

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
7 September 2001 (07.09.2001)

PCT

(10) International Publication Number
WO 01/64835 A2

(51) International Patent Classification⁷: C12N

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(21) International Application Number: PCT/US01/04927

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(22) International Filing Date: 26 February 2001 (26.02.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
09/515,126 28 February 2000 (28.02.2000) US
09/577,409 18 May 2000 (18.05.2000) US

(63) Related by continuation (CON) or continuation-in-part
(CIP) to earlier applications:

US 09/515,126 (CIP)
Filed on 28 February 2000 (28.02.2000)
US 09/577,409 (CIP)
Filed on 18 May 2000 (18.05.2000)

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(81) Designated States (national): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ,
DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF,
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

- without international search report and to be republished
upon receipt of that report
- with sequence listing part of description published sepa-
rately in electronic form and available upon request from
the International Bureau

For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.

WO 01/64835 A2

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and
uses thereof.

NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

1. TECHNICAL FIELD

4 The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with uses for these polynucleotides and proteins, for example in therapeutic, diagnostic and research methods.

8 2. BACKGROUND

Technology aimed at the discovery of protein factors (including *e.g.*, cytokines, such as lymphokines, interferons, CSFs, chemokines, and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel
12 polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (*i.e.*, partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent
"indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences
16 based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization-based cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity, for example, by virtue of their secreted nature in the
20 case of leader sequence cloning, by virtue of their cell or tissue source in the case of PCR-based techniques, or by virtue of structural similarity to other genes of known biological activity.

Identified polynucleotide and polypeptide sequences have numerous applications in, for example, diagnostics, forensics, gene mapping; identification of mutations responsible for
24 genetic disorders or other traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences.

3. SUMMARY OF THE INVENTION

28 The compositions of the present invention include novel isolated polypeptides, novel isolated polynucleotides encoding such polypeptides, including recombinant DNA molecules, cloned genes or degenerate variants thereof, especially naturally occurring variants such as allelic variants, antisense polynucleotide molecules, and antibodies that specifically recognize one or more
32 epitopes present on such polypeptides, as well as hybridomas producing such antibodies.

The compositions of the present invention additionally include vectors, including expression vectors, containing the polynucleotides of the invention, cells genetically engineered to contain such polynucleotides and cells genetically engineered to express such polynucleotides.

The present invention relates to a collection or library of at least one novel nucleic acid sequence assembled from expressed sequence tags (ESTs) isolated mainly by sequencing by hybridization (SBH), and in some cases, sequences obtained from one or more public databases.

- 4 The invention relates also to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. These nucleic acid sequences are designated as SEQ ID NOS: 1-13901. The polypeptides sequences are designated SEQ ID NOS: 13902-27802. The nucleic acids and polypeptides are provided in the Sequence
- 8 Listing. In the nucleic acids provided in the Sequence Listing, A is adenosine; C is cytosine; G is guanine; T is thymine; and N is any of the four bases. In the amino acids provided in the Sequence Listing, * corresponds to the stop codon.

- The nucleic acid sequences of the present invention also include, nucleic acid sequences that
- 12 hybridize to the complement of SEQ ID NO: 1-13901 under stringent hybridization conditions; nucleic acid sequences which are allelic variants or species homologues of any of the nucleic acid sequences recited above, or nucleic acid sequences that encode a peptide comprising a specific domain or truncation of the peptides encoded by SEQ ID NOS: 1-13901. A polynucleotide
- 16 comprising a nucleotide sequence having at least 90% identity to an identifying sequence of SEQ ID NO: 1-13901 or a degenerate variant or fragment thereof. The identifying sequence can be 100 base pairs in length.

- The nucleic acid sequences of the present invention also include the sequence information
- 20 from the nucleic acid sequences of SEQ ID NO: 1-13901. The sequence information can be a segment of any one of SEQ ID NO: 1-13901 that uniquely identifies or represents the sequence information of SEQ ID NOS: 1-13901.

- A collection as used in this application can be a collection of only one polynucleotide. The
- 24 collection of sequence information or identifying information of each sequence can be provided on a nucleic acid array. In one embodiment, segments of sequence information is provided on a nucleic acid array to detect the polynucleotide that contains the segment. The array can be designed to detect full-match or mismatch to the polynucleotide that contains the segment. The collection
- 28 can also be provided in a computer-readable format.

- This invention also includes the reverse or direct complement of any of the nucleic acid sequences recited above; cloning or expression vectors containing the nucleic acid sequences; and host cells or organisms transformed with these expression vectors. Nucleic acid sequences (or their
- 32 reverse or direct complements) according to the invention have numerous applications in a variety of techniques known to those skilled in the art of molecular biology, such as use as hybridization probes, use as primers for PCR, use in an array, use in computer-readable media, use in sequencing

full-length genes, use for chromosome and gene mapping, use in the recombinant production of protein, and use in the generation of anti-sense DNA or RNA, their chemical analogs and the like.

4 In a preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-13901 or novel segments or parts of the nucleic acids of the invention are used as primers in expression assays that are well known in the art. In a particularly preferred embodiment, the nucleic acid sequences of SEQ ID NO: 1-13901 or novel segments or parts of the nucleic acids provided herein are used in diagnostics for identifying expressed genes or, as well known in the art and exemplified by Vollrath
8 et al., *Science* 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

The isolated polynucleotides of the invention include, but are not limited to, a polynucleotide comprising any one of the nucleotide sequences set forth in SEQ ID NO: 1-13901; a
12 polynucleotide comprising any of the full length protein coding sequences of SEQ ID NOS: 1-13901; and a polynucleotide comprising any of the nucleotide sequences of the mature protein coding sequences of SEQ ID NOS: 1-13901. The polynucleotides of the present invention also include, but are not limited to, a polynucleotide that hybridizes under stringent hybridization
16 conditions to (a) the complement of any one of the nucleotide sequences set forth in SEQ ID NO: 1-13901; (b) a nucleotide sequence encoding any one of the amino acid sequences set forth in the Sequence Listing (*e.g.*, SEQ ID NOS: 13902-27802); (c) a polynucleotide which is an allelic variant of any polynucleotides recited above; (d) a polynucleotide which encodes a species homolog (*e.g.*
20 orthologs) of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of any of the polypeptides comprising an amino acid sequence set forth in the Sequence Listing.

The isolated polypeptides of the invention include, but are not limited to, a polypeptide
24 comprising any of the amino acid sequences set forth in the Sequence Listing; or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides with biological activity that are encoded by (a) any of the polynucleotides having a nucleotide sequence set forth in SEQ ID NO: 1-13901; or (b) polynucleotides that hybridize to the complement of the
28 polynucleotides of (a) under stringent hybridization conditions. Biologically or immunologically active variants of any of the polypeptide sequences in the Sequence Listing, and "substantial equivalents" thereof (*e.g.*, with at least about 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% amino acid sequence identity) that preferably retain biological activity are also contemplated. The
32 polypeptides of the invention may be wholly or partially chemically synthesized but are preferably produced by recombinant means using the genetically engineered cells (*e.g.* host cells) of the invention.

The invention also provides compositions comprising a polypeptide of the invention. Polypeptide compositions of the invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

4 The invention also provides host cells transformed or transfected with a polynucleotide of the invention.

 The invention also relates to methods for producing a polypeptide of the invention comprising growing a culture of the host cells of the invention in a suitable culture medium
8 under conditions permitting expression of the desired polypeptide, and purifying the polypeptide from the culture or from the host cells. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

 Polynucleotides according to the invention have numerous applications in a variety of
12 techniques known to those skilled in the art of molecular biology. These techniques include use as hybridization probes, use as oligomers, or primers, for PCR, use for chromosome and gene mapping, use in the recombinant production of protein, and use in generation of anti-sense DNA or RNA, their chemical analogs and the like. For example, when the expression of an mRNA is
16 largely restricted to a particular cell or tissue type, polynucleotides of the invention can be used as hybridization probes to detect the presence of the particular cell or tissue mRNA in a sample using, *e.g.*, *in situ* hybridization.

 In other exemplary embodiments, the polynucleotides are used in diagnostics as
20 expressed sequence tags for identifying expressed genes or, as well known in the art and exemplified by Vollrath et al., Science 258:52-59 (1992), as expressed sequence tags for physical mapping of the human genome.

 The polypeptides according to the invention can be used in a variety of conventional
24 procedures and methods that are currently applied to other proteins. For example, a polypeptide of the invention can be used to generate an antibody that specifically binds the polypeptide. Such antibodies, particularly monoclonal antibodies, are useful for detecting or quantitating the polypeptide in tissue. The polypeptides of the invention can also be used as molecular weight
28 markers, and as a food supplement.

 Methods are also provided for preventing, treating, or ameliorating a medical condition which comprises the step of administering to a mammalian subject a therapeutically effective amount of a composition comprising a polypeptide of the present invention and a
32 pharmaceutically acceptable carrier.

 In particular, the polypeptides and polynucleotides of the invention can be utilized, for example, in methods for the prevention and/or treatment of disorders involving aberrant protein expression or biological activity.

The present invention further relates to methods for detecting the presence of the polynucleotides or polypeptides of the invention in a sample. Such methods can, for example, be utilized as part of prognostic and diagnostic evaluation of disorders as recited herein and for the identification of subjects exhibiting a predisposition to such conditions. The invention provides a method for detecting the polynucleotides of the invention in a sample, comprising contacting the sample with a compound that binds to and forms a complex with the polynucleotide of interest for a period sufficient to form the complex and under conditions sufficient to form a complex and detecting the complex such that if a complex is detected, the polynucleotide of interest is detected. The invention also provides a method for detecting the polypeptides of the invention in a sample comprising contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex and detecting the formation of the complex such that if a complex is formed, the polypeptide is detected.

The invention also provides kits comprising polynucleotide probes and/or monoclonal antibodies, and optionally quantitative standards, for carrying out methods of the invention. Furthermore, the invention provides methods for evaluating the efficacy of drugs, and monitoring the progress of patients, involved in clinical trials for the treatment of disorders as recited above.

The invention also provides methods for the identification of compounds that modulate (*i.e.*, increase or decrease) the expression or activity of the polynucleotides and/or polypeptides of the invention. Such methods can be utilized, for example, for the identification of compounds that can ameliorate symptoms of disorders as recited herein. Such methods can include, but are not limited to, assays for identifying compounds and other substances that interact with (*e.g.*, bind to) the polypeptides of the invention. The invention provides a method for identifying a compound that binds to the polypeptides of the invention comprising contacting the compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and detecting the complex by detecting the reporter gene sequence expression such that if expression of the reporter gene is detected the compound the binds to a polypeptide of the invention is identified.

The methods of the invention also provides methods for treatment which involve the administration of the polynucleotides or polypeptides of the invention to individuals exhibiting symptoms or tendencies. In addition, the invention encompasses methods for treating diseases or disorders as recited herein comprising administering compounds and other substances that modulate the overall activity of the target gene products. Compounds and other substances can

effect such modulation either on the level of target gene/protein expression or target protein activity.

The polypeptides of the present invention and the polynucleotides encoding them are also useful for the same functions known to one of skill in the art as the polypeptides and polynucleotides to which they have homology (set forth in Table 2). If no homology is set forth for a sequence, then the polypeptides and polynucleotides of the present invention are useful for a variety of applications, as described herein, including use in arrays for detection.

4. DETAILED DESCRIPTION OF THE INVENTION

4.1 DEFINITIONS

It must be noted that as used herein and in the appended claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise.

The term "active" refers to those forms of the polypeptide which retain the biologic and/or immunologic activities of any naturally occurring polypeptide. According to the invention, the terms "biologically active" or "biological activity" refer to a protein or peptide having structural, regulatory or biochemical functions of a naturally occurring molecule. Likewise "immunologically active" or "immunological activity" refers to the capability of the natural, recombinant or synthetic polypeptide to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "activated cells" as used in this application are those cells which are engaged in extracellular or intracellular membrane trafficking, including the export of secretory or enzymatic molecules as part of a normal or disease process.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence 5'-AGT-3' binds to the complementary sequence 3'-TCA-5'. Complementarity between two single-stranded molecules may be "partial" such that only some of the nucleic acids bind or it may be "complete" such that total complementarity exists between the single stranded molecules. The degree of complementarity between the nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands.

The term "embryonic stem cells (ES)" refers to a cell that can give rise to many differentiated cell types in an embryo or an adult, including the germ cells. The term "germ line stem cells (GSCs)" refers to stem cells derived from primordial stem cells that provide a steady and continuous source of germ cells for the production of gametes. The term "primordial germ

cells (PGCs)" refers to a small population of cells set aside from other cell lineages particularly from the yolk sac, mesenteries, or gonadal ridges during embryogenesis that have the potential to differentiate into germ cells and other cells. PGCs are the source from which GSCs and ES cells are derived. The PGCs, the GSCs and the ES cells are capable of self-renewal. Thus these cells not only populate the germ line and give rise to a plurality of terminally differentiated cells that comprise the adult specialized organs, but are able to regenerate themselves.

The term "expression modulating fragment," EMF, means a series of nucleotides which modulates the expression of an operably linked ORF or another EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are nucleic acid fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

The terms "nucleotide sequence" or "nucleic acid" or "polynucleotide" or "oligonucleotide" are used interchangeably and refer to a heteropolymer of nucleotides or the sequence of these nucleotides. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA) or to any DNA-like or RNA-like material. In the sequences herein A is adenine, C is cytosine, T is thymine, G is guanine and N is A, C, G or T (U). It is contemplated that where the polynucleotide is RNA, the T (thymine) in the sequences provided herein is substituted with U (uracil). Generally, nucleic acid segments provided by this invention may be assembled from fragments of the genome and short oligonucleotide linkers, or from a series of oligonucleotides, or from individual nucleotides, to provide a synthetic nucleic acid which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon, or a eukaryotic gene.

The terms "oligonucleotide fragment" or a "polynucleotide fragment", "portion," or "segment" or "probe" or "primer" are used interchangeably and refer to a sequence of nucleotide residues which are at least about 5 nucleotides, more preferably at least about 7 nucleotides, more preferably at least about 9 nucleotides, more preferably at least about 11 nucleotides and most preferably at least about 17 nucleotides. The fragment is preferably less than about 500 nucleotides, preferably less than about 200 nucleotides, more preferably less than about 100 nucleotides, more preferably less than about 50 nucleotides and most preferably less than 30 nucleotides. Preferably the probe is from about 6 nucleotides to about 200 nucleotides, preferably from about 15 to about 50 nucleotides, more preferably from about 17 to 30 nucleotides and most preferably from about 20 to 25 nucleotides. Preferably the fragments can

be used in polymerase chain reaction (PCR), various hybridization procedures or microarray procedures to identify or amplify identical or related parts of mRNA or DNA molecules. A fragment or segment may uniquely identify each polynucleotide sequence of the present invention. Preferably the fragment comprises a sequence substantially similar to any one of SEQ ID NOS: 1-13901.

Probes may, for example, be used to determine whether specific mRNA molecules are present in a cell or tissue or to isolate similar nucleic acid sequences from chromosomal DNA as described by Walsh et al. (Walsh, P.S. et al., 1992, PCR Methods Appl 1:241-250). They may be labeled by nick translation, Klenow fill-in reaction, PCR, or other methods well known in the art. Probes of the present invention, their preparation and/or labeling are elaborated in Sambrook, J. et al., 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY; or Ausubel, F.M. et al., 1989, Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, both of which are incorporated herein by reference in their entirety.

The nucleic acid sequences of the present invention also include the sequence information from the nucleic acid sequences of SEQ ID NOS: 1-13901. The sequence information can be a segment of any one of SEQ ID NO: 1-13901 that uniquely identifies or represents the sequence information of that sequence of SEQ ID NOS: 1-13901. One such segment can be a twenty-mer nucleic acid sequence because the probability that a twenty-mer is fully matched in the human genome is 1 in 300. In the human genome, there are three billion base pairs in one set of chromosomes. Because 4^{20} possible twenty-mers exist, there are 300 times more twenty-mers than there are base pairs in a set of human chromosomes. Using the same analysis, the probability for a seventeen-mer to be fully matched in the human genome is approximately 1 in 5. When these segments are used in arrays for expression studies, fifteen-mer segments can be used. The probability that the fifteen-mer is fully matched in the expressed sequences is also approximately one in five because expressed sequences comprise less than approximately 5% of the entire genome sequence.

Similarly, when using sequence information for detecting a single mismatch, a segment can be a twenty-five mer. The probability that the twenty-five mer would appear in a human genome with a single mismatch is calculated by multiplying the probability for a full match ($1/4^{25}$) times the increased probability for mismatch at each nucleotide position (3×25). The probability that an eighteen mer with a single mismatch can be detected in an array for expression studies is approximately one in five. The probability that a twenty-mer with a single mismatch can be detected in a human genome is approximately one in five.

The term "open reading frame," ORF, means a series of nucleotide triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

4 The terms "operably linked" or "operably associated" refer to functionally related nucleic acid sequences. For example, a promoter is operably associated or operably linked with a coding sequence if the promoter controls the transcription of the coding sequence. While operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements *e.g.* repressor genes are not contiguously linked to the coding sequence but still control
8 transcription/translation of the coding sequence.

The term "pluripotent" refers to the capability of a cell to differentiate into a number of differentiated cell types that are present in an adult organism. A pluripotent cell is restricted in its differentiation capability in comparison to a totipotent cell.

12 The terms "polypeptide" or "peptide" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide or protein sequence or fragment thereof and to naturally occurring or synthetic molecules. A polypeptide "fragment," "portion," or "segment" is a stretch of amino acid residues of at least about 5 amino acids, preferably at least about 7 amino acids, more
16 preferably at least about 9 amino acids and most preferably at least about 17 or more amino acids. The peptide preferably is not greater than about 200 amino acids, more preferably less than 150 amino acids and most preferably less than 100 amino acids. Preferably the peptide is from about 5 to about 200 amino acids. To be active, any polypeptide must have sufficient
20 length to display biological and/or immunological activity.

The term "naturally occurring polypeptide" refers to polypeptides produced by cells that have not been genetically engineered and specifically contemplates various polypeptides arising from post-translational modifications of the polypeptide including, but not limited to,
24 acetylation, carboxylation, glycosylation, phosphorylation, lipidation and acylation.

The term "translated protein coding portion" means a sequence which encodes for the full length protein which may include any leader sequence or any processing sequence.

28 The term "mature protein coding sequence" means a sequence which encodes a peptide or protein without a signal or leader sequence. The "mature protein portion" means that portion of the protein which does not include a signal or leader sequence. The peptide may have been produced by processing in the cell which removes any leader/signal sequence. The mature protein portion may or may not include the initial methionine residue. The methionine residue
32 may be removed from the protein during processing in the cell. The peptide may be produced synthetically or the protein may have been produced using a polynucleotide only encoding for the mature protein coding sequence.

The term "derivative" refers to polypeptides chemically modified by such techniques as ubiquitination, labeling (*e.g.*, with radionuclides or various enzymes), covalent polymer attachment such as pegylation (derivatization with polyethylene glycol) and insertion or substitution by chemical synthesis of amino acids such as ornithine, which do not normally occur in human proteins.

The term "variant" (or "analog") refers to any polypeptide differing from naturally occurring polypeptides by amino acid insertions, deletions, and substitutions, created using, *e.g.*, recombinant DNA techniques. Guidance in determining which amino acid residues may be replaced, added or deleted without abolishing activities of interest, may be found by comparing the sequence of the particular polypeptide with that of homologous peptides and minimizing the number of amino acid sequence changes made in regions of high homology (conserved regions) or by replacing amino acids with consensus sequence.

Alternatively, recombinant variants encoding these same or similar polypeptides may be synthesized or selected by making use of the "redundancy" in the genetic code. Various codon substitutions, such as the silent changes which produce various restriction sites, may be introduced to optimize cloning into a plasmid or viral vector or expression in a particular prokaryotic or eukaryotic system. Mutations in the polynucleotide sequence may be reflected in the polypeptide or domains of other peptides added to the polypeptide to modify the properties of any part of the polypeptide, to change characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate.

Preferably, amino acid "substitutions" are the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, *i.e.*, conservative amino acid replacements. "Conservative" amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid. "Insertions" or "deletions" are preferably in the range of about 1 to 20 amino acids, more preferably 1 to 10 amino acids. The variation allowed may be experimentally determined by systematically making insertions, deletions, or substitutions of amino acids in a polypeptide molecule using recombinant DNA techniques and assaying the resulting recombinant variants for activity.

Alternatively, where alteration of function is desired, insertions, deletions or non-conservative alterations can be engineered to produce altered polypeptides. Such alterations

can, for example, alter one or more of the biological functions or biochemical characteristics of the polypeptides of the invention. For example, such alterations may change polypeptide characteristics such as ligand-binding affinities, interchain affinities, or degradation/turnover rate. Further, such alterations can be selected so as to generate polypeptides that are better suited for expression, scale up and the like in the host cells chosen for expression. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

The terms "purified" or "substantially purified" as used herein denotes that the indicated nucleic acid or polypeptide is present in the substantial absence of other biological macromolecules, *e.g.*, polynucleotides, proteins, and the like. In one embodiment, the polynucleotide or polypeptide is purified such that it constitutes at least 95% by weight, more preferably at least 99% by weight, of the indicated biological macromolecules present (but water, buffers, and other small molecules, especially molecules having a molecular weight of less than 1000 daltons, can be present).

The term "isolated" as used herein refers to a nucleic acid or polypeptide separated from at least one other component (*e.g.*, nucleic acid or polypeptide) present with the nucleic acid or polypeptide in its natural source. In one embodiment, the nucleic acid or polypeptide is found in the presence of (if anything) only a solvent, buffer, ion, or other component normally present in a solution of the same. The terms "isolated" and "purified" do not encompass nucleic acids or polypeptides present in their natural source.

The term "recombinant," when used herein to refer to a polypeptide or protein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial, insect, or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern in general different from those expressed in mammalian cells.

The term "recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. An expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use

in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an amino terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

The term "recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extrachromosomally. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed. This term also means host cells which have stably integrated a recombinant genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers. Recombinant expression systems as defined herein will express polypeptides or proteins endogenous to the cell upon induction of the regulatory elements linked to the endogenous DNA segment or gene to be expressed. The cells can be prokaryotic or eukaryotic.

The term "secreted" includes a protein that is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence when it is expressed in a suitable host cell. "Secreted" proteins include without limitation proteins secreted wholly (*e.g.*, soluble proteins) or partially (*e.g.*, receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins that are transported across the membrane of the endoplasmic reticulum. "Secreted" proteins are also intended to include proteins containing non-typical signal sequences (*e.g.* Interleukin-1 Beta, see Krasney, P.A. and Young, P.R. (1992) Cytokine 4(2):134-143) and factors released from damaged cells (*e.g.* Interleukin-1 Receptor Antagonist, see Arend, W.P. et. al. (1998) Annu. Rev. Immunol. 16:27-55)

Where desired, an expression vector may be designed to contain a "signal or leader sequence" which will direct the polypeptide through the membrane of a cell. Such a sequence may be naturally present on the polypeptides of the present invention or provided from heterologous protein sources by recombinant DNA techniques.

The term "stringent" is used to refer to conditions that are commonly understood in the art as stringent. Stringent conditions can include highly stringent conditions (*i.e.*, hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1X SSC/0.1% SDS at 68°C), and moderately stringent conditions (*i.e.*, washing in 0.2X SSC/0.1% SDS at 42°C). Other exemplary hybridization conditions are described herein in the examples.

In instances of hybridization of deoxyoligonucleotides, additional exemplary stringent hybridization conditions include washing in 6X SSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligonucleotides), 48°C (for 17-base oligos), 55°C (for 20-base oligonucleotides), and 60°C (for 23-base oligonucleotides).

As used herein, "substantially equivalent" can refer both to nucleotide and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between the reference and subject sequences. Typically, such a substantially equivalent sequence varies from one of those listed herein by no more than about 35% (*i.e.*, the number of individual residue substitutions, additions, and/or deletions in a substantially equivalent sequence, as compared to the corresponding reference sequence, divided by the total number of residues in the substantially equivalent sequence is about 0.35 or less). Such a sequence is said to have 65% sequence identity to the listed sequence. In one embodiment, a substantially equivalent, *e.g.*, mutant, sequence of the invention varies from a listed sequence by no more than 30% (70% sequence identity); in a variation of this embodiment, by no more than 25% (75% sequence identity); and in a further variation of this embodiment, by no more than 20% (80% sequence identity) and in a further variation of this embodiment, by no more than 10% (90% sequence identity) and in a further variation of this embodiment, by no more than 5% (95% sequence identity). Substantially equivalent, *e.g.*, mutant, amino acid sequences according to the invention preferably have at least 80% sequence identity with a listed amino acid sequence, more preferably at least 85% sequence identity, more preferably at least 90% sequence identity, more preferably at least 95% identity, more preferably at least 98% identity, and most preferably at least 99% identity. Substantially equivalent nucleotide sequences of the invention can have lower percent sequence identities, taking into account, for example, the redundancy or degeneracy of the genetic code. Preferably, nucleotide sequence has at least about 65% identity, more preferably at least about 75% identity, more preferably at least about 80% sequence identity, more preferably at least about 85% sequence identity, more preferably at least about 90% sequence identity, and most preferably at least about 95% identity, more preferably at least about 98% sequence identity, and most preferably at least about 99% sequence identity. For the purposes of the present invention, sequences having substantially equivalent biological activity and substantially equivalent expression characteristics are considered substantially equivalent. For the purposes of determining equivalence, truncation of the mature sequence (*e.g.*, via a mutation which creates a spurious stop codon) should be disregarded. Sequence identity may be determined, *e.g.*, using the Jotun Hein method (Hein, J.

(1990) Methods Enzymol. 183:626-645). Identity between sequences can also be determined by other methods known in the art, *e.g.* by varying hybridization conditions.

4 The term "totipotent" refers to the capability of a cell to differentiate into all of the cell types of an adult organism.

The term "transformation" means introducing DNA into a suitable host cell so that the DNA is replicable, either as an extrachromosomal element, or by chromosomal integration. The term "transfection" refers to the taking up of an expression vector by a suitable host cell, whether
8 or not any coding sequences are in fact expressed. The term "infection" refers to the introduction of nucleic acids into a suitable host cell by use of a virus or viral vector.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotides which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified
12 using known UMFs as a target sequence or target motif with the computer-based systems described below. The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is
16 determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence.

Each of the above terms is meant to encompass all that is described for each, unless the context dictates otherwise.

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4.2 NUCLEIC ACIDS OF THE INVENTION

Nucleotide sequences of the invention are set forth in the Sequence Listing.

The isolated polynucleotides of the invention include a polynucleotide comprising the
24 nucleotide sequences of SEQ ID NO: 1-13901 ; a polynucleotide encoding any one of the peptide sequences of SEQ ID NOS: 13902-27802; and a polynucleotide comprising the nucleotide sequence encoding the mature protein coding sequence of the polypeptides of any one of SEQ ID NOS: 13902-27802. The polynucleotides of the present invention also include, but
28 are not limited to, a polynucleotide that hybridizes under stringent conditions to (a) the complement of any of the nucleotides sequences of SEQ ID NO: 1-13901; (b) nucleotide sequences encoding any one of the amino acid sequences set forth in the Sequence Listing; (c) a polynucleotide which is an allelic variant of any polynucleotide recited above; (d) a
32 polynucleotide which encodes a species homolog of any of the proteins recited above; or (e) a polynucleotide that encodes a polypeptide comprising a specific domain or truncation of the polypeptides of SEQ ID NOS: 13902-27802. Domains of interest may depend on the nature of the encoded polypeptide; *e.g.*, domains in receptor-like polypeptides include ligand-binding,

extracellular, transmembrane, or cytoplasmic domains, or combinations thereof; domains in immunoglobulin-like proteins include the variable immunoglobulin-like domains; domains in enzyme-like polypeptides include catalytic and substrate binding domains; and domains in ligand polypeptides include receptor-binding domains.

The polynucleotides of the invention include naturally occurring or wholly or partially synthetic DNA, *e.g.*, cDNA and genomic DNA, and RNA, *e.g.*, mRNA. The polynucleotides may include all of the coding region of the cDNA or may represent a portion of the coding region of the cDNA.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. Further 5' and 3' sequence can be obtained using methods known in the art. For example, full length cDNA or genomic DNA that corresponds to any of the polynucleotides of SEQ ID NO: 1-13901 can be obtained by screening appropriate cDNA or genomic DNA libraries under suitable hybridization conditions using any of the polynucleotides of SEQ ID NO: 1-13901 or a portion thereof as a probe. Alternatively, the polynucleotides of SEQ ID NO: 1-13901 may be used as the basis for suitable primer(s) that allow identification and/or amplification of genes in appropriate genomic DNA or cDNA libraries.

The nucleic acid sequences of the invention can be assembled from ESTs and sequences (including cDNA and genomic sequences) obtained from one or more public databases, such as dbEST, gbpr, and UniGene. The EST sequences can provide identifying sequence information, representative fragment or segment information, or novel segment information for the full-length gene.

The polynucleotides of the invention also provide polynucleotides including nucleotide sequences that are substantially equivalent to the polynucleotides recited above. Polynucleotides according to the invention can have, *e.g.*, at least about 65%, at least about 70%, at least about 75%, at least about 80%, 81%, 82%, 83%, 84%, more typically at least about 85%, 86%, 87%, 88%, 89%, more typically at least about 90%, 91%, 92%, 93%, 94%, and even more typically at least about 95%, 96%, 97%, 98%, 99%, sequence identity to a polynucleotide recited above.

Included within the scope of the nucleic acid sequences of the invention are nucleic acid sequence fragments that hybridize under stringent conditions to any of the nucleotide sequences of SEQ ID NO: 1-13901, or complements thereof, which fragment is greater than about 5 nucleotides, preferably 7 nucleotides, more preferably greater than 9 nucleotides and most preferably greater than 17 nucleotides. Fragments of, *e.g.* 15, 17, or 20 nucleotides or more that

are selective for (*i.e.* specifically hybridize to any one of the polynucleotides of the invention) are contemplated. Probes capable of specifically hybridizing to a polynucleotide can differentiate polynucleotide sequences of the invention from other polynucleotide sequences in the same family of genes or can differentiate human genes from genes of other species, and are preferably based on unique nucleotide sequences.

The sequences falling within the scope of the present invention are not limited to these specific sequences, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided SEQ ID NO: 1-13901, a representative fragment thereof, or a nucleotide sequence at least 90% identical, preferably 95% identical, to SEQ ID NO: 1-13901 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another codon that encodes the same amino acid is expressly contemplated.

The nearest neighbor or homology result for the nucleic acids of the present invention, including SEQ ID NO: 1-13901 can be obtained by searching a database using an algorithm or a program. Preferably, a BLAST which stands for Basic Local Alignment Search Tool is used to search for local sequence alignments (Altschul, S.F. J Mol. Evol. 36 290-300 (1993) and Altschul S.F. et al. J. Mol. Biol. 21:403-410 (1990)). Alternatively a FASTA version 3 search against Genpept, using Fastxy algorithm.

Species homologs (or orthologs) of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the polynucleotides.

The nucleic acid sequences of the invention are further directed to sequences which encode variants of the described nucleic acids. These amino acid sequence variants may be prepared by methods known in the art by introducing appropriate nucleotide changes into a native or variant polynucleotide. There are two variables in the construction of amino acid sequence variants: the location of the mutation and the nature of the mutation. Nucleic acids encoding the amino acid sequence variants are preferably constructed by mutating the polynucleotide to encode an amino acid sequence that does not occur in nature. These nucleic

acid alterations can be made at sites that differ in the nucleic acids from different species (variable positions) or in highly conserved regions (constant regions). Sites at such locations will typically be modified in series, e.g., by substituting first with conservative choices (e.g., hydrophobic amino acid to a different hydrophobic amino acid) and then with more distant choices (e.g., hydrophobic amino acid to a charged amino acid), and then deletions or insertions may be made at the target site. Amino acid sequence deletions generally range from about 1 to 30 residues, preferably about 1 to 10 residues, and are typically contiguous. Amino acid insertions include amino- and/or carboxyl-terminal fusions ranging in length from one to one hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Intrasequence insertions may range generally from about 1 to 10 amino residues, preferably from 1 to 5 residues. Examples of terminal insertions include the heterologous signal sequences necessary for secretion or for intracellular targeting in different host cells and sequences such as FLAG or poly-histidine sequences useful for purifying the expressed protein.

In a preferred method, polynucleotides encoding the novel amino acid sequences are changed via site-directed mutagenesis. This method uses oligonucleotide sequences to alter a polynucleotide to encode the desired amino acid variant, as well as sufficient adjacent nucleotides on both sides of the changed amino acid to form a stable duplex on either side of the site of being changed. In general, the techniques of site-directed mutagenesis are well known to those of skill in the art and this technique is exemplified by publications such as, Edelman et al., *DNA* 2:183 (1983). A versatile and efficient method for producing site-specific changes in a polynucleotide sequence was published by Zoller and Smith, *Nucleic Acids Res.* 10:6487-6500 (1982). PCR may also be used to create amino acid sequence variants of the novel nucleic acids. When small amounts of template DNA are used as starting material, primer(s) that differs slightly in sequence from the corresponding region in the template DNA can generate the desired amino acid variant. PCR amplification results in a population of product DNA fragments that differ from the polynucleotide template encoding the polypeptide at the position specified by the primer. The product DNA fragments replace the corresponding region in the plasmid and this gives a polynucleotide encoding the desired amino acid variant.

A further technique for generating amino acid variants is the cassette mutagenesis technique described in Wells et al., *Gene* 34:315 (1985); and other mutagenesis techniques well known in the art, such as, for example, the techniques in Sambrook et al., *supra*, and *Current Protocols in Molecular Biology*, Ausubel et al. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be used in the practice of the invention for the cloning and expression

of these novel nucleic acids. Such DNA sequences include those which are capable of hybridizing to the appropriate novel nucleic acid sequence under stringent conditions.

Polynucleotides encoding preferred polypeptide truncations of the invention can be used to generate polynucleotides encoding chimeric or fusion proteins comprising one or more domains of the invention and heterologous protein sequences.

The polynucleotides of the invention additionally include the complement of any of the polynucleotides recited above. The polynucleotide can be DNA (genomic, cDNA, amplified, or synthetic) or RNA. Methods and algorithms for obtaining such polynucleotides are well known to those of skill in the art and can include, for example, methods for determining hybridization conditions that can routinely isolate polynucleotides of the desired sequence identities.

In accordance with the invention, polynucleotide sequences comprising the mature protein coding sequences corresponding to any one of SEQ ID NO: 1-13901, or functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of that nucleic acid, or a functional equivalent thereof, in appropriate host cells. Also included are the cDNA inserts of any of the clones identified herein.

A polynucleotide according to the invention can be joined to any of a variety of other nucleotide sequences by well-established recombinant DNA techniques (see Sambrook J et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, NY). Useful nucleotide sequences for joining to polynucleotides include an assortment of vectors, *e.g.*, plasmids, cosmids, lambda phage derivatives, phagemids, and the like, that are well known in the art. Accordingly, the invention also provides a vector including a polynucleotide of the invention and a host cell containing the polynucleotide. In general, the vector contains an origin of replication functional in at least one organism, convenient restriction endonuclease sites, and a selectable marker for the host cell. Vectors according to the invention include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. A host cell according to the invention can be a prokaryotic or eukaryotic cell and can be a unicellular organism or part of a multicellular organism.

The present invention further provides recombinant constructs comprising a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-13901 or a fragment thereof or any other polynucleotides of the invention. In one embodiment, the recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a nucleic acid having any of the nucleotide sequences of SEQ ID NO: 1-13901 or a fragment thereof is inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. Large numbers of suitable vectors and

promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, PXTI, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), a-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an amino terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or

more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotech, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced or derepressed by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Polynucleotides of the invention can also be used to induce immune responses. For example, as described in Fan et al., *Nat. Biotech.* 17:870-872 (1999), incorporated herein by reference, nucleic acid sequences encoding a polypeptide may be used to generate antibodies against the encoded polypeptide following topical administration of naked plasmid DNA or following injection, and preferably intramuscular injection of the DNA. The nucleic acid sequences are preferably inserted in a recombinant expression vector and may be in the form of naked DNA.

4.3 ANTISENSE

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1-13901, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a protein of any of SEQ ID

NOS: 13902-27802 or antisense nucleic acids complementary to a nucleic acid sequence of SEQ ID NO: 1-13901 are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding a nucleic acid disclosed herein (*e.g.*, SEQ ID NO: 1-13901), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of a mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of a mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of a mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the

antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a protein according to the invention to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-O-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

4.4 RIBOZYMES AND PNA MOIETIES

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as a mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave a mRNA transcripts to thereby inhibit translation of a mRNA. A ribozyme having specificity for a nucleic acid of the invention can be

designed based upon the nucleotide sequence of a DNA disclosed herein (*i.e.*, SEQ ID NO: 1-13901). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SECX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742. Alternatively, SECX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region (*e.g.*, promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of the invention can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of the invention can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of the invention can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated that may

combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

4.5 HOSTS

The present invention further provides host cells genetically engineered to contain the polynucleotides of the invention. For example, such host cells may contain nucleic acids of the invention introduced into the host cell using known transformation, transfection or infection methods. The present invention still further provides host cells genetically engineered to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in the cell.

Knowledge of nucleic acid sequences allows for modification of cells to permit, or increase, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous

recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the polypeptide at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the encoding sequences. See, for example, PCT International Publication No. WO94/12650, PCT International Publication No. WO92/20808, and PCT International Publication No. WO91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (e.g., *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. et al., *Basic Methods in Molecular Biology* (1986)). The host cells containing one of the polynucleotides of the invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, 293 cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981). Other cell lines capable of expressing a compatible vector are, for example, the C127, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3

cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements. Recombinant polypeptides and proteins produced in bacterial culture are usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or insects or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequence include polyadenylation signals, mRNA stability elements, splice

sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

- 4 The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element.
- 8 Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are added. In all cases, the identification of the targeting event may be facilitated by
- 12 the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the host cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively
- 16 selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the
- 20 Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (*gpt*) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to

24 Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

28

4.6 POLYPEPTIDES OF THE INVENTION

The isolated polypeptides of the invention include, but are not limited to, a polypeptide comprising: the amino acid sequences set forth as any one of SEQ ID NOS: 13902-27802 or an

32 amino acid sequence encoded by any one of the nucleotide sequences SEQ ID NO: 1-13901 or the corresponding full length or mature protein. Polypeptides of the invention also include polypeptides preferably with biological or immunological activity that are encoded by: (a) a polynucleotide having any one of the nucleotide sequences set forth in SEQ ID NO: 1-13901 or

(b) polynucleotides encoding any one of the amino acid sequences set forth as SEQ ID NOS: 13902-27802 or (c) polynucleotides that hybridize to the complement of the polynucleotides of either (a) or (b) under stringent hybridization conditions. The invention also provides

- 4 biologically active or immunologically active variants of any of the amino acid sequences set forth as SEQ ID NOS: 13902-27802 or the corresponding full length or mature protein; and "substantial equivalents" thereof (*e.g.*, with at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, 86%, 87%, 88%, 89%, at least about 90%, 91%,
8 92%, 93%, 94%, typically at least about 95%, 96%, 97%, more typically at least about 98%, or most typically at least about 99% amino acid identity) that retain biological activity.

Polypeptides encoded by allelic variants may have a similar, increased, or decreased activity compared to polypeptides comprising SEQ ID NOS: 13902-27802.

- 12 Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H. U. Saragovi, et al., *Bio/Technology* 10, 773-778 (1992) and in R. S. McDowell, et al., *J. Amer.*
16 *Chem. Soc.* 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites.

- The present invention also provides both full-length and mature forms (for example,
20 without a signal sequence or precursor sequence) of the disclosed proteins. The protein coding sequence is identified in the sequence listing by translation of the disclosed nucleotide sequences. The mature form of such protein may be obtained by expression of a full-length polynucleotide in a suitable mammalian cell or other host cell. The sequence of the mature form
24 of the protein is also determinable from the amino acid sequence of the full-length form. Where proteins of the present invention are membrane bound, soluble forms of the proteins are also provided. In such forms, part or all of the regions causing the proteins to be membrane bound are deleted so that the proteins are fully secreted from the cell in which they are expressed.

- 28 Protein compositions of the present invention may further comprise an acceptable carrier, such as a hydrophilic, *e.g.*, pharmaceutically acceptable, carrier.

- The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a
32 nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the genetic code, encode an identical polypeptide sequence. Preferred nucleic acid fragments of the present invention are the ORFs that encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. This technique is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

The invention also relates to methods for producing a polypeptide comprising growing a culture of host cells of the invention in a suitable culture medium, and purifying the protein from the cells or the culture in which the cells are grown. For example, the methods of the invention include a process for producing a polypeptide in which a host cell containing a suitable expression vector that includes a polynucleotide of the invention is cultured under conditions that allow expression of the encoded polypeptide. The polypeptide can be recovered from the culture, conveniently from the culture medium, or from a lysate prepared from the host cells and further purified. Preferred embodiments include those in which the protein produced by such process is a full length or mature form of the protein.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography. See, e.g., Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag (1994); Sambrook, et al., in *Molecular Cloning: A Laboratory Manual*; Ausubel et al., *Current Protocols in Molecular Biology*. Polypeptide fragments that

retain biological/immunological activity include fragments comprising greater than about 100 amino acids, or greater than about 200 amino acids, and fragments that encode specific protein domains.

4 The purified polypeptides can be used in *in vitro* binding assays which are well known in the art to identify molecules which bind to the polypeptides. These molecules include but are not limited to, for *e.g.*, small molecules, molecules from combinatorial libraries, antibodies or other proteins. The molecules identified in the binding assay are then tested for antagonist or agonist
8 activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

12 In addition, the peptides of the invention or molecules capable of binding to the peptides may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for SEQ ID NOS: 13902-27802.

16 The protein of the invention may also be expressed as a product of transgenic animals, *e.g.*, as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

20 The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications, in the peptide or DNA sequence, can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a
24 selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, *e.g.*, U.S. Pat. No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the
28 protein. Regions of the protein that are important for the protein function can be determined by various methods known in the art including the alanine-scanning method which involved systematic substitution of single or strings of amino acids with alanine, followed by testing the resulting alanine-containing variant for biological activity. This type of analysis determines the
32 importance of the substituted amino acid(s) in biological activity. Regions of the protein that are important for protein function may be determined by the eMATRIX program.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and are useful for screening or other immunological

methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are encompassed by the present invention.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBat™ kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl™ or Cibacrom blue 3GA Sepharose™; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX), or as a His tag. Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, Mass.), Pharmacia (Piscataway, N.J.) and Invitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("FLAG®") is commercially available from Kodak (New Haven, Conn.).

Finally, one or more reverse-phase high performance liquid chromatography (RP- HPLC) steps employing hydrophobic RP-HPLC media, *e.g.*, silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The polypeptides of the invention include analogs (variants). This embraces fragments, as well as peptides in which one or more amino acids has been deleted, inserted, or substituted. Also, analogs of the polypeptides of the invention embrace fusions of the polypeptides or modifications of the polypeptides of the invention, wherein the polypeptide or analog is fused to another moiety or moieties, *e.g.*, targeting moiety or another therapeutic agent. Such analogs may exhibit improved properties such as activity and/or stability. Examples of moieties which may be fused to the polypeptide or an analog include, for example, targeting moieties which provide for the delivery of polypeptide to pancreatic cells, *e.g.*, antibodies to pancreatic cells, antibodies to immune cells such as T-cells, monocytes, dendritic cells, granulocytes, etc., as well as receptor and ligands expressed on pancreatic or immune cells. Other moieties which may be fused to the polypeptide include therapeutic agents which are used for treatment, for example, immunosuppressive drugs such as cyclosporin, SK506, azathioprine, CD3 antibodies and steroids. Also, polypeptides may be fused to immune modulators, and other cytokines such as alpha or beta interferon.

4.6.1 DETERMINING POLYPEPTIDE AND POLYNUCLEOTIDE IDENTITY AND SIMILARITY

Preferred identity and/or similarity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in computer programs including, but are not limited to, the GCG program package, including GAP (Devereux, J., et al., *Nucleic Acids Research* 12(1):387 (1984); Genetics Computer Group, University of Wisconsin, Madison, WI), BLASTP, BLASTN, BLASTX, FASTA (Altschul, S.F. et al., *J. Molec. Biol.* 215:403-410 (1990), PSI-BLAST (Altschul S.F. et al., *Nucleic Acids Res.* vol. 25, pp. 3389-3402, herein incorporated by reference), eMatrix software (Wu et al., *J. Comp. Biol.*, Vol. 6, pp. 219-235 (1999), herein incorporated by reference), eMotif software (Nevill-Manning et al, *ISMB-97*, Vol. 4, pp. 202-209, herein incorporated by reference), pFam software (Sonnhammer et al., *Nucleic Acids Res.*, Vol. 26(1), pp. 320-322 (1998), herein incorporated by reference) and the Kyte-Doolittle hydrophobicity prediction algorithm (*J. Mol Biol*, 157, pp. 105-31 (1982), incorporated herein by reference). The BLAST programs are publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul, S., et al. NCB NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215:403-410 (1990).

4.7 CHIMERIC AND FUSION PROTEINS

The invention also provides chimeric or fusion proteins. As used herein, a "chimeric protein" or "fusion protein" comprises a polypeptide of the invention operatively linked to

another polypeptide. Within a fusion protein the polypeptide according to the invention can correspond to all or a portion of a protein according to the invention. In one embodiment, a fusion protein comprises at least one biologically active portion of a protein according to the invention. In another embodiment, a fusion protein comprises at least two biologically active portions of a protein according to the invention. Within the fusion protein, the term "operatively linked" is intended to indicate that the polypeptide according to the invention and the other polypeptide are fused in-frame to each other. The polypeptide can be fused to the N-terminus or C-terminus.

For example, in one embodiment a fusion protein comprises a polypeptide according to the invention operably linked to the extracellular domain of a second protein.

In another embodiment, the fusion protein is a GST-fusion protein in which the polypeptide sequences of the invention are fused to the C-terminus of the GST (*i.e.*, glutathione S-transferase) sequences.

In another embodiment, the fusion protein is an immunoglobulin fusion protein in which the polypeptide sequences according to the invention comprises one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand and a protein of the invention on the surface of a cell, to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion proteins can be used to affect the bioavailability of a cognate ligand. Inhibition of the ligand/protein interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, *e.g.*, cancer as well as modulating (*e.g.*, promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies in a subject, to purify ligands, and in screening assays to identify molecules that inhibit the interaction of a polypeptide of the invention with a ligand.

A chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for

example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the protein of the invention.

4.8 GENE THERAPY

Mutations in the polynucleotides of the invention gene may result in loss of normal function of the encoded protein. The invention thus provides gene therapy to restore normal activity of the polypeptides of the invention; or to treat disease states involving polypeptides of the invention. Delivery of a functional gene encoding polypeptides of the invention to appropriate cells is effected *ex vivo*, *in situ*, or *in vivo* by use of vectors, and more particularly viral vectors (e.g., adenovirus, adeno-associated virus, or a retrovirus), or *ex vivo* by use of physical DNA transfer methods (e.g., liposomes or chemical treatments). See, for example, Anderson, Nature, supplement to vol. 392, no. 6679, pp.25-20 (1998). For additional reviews of gene therapy technology see Friedmann, Science, 244: 1275-1281 (1989); Verma, Scientific American: 68-84 (1990); and Miller, Nature, 357: 455-460 (1992). Introduction of any one of the nucleotides of the present invention or a gene encoding the polypeptides of the present invention can also be accomplished with extrachromosomal substrates (transient expression) or artificial chromosomes (stable expression). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes. Alternatively, it is contemplated that in other human disease states, preventing the expression of or inhibiting the activity of polypeptides of the invention will be useful in treating the disease states. It is contemplated that antisense therapy or gene therapy could be applied to negatively regulate the expression of polypeptides of the invention.

Other methods inhibiting expression of a protein include the introduction of antisense molecules to the nucleic acids of the present invention, their complements, or their translated RNA sequences, by methods known in the art. Further, the polypeptides of the present invention can be inhibited by using targeted deletion methods, or the insertion of a negative regulatory element such as a silencer, which is tissue specific.

The present invention still further provides cells genetically engineered *in vivo* to express the polynucleotides of the invention, wherein such polynucleotides are in operative association with a regulatory sequence heterologous to the host cell which drives expression of the polynucleotides in

the cell. These methods can be used to increase or decrease the expression of the polynucleotides of the present invention.

Knowledge of DNA sequences provided by the invention allows for modification of cells to permit, increase, or decrease, expression of endogenous polypeptide. Cells can be modified (*e.g.*, by homologous recombination) to provide increased polypeptide expression by replacing, in whole or in part, the naturally occurring promoter with all or part of a heterologous promoter so that the cells express the protein at higher levels. The heterologous promoter is inserted in such a manner that it is operatively linked to the desired protein encoding sequences. See, for example, PCT International Publication No. WO 94/12650, PCT International Publication No. WO 92/20808, and PCT International Publication No. WO 91/09955. It is also contemplated that, in addition to heterologous promoter DNA, amplifiable marker DNA (*e.g.*, *ada*, *dhfr*, and the multifunctional CAD gene which encodes carbamyl phosphate synthase, aspartate transcarbamylase, and dihydroorotase) and/or intron DNA may be inserted along with the heterologous promoter DNA. If linked to the desired protein coding sequence, amplification of the marker DNA by standard selection methods results in co-amplification of the desired protein coding sequences in the cells.

In another embodiment of the present invention, cells and tissues may be engineered to express an endogenous gene comprising the polynucleotides of the invention under the control of inducible regulatory elements, in which case the regulatory sequences of the endogenous gene may be replaced by homologous recombination. As described herein, gene targeting can be used to replace a gene's existing regulatory region with a regulatory sequence isolated from a different gene or a novel regulatory sequence synthesized by genetic engineering methods. Such regulatory sequences may be comprised of promoters, enhancers, scaffold-attachment regions, negative regulatory elements, transcriptional initiation sites, regulatory protein binding sites or combinations of said sequences. Alternatively, sequences which affect the structure or stability of the RNA or protein produced may be replaced, removed, added, or otherwise modified by targeting. These sequences include polyadenylation signals, mRNA stability elements, splice sites, leader sequences for enhancing or modifying transport or secretion properties of the protein, or other sequences which alter or improve the function or stability of protein or RNA molecules.

The targeting event may be a simple insertion of the regulatory sequence, placing the gene under the control of the new regulatory sequence, *e.g.*, inserting a new promoter or enhancer or both upstream of a gene. Alternatively, the targeting event may be a simple deletion of a regulatory element, such as the deletion of a tissue-specific negative regulatory element. Alternatively, the targeting event may replace an existing element; for example, a tissue-specific enhancer can be replaced by an enhancer that has broader or different cell-type specificity than the naturally occurring elements. Here, the naturally occurring sequences are deleted and new sequences are

added. In all cases, the identification of the targeting event may be facilitated by the use of one or more selectable marker genes that are contiguous with the targeting DNA, allowing for the selection of cells in which the exogenous DNA has integrated into the cell genome. The identification of the targeting event may also be facilitated by the use of one or more marker genes exhibiting the property of negative selection, such that the negatively selectable marker is linked to the exogenous DNA, but configured such that the negatively selectable marker flanks the targeting sequence, and such that a correct homologous recombination event with sequences in the host cell genome does not result in the stable integration of the negatively selectable marker. Markers useful for this purpose include the Herpes Simplex Virus thymidine kinase (TK) gene or the bacterial xanthine-guanine phosphoribosyl-transferase (gpt) gene.

The gene targeting or gene activation techniques which can be used in accordance with this aspect of the invention are more particularly described in U.S. Patent No. 5,272,071 to Chappel; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

4.9 TRANSGENIC ANIMALS

In preferred methods to determine biological functions of the polypeptides of the invention in vivo, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

Transgenic animals can be prepared wherein all or part of a promoter of the polynucleotides of the invention is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous

promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

4 The polynucleotides of the present invention also make possible the development, through, *e.g.*, homologous recombination or knock out strategies, of animals that fail to express polypeptides of the invention or that express a variant polypeptide. Such animals are useful as models for studying the *in vivo* activities of polypeptide as well as for studying modulators of the polypeptides of the invention.

8 In preferred methods to determine biological functions of the polypeptides of the invention *in vivo*, one or more genes provided by the invention are either over expressed or inactivated in the germ line of animals using homologous recombination [Capecchi, Science 244:1288-1292 (1989)]. Animals in which the gene is over expressed, under the regulatory control of exogenous or endogenous promoter elements, are known as transgenic animals. Animals in which an endogenous gene has been inactivated by homologous recombination are referred to as "knockout" animals. Knockout animals, preferably non-human mammals, can be prepared as described in U.S. Patent No. 5,557,032, incorporated herein by reference. Transgenic animals are useful to determine the roles polypeptides of the invention play in biological processes, and preferably in disease states. Transgenic animals are useful as model systems to identify compounds that modulate lipid metabolism. Transgenic animals, preferably non-human mammals, are produced using methods as described in U.S. Patent No. 5,489,743 and PCT Publication No. WO94/28122, incorporated herein by reference.

24 Transgenic animals can be prepared wherein all or part of the polynucleotides of the invention promoter is either activated or inactivated to alter the level of expression of the polypeptides of the invention. Inactivation can be carried out using homologous recombination methods described above. Activation can be achieved by supplementing or even replacing the homologous promoter to provide for increased protein expression. The homologous promoter can be supplemented by insertion of one or more heterologous enhancer elements known to confer promoter activation in a particular tissue.

28

4.10 USES AND BIOLOGICAL ACTIVITY

32 The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified herein. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA). The mechanism underlying the particular condition or pathology will dictate whether the

polypeptides of the invention, the polynucleotides of the invention or modulators (activators or inhibitors) thereof would be beneficial to the subject in need of treatment. Thus, "therapeutic compositions of the invention" include compositions comprising isolated polynucleotides (including recombinant DNA molecules, cloned genes and degenerate variants thereof) or polypeptides of the invention (including full length protein, mature protein and truncations or domains thereof), or compounds and other substances that modulate the overall activity of the target gene products, either at the level of target gene/protein expression or target protein activity. Such modulators include polypeptides, analogs, (variants), including fragments and fusion proteins, antibodies and other binding proteins; chemical compounds that directly or indirectly activate or inhibit the polypeptides of the invention (identified, *e.g.*, via drug screening assays as described herein); antisense polynucleotides and polynucleotides suitable for triple helix formation; and in particular antibodies or other binding partners that specifically recognize one or more epitopes of the polypeptides of the invention.

The polypeptides of the present invention may likewise be involved in cellular activation or in one of the other physiological pathways described herein.

4.10.1 RESEARCH USES AND UTILITIES

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., *Cell* 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding polypeptide is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands.

Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987.

4.10.2 NUTRITIONAL USES

Polynucleotides and polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the polypeptide or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the polypeptide or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

4.10.3 CYTOKINE AND CELL PROLIFERATION/DIFFERENTIATION ACTIVITY

A polypeptide of the present invention may exhibit activity relating to cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient

confirmation of cytokine activity. The activity of therapeutic compositions of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+(preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e, CMK, HUVEC, and Caco. Therapeutic compositions of the invention can be used in the following:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin- γ , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6--Nordan, R. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11--Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9--Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober,

- Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

4.10.4 STEM CELL GROWTH FACTOR ACTIVITY

- 8 A polypeptide of the present invention may exhibit stem cell growth factor activity and be involved in the proliferation, differentiation and survival of pluripotent and totipotent stem cells including primordial germ cells, embryonic stem cells, hematopoietic stem cells and/or germ line stem cells. Administration of the polypeptide of the invention to stem cells *in vivo* or
12 *ex vivo* is expected to maintain and expand cell populations in a totipotent or pluripotent state which would be useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals and the development of bio-sensors. The ability to produce large quantities of human cells has important working applications for the production of human
16 proteins which currently must be obtained from non-human sources or donors, implantation of cells to treat diseases such as Parkinson's, Alzheimer's and other neurodegenerative diseases; tissues for grafting such as bone marrow, skin, cartilage, tendons, bone, muscle (including cardiac muscle), blood vessels, cornea, neural cells, gastrointestinal cells and others; and organs
20 for transplantation such as kidney, liver, pancreas (including islet cells), heart and lung.

- It is contemplated that multiple different exogenous growth factors and/or cytokines may be administered in combination with the polypeptide of the invention to achieve the desired effect, including any of the growth factors listed herein, other stem cell maintenance factors, and
24 specifically including stem cell factor (SCF), leukemia inhibitory factor (LIF), Flt-3 ligand (Flt-3L), any of the interleukins, recombinant soluble IL-6 receptor fused to IL-6, macrophage inflammatory protein 1-alpha (MIP-1-alpha), G-CSF, GM-CSF, thrombopoietin (TPO), platelet factor 4 (PF-4), platelet-derived growth factor (PDGF), neural growth factors and basic
28 fibroblast growth factor (bFGF).

- Since totipotent stem cells can give rise to virtually any mature cell type, expansion of these cells in culture will facilitate the production of large quantities of mature cells. Techniques for culturing stem cells are known in the art and administration of polypeptides of the invention, optionally with other growth factors and/or cytokines, is expected to enhance the survival and
32 proliferation of the stem cell populations. This can be accomplished by direct administration of the polypeptide of the invention to the culture medium. Alternatively, stroma cells transfected with a polynucleotide that encodes for the polypeptide of the invention can be used as a feeder

layer for the stem cell populations in culture or in vivo. Stromal support cells for feeder layers may include embryonic bone marrow fibroblasts, bone marrow stromal cells, fetal liver cells, or cultured embryonic fibroblasts (see U.S. Patent No. 5,690,926).

4 Stem cells themselves can be transfected with a polynucleotide of the invention to induce autocrine expression of the polypeptide of the invention. This will allow for generation of undifferentiated totipotent/pluripotent stem cell lines that are useful as is or that can then be differentiated into the desired mature cell types. These stable cell lines can also serve as a source
8 of undifferentiated totipotent/pluripotent mRNA to create cDNA libraries and templates for polymerase chain reaction experiments. These studies would allow for the isolation and identification of differentially expressed genes in stem cell populations that regulate stem cell proliferation and/or maintenance.

12 Expansion and maintenance of totipotent stem cell populations will be useful in the treatment of many pathological conditions. For example, polypeptides of the present invention may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or
16 genetic disorders. The polypeptide of the invention may be useful for inducing the proliferation of neural cells and for the regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders which involve degeneration, death or trauma to neural cells or nerve tissue. In addition,
20 the expanded stem cell populations can also be genetically altered for gene therapy purposes and to decrease host rejection of replacement tissues after grafting or implantation.

Expression of the polypeptide of the invention and its effect on stem cells can also be manipulated to achieve controlled differentiation of the stem cells into more differentiated cell
24 types. A broadly applicable method of obtaining pure populations of a specific differentiated cell type from undifferentiated stem cell populations involves the use of a cell-type specific promoter driving a selectable marker. The selectable marker allows only cells of the desired type to survive. For example, stem cells can be induced to differentiate into cardiomyocytes (Wobus et al., *Differentiation*, 48: 173-182, (1991); Klug et al., *J. Clin. Invest.*, 98(1): 216-224, (1998))
28 or skeletal muscle cells (Browder, L. W. In: *Principles of Tissue Engineering* eds. Lanza et al., Academic Press (1997)). Alternatively, directed differentiation of stem cells can be accomplished by culturing the stem cells in the presence of a differentiation factor such as
32 retinoic acid and an antagonist of the polypeptide of the invention which would inhibit the effects of endogenous stem cell factor activity and allow differentiation to proceed.

In vitro cultures of stem cells can be used to determine if the polypeptide of the invention exhibits stem cell growth factor activity. Stem cells are isolated from any one of various cell

sources (including hematopoietic stem cells and embryonic stem cells) and cultured on a feeder layer, as described by Thompson et al. Proc. Natl. Acad. Sci, U.S.A., 92: 7844-7848 (1995), in the presence of the polypeptide of the invention alone or in combination with other growth factors or cytokines. The ability of the polypeptide of the invention to induce stem cells proliferation is determined by colony formation on semi-solid support *e.g.* as described by Bernstein et al., Blood, 77: 2316-2321 (1991).

4.10.5 HEMATOPOIESIS REGULATING ACTIVITY

A polypeptide of the present invention may be involved in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell disorders. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (*i.e.*, in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

Therapeutic compositions of the invention can be used in the following:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

- Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in:
- Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

16 4.10.6 TISSUE GROWTH ACTIVITY

A polypeptide of the present invention also may be involved in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as in wound healing and tissue repair and replacement, and in healing of burns, incisions and ulcers.

- 20 A polypeptide of the present invention which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Compositions of a polypeptide, antibody, binding partner, or other modulator of the invention may have
- 24 prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

- 28 A polypeptide of this invention may also be involved in attracting bone-forming cells, stimulating growth of bone-forming cells, or inducing differentiation of progenitors of bone-forming cells. Treatment of osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease, such as through stimulation of bone and/or cartilage repair or by blocking
- 32 inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes may also be possible using the composition of the invention.

Another category of tissue regeneration activity that may involve the polypeptide of the present invention is tendon/ligament formation. Induction of tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The compositions of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a composition may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a composition of the invention.

Compositions of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

Compositions of the present invention may also be involved in the generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine,

kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring may allow normal tissue to regenerate. A polypeptide of the present invention may also exhibit angiogenic activity.

A composition of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A composition of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Therapeutic compositions of the invention can be used in the following:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

4.10.7 IMMUNE STIMULATING OR SUPPRESSING ACTIVITY

A polypeptide of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A polynucleotide of the invention can encode a polypeptide exhibiting such activities. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpes viruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, proteins of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein (or antagonists thereof, including antibodies) of the present invention may also be useful in the treatment of allergic reactions and conditions (e.g., anaphylaxis, serum sickness, drug reactions, food allergies, insect venom allergies, mastocytosis, allergic rhinitis, hypersensitivity pneumonitis, urticaria, angioedema, eczema, atopic dermatitis, allergic contact dermatitis, erythema multiforme, Stevens-Johnson syndrome, allergic conjunctivitis, atopic keratoconjunctivitis, venereal keratoconjunctivitis, giant papillary conjunctivitis and contact allergies), such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein (or antagonists thereof) of the present invention. The therapeutic effects of the polypeptides or antagonists thereof on allergic reactions can be evaluated by in vivo animals models such as the cumulative contact enhancement test (Lastbom et al., Toxicology 125: 59-66, 1998), skin prick test (Hoffmann et al., Allergy 54: 446-54, 1999), guinea pig skin sensitization test (Vohr et al., Arch. Toxicol. 73: 501-9), and murine local lymph node assay (Kimber et al., J. Toxicol. Environ. Health 53: 563-79).

Using the proteins of the invention it may also be possible to modulate immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue

transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a therapeutic composition of the invention may prevent cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, a lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular therapeutic compositions in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of therapeutic compositions of the invention on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block stimulation of T cells can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (e.g., a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial

immune response. For example, enhancing an immune response may be useful in cases of viral infection, including systemic viral diseases such as influenza, the common cold, and encephalitis.

4 Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the
8 patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be
12 capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

 A polypeptide of the present invention may provide the necessary stimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to
16 reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and β_2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II
20 proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as
24 the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

28 The activity of a protein of the invention may, among other means, be measured by the following methods:

 Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D.
32 H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J.

Immunol. 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bowman et al., *J. Virology* 61:1992-1998; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Brown et al., *J. Immunol.* 153:3079-3092, 1994.

- 4 Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. *Immunol.* 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In *Current Protocols in Immunology*. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

- Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *J. Immunol.* 149:3778-3783, 1992.

- Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., *J. Immunol.* 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation* 94:797-807, 1994; and Inaba et al., *Journal of Experimental Medicine* 172:631-640, 1990.

- Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., *Cytometry* 13:795-808, 1992; Gorczyca et al., *Leukemia* 7:659-670, 1993; Gorczyca et al., *Cancer Research* 53:1945-1951, 1993; Itoh et al., *Cell* 66:233-243, 1991; Zacharchuk, *Journal of Immunology* 145:4037-4045, 1990; Zamai et al., *Cytometry* 14:891-897, 1993; Gorczyca et al., *International Journal of Oncology* 1:639-648, 1992.

- Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., *Blood* 84:111-117, 1994; Fine et al., *Cellular Immunology* 155:111-122, 1994; Galy et al., *Blood* 85:2770-2778, 1995; Toki et al., *Proc. Nat. Acad. Sci. USA* 88:7548-7551, 1991.

4.10.8 ACTIVIN/INHIBIN ACTIVITY

A polypeptide of the present invention may also exhibit activin- or inhibin-related activities. A polynucleotide of the invention may encode a polypeptide exhibiting such characteristics. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as, but not limited to, cows, sheep and pigs.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods.

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

4.10.9 CHEMOTACTIC/CHEMOKINETIC ACTIVITY

A polypeptide of the present invention may be involved in chemotactic or chemokinetic activity for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Chemotactic and chemokinetic receptor activation can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic compositions (e.g. proteins, antibodies, binding partners, or modulators of the invention) provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells.

- 4 Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

Therapeutic compositions of the invention can be used in the following:

- 8 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

4.10.10 HEMOSTATIC AND THROMBOLYTIC ACTIVITY

- 20 A polypeptide of the invention may also be involved in hemostasis or thrombolysis or thrombosis. A polynucleotide of the invention can encode a polypeptide exhibiting such attributes. Compositions may be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A composition of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

Therapeutic compositions of the invention can be used in the following:

- 28 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

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4.10.11 CANCER DIAGNOSIS AND THERAPY

Polypeptides of the invention may be involved in cancer cell generation, proliferation or metastasis. Detection of the presence or amount of polynucleotides or polypeptides of the

invention may be useful for the diagnosis and/or prognosis of one or more types of cancer. For example, the presence or increased expression of a polynucleotide/polypeptide of the invention may indicate a hereditary risk of cancer, a precancerous condition, or an ongoing malignancy.

4 Conversely, a defect in the gene or absence of the polypeptide may be associated with a cancer condition. Identification of single nucleotide polymorphisms associated with cancer or a predisposition to cancer may also be useful for diagnosis or prognosis.

Cancer treatments promote tumor regression by inhibiting tumor cell proliferation,
8 inhibiting angiogenesis (growth of new blood vessels that is necessary to support tumor growth) and/or prohibiting metastasis by reducing tumor cell motility or invasiveness. Therapeutic compositions of the invention may be effective in adult and pediatric oncology including in solid phase tumors/malignancies, locally advanced tumors, human soft tissue sarcomas, metastatic
12 cancer, including lymphatic metastases, blood cell malignancies including multiple myeloma, acute and chronic leukemias, and lymphomas, head and neck cancers including mouth cancer, larynx cancer and thyroid cancer, lung cancers including small cell carcinoma and non-small cell cancers, breast cancers including small cell carcinoma and ductal carcinoma, gastrointestinal
16 cancers including esophageal cancer, stomach cancer, colon cancer, colorectal cancer and polyps associated with colorectal neoplasia, pancreatic cancers, liver cancer, urologic cancers including bladder cancer and prostate cancer, malignancies of the female genital tract including ovarian carcinoma, uterine (including endometrial) cancers, and solid tumor in the ovarian follicle,
20 kidney cancers including renal cell carcinoma, brain cancers including intrinsic brain tumors, neuroblastoma, astrocytic brain tumors, gliomas, metastatic tumor cell invasion in the central nervous system, bone cancers including osteomas, skin cancers including malignant melanoma, tumor progression of human skin keratinocytes, squamous cell carcinoma, basal cell carcinoma,
24 hemangiopericytoma and Kaposi's sarcoma.

Polypeptides, polynucleotides, or modulators of polypeptides of the invention (including inhibitors and stimulators of the biological activity of the polypeptide of the invention) may be administered to treat cancer. Therapeutic compositions can be administered in therapeutically
28 effective dosages alone or in combination with adjuvant cancer therapy such as surgery, chemotherapy, radiotherapy, thermotherapy, and laser therapy, and may provide a beneficial effect, e.g. reducing tumor size, slowing rate of tumor growth, inhibiting metastasis, or otherwise improving overall clinical condition, without necessarily eradicating the cancer.

32 The composition can also be administered in therapeutically effective amounts as a portion of an anti-cancer cocktail. An anti-cancer cocktail is a mixture of the polypeptide or modulator of the invention with one or more anti-cancer drugs in addition to a pharmaceutically acceptable carrier for delivery. The use of anti-cancer cocktails as a cancer treatment is routine.

Anti-cancer drugs that are well known in the art and can be used as a treatment in combination with the polypeptide or modulator of the invention include: Actinomycin D, Aminoglutethimide, Asparaginase, Bleomycin, Busulfan, Carboplatin, Carmustine, Chlorambucil, Cisplatin (cis-
 4 DDP), Cyclophosphamide, Cytarabine HCl (Cytosine arabinoside), Daçãrbazine, Dactinomycin, Daunorubicin HCl, Doxorubicin HCl, Estramustine phosphate sodium, Etoposide (V16-213), Floxuridine, 5-Fluorouracil (5-Fu), Flutamide, Hydroxyurea (hydroxycarbamide), Ifosfamide, Interferon Alpha-2a, Interferon Alpha-2b, Leuprolide acetate (LHRH-releasing factor analog),
 8 Lomustine, Mechlorethamine HCl (nitrogen mustard), Melphalan, Mercaptopurine, Mesna, Methotrexate (MTX), Mitomycin, Mitoxantrone HCl, Octreotide, Plicamycin, Procarbazine HCl, Streptozocin, Tamoxifen citrate, Thioguanine, Thiotepa, Vinblastine sulfate, Vincristine sulfate, Amsacrine, Azacitidine, Hexamethylmelamine, Interleukin-2, Mitoguazone, Pentostatin,
 12 Semustine, Teniposide, and Vindesine sulfate.

In addition, therapeutic compositions of the invention may be used for prophylactic treatment of cancer. There are hereditary conditions and/or environmental situations (*e.g.* exposure to carcinogens) known in the art that predispose an individual to developing cancers.
 16 Under these circumstances, it may be beneficial to treat these individuals with therapeutically effective doses of the polypeptide of the invention to reduce the risk of developing cancers.

In vitro models can be used to determine the effective doses of the polypeptide of the invention as a potential cancer treatment. These *in vitro* models include proliferation assays of
 20 cultured tumor cells, growth of cultured tumor cells in soft agar (see Freshney, (1987) Culture of Animal Cells: A Manual of Basic Technique, Wiley-Liss, New York, NY Ch 18 and Ch 21), tumor systems in nude mice as described in Giovanella et al., J. Natl. Can. Inst., 52: 921-30 (1974), mobility and invasive potential of tumor cells in Boyden Chamber assays as described in
 24 Pilkington et al., Anticancer Res., 17: 4107-9 (1997), and angiogenesis assays such as induction of vascularization of the chick chorioallantoic membrane or induction of vascular endothelial cell migration as described in Ribatta et al., Intl. J. Dev. Biol., 40: 1189-97 (1999) and Li et al., Clin. Exp. Metastasis, 17:423-9 (1999), respectively. Suitable tumor cells lines are available,
 28 *e.g.* from American Type Tissue Culture Collection catalogs.

4.10.12 RECEPTOR/LIGAND ACTIVITY

A polypeptide of the present invention may also demonstrate activity as receptor,
 32 receptor ligand or inhibitor or agonist of receptor/ligand interactions. A polynucleotide of the invention can encode a polypeptide exhibiting such characteristics. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions

and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses. Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a polypeptide of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley- Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1- 7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

By way of example, the polypeptides of the invention may be used as a receptor for a ligand(s) thereby transmitting the biological activity of that ligand(s). Ligands may be identified through binding assays, affinity chromatography, dihybrid screening assays, BIAcore assays, gel overlay assays, or other methods known in the art.

Studies characterizing drugs or proteins as agonist or antagonist or partial agonists or a partial antagonist require the use of other proteins as competing ligands. The polypeptides of the present invention or ligand(s) thereof may be labeled by being coupled to radioisotopes, colorimetric molecules or a toxin molecules by conventional methods. ("Guide to Protein Purification" Murray P. Deutscher (ed) Methods in Enzymology Vol. 182 (1990) Academic Press, Inc. San Diego). Examples of radioisotopes include, but are not limited to, tritium and carbon-14. Examples of colorimetric molecules include, but are not limited to, fluorescent molecules such as fluorescamine, or rhodamine or other colorimetric molecules. Examples of toxins include, but are not limited, to ricin.

4.10.13 DRUG SCREENING

This invention is particularly useful for screening chemical compounds by using the novel polypeptides or binding fragments thereof in any of a variety of drug screening techniques. The polypeptides or fragments employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface or located intracellularly. One method of drug screening

utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or a fragment thereof. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between polypeptides of the invention or fragments and the agent being tested or examine the diminution in complex formation between the novel polypeptides and an appropriate cell line, which are well known in the art.

Sources for test compounds that may be screened for ability to bind to or modulate (*i.e.*, increase or decrease) the activity of polypeptides of the invention include (1) inorganic and organic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of either random or mimetic peptides, oligonucleotides or organic molecules.

Chemical libraries may be readily synthesized or purchased from a number of commercial sources, and may include structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening.

The sources of natural product libraries are microorganisms (including bacteria and fungi), animals, plants or other vegetation, or marine organisms, and libraries of mixtures for screening may be created by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of the organisms themselves. Natural product libraries include polyketides, non-ribosomal peptides, and (non-naturally occurring) variants thereof. For a review, see *Science* 282:63-68 (1998).

Combinatorial libraries are composed of large numbers of peptides, oligonucleotides or organic compounds and can be readily prepared by traditional automated synthesis methods, PCR, cloning or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). For reviews and examples of peptidomimetic libraries, see Al-Obeidi et al., *Mol. Biotechnol.*, 9(3):205-23 (1998); Hruby et al., *Curr Opin Chem Biol*, 1(1):114-19 (1997); Dorner et al., *Bioorg Med Chem*, 4(5):709-15 (1996) (alkylated dipeptides).

Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to bind a polypeptide of the invention. The molecules identified in the binding assay are then tested for antagonist or agonist activity in *in vivo* tissue culture or animal models that are well known in the art. In brief, the molecules are titrated into a plurality of cell cultures or animals and then tested for either cell/animal death or prolonged survival of the animal/cells.

The binding molecules thus identified may be complexed with toxins, *e.g.*, ricin or cholera, or with other compounds that are toxic to cells such as radioisotopes. The toxin-binding molecule complex is then targeted to a tumor or other cell by the specificity of the binding molecule for a polypeptide of the invention. Alternatively, the binding molecules may be complexed with imaging agents for targeting and imaging purposes.

4.10.14 ASSAY FOR RECEPTOR ACTIVITY

The invention also provides methods to detect specific binding of a polypeptide *e.g.* a ligand or a receptor. The art provides numerous assays particularly useful for identifying previously unknown binding partners for receptor polypeptides of the invention. For example, expression cloning using mammalian or bacterial cells, or dihybrid screening assays can be used to identify polynucleotides encoding binding partners. As another example, affinity chromatography with the appropriate immobilized polypeptide of the invention can be used to isolate polypeptides that recognize and bind polypeptides of the invention. There are a number of different libraries used for the identification of compounds, and in particular small molecules, that modulate (*i.e.*, increase or decrease) biological activity of a polypeptide of the invention. Ligands for receptor polypeptides of the invention can also be identified by adding exogenous ligands, or cocktails of ligands to two cells populations that are genetically identical except for the expression of the receptor of the invention: one cell population expresses the receptor of the invention whereas the other does not. The response of the two cell populations to the addition of ligand(s) are then compared. Alternatively, an expression library can be co-expressed with the polypeptide of the invention in cells and assayed for an autocrine response to identify potential ligand(s). As still another example, BIAcore assays, gel overlay assays, or other methods known in the art can be used to identify binding partner polypeptides, including, (1) organic and inorganic chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules.

The role of downstream intracellular signaling molecules in the signaling cascade of the polypeptide of the invention can be determined. For example, a chimeric protein in which the cytoplasmic domain of the polypeptide of the invention is fused to the extracellular portion of a protein, whose ligand has been identified, is produced in a host cell. The cell is then incubated with the ligand specific for the extracellular portion of the chimeric protein, thereby activating the chimeric receptor. Known downstream proteins involved in intracellular signaling can then be assayed for expected modifications *i.e.* phosphorylation. Other methods known to those in the art can also be used to identify signaling molecules involved in receptor activity.

4.10.15 ANTI-INFLAMMATORY ACTIVITY

Compositions of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Compositions with such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Compositions of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Compositions of this invention may be utilized to prevent or treat conditions such as, but not limited to, sepsis, acute pancreatitis, endotoxin shock, cytokine induced shock, rheumatoid arthritis, chronic inflammatory arthritis, pancreatic cell damage from diabetes mellitus type 1, graft versus host disease, inflammatory bowel disease, inflammation associated with pulmonary disease, other autoimmune disease or inflammatory disease, an antiproliferative agent such as for acute or chronic myelogenous leukemia or in the prevention of premature labor secondary to intrauterine infections.

4.10.16 LEUKEMIAS

Leukemias and related disorders may be treated or prevented by administration of a therapeutic that promotes or inhibits function of the polynucleotides and/or polypeptides of the invention. Such leukemias and related disorders include but are not limited to acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblastic, promyelocytic, myelomonocytic, monocytic, erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia (for a review of such disorders, see Fishman et al., 1985, Medicine, 2d Ed., J.B. Lippincott Co., Philadelphia).

4.10.17 NERVOUS SYSTEM DISORDERS

Nervous system disorders, involving cell types which can be tested for efficacy of intervention with compounds that modulate the activity of the polynucleotides and/or polypeptides of the invention, and which can be treated upon thus observing an indication of

therapeutic utility, include but are not limited to nervous system injuries, and diseases or disorders which result in either a disconnection of axons, a diminution or degeneration of neurons, or demyelination. Nervous system lesions which may be treated in a patient (including human and non-human mammalian patients) according to the invention include but are not limited to the following lesions of either the central (including spinal cord, brain) or peripheral nervous systems:

(i) traumatic lesions, including lesions caused by physical injury or associated with surgery, for example, lesions which sever a portion of the nervous system, or compression injuries;

(ii) ischemic lesions, in which a lack of oxygen in a portion of the nervous system results in neuronal injury or death, including cerebral infarction or ischemia, or spinal cord infarction or ischemia;

(iii) infectious lesions, in which a portion of the nervous system is destroyed or injured as a result of infection, for example, by an abscess or associated with infection by human immunodeficiency virus, herpes zoster, or herpes simplex virus or with Lyme disease, tuberculosis, syphilis;

(iv) degenerative lesions, in which a portion of the nervous system is destroyed or injured as a result of a degenerative process including but not limited to degeneration associated with Parkinson's disease, Alzheimer's disease, Huntington's chorea, or amyotrophic lateral sclerosis;

(v) lesions associated with nutritional diseases or disorders, in which a portion of the nervous system is destroyed or injured by a nutritional disorder or disorder of metabolism including but not limited to, vitamin B12 deficiency, folic acid deficiency, Wernicke disease, tobacco-alcohol amblyopia, Marchiafava-Bignami disease (primary degeneration of the corpus callosum), and alcoholic cerebellar degeneration;

(vi) neurological lesions associated with systemic diseases including but not limited to diabetes (diabetic neuropathy, Bell's palsy), systemic lupus erythematosus, carcinoma, or sarcoidosis;

(vii) lesions caused by toxic substances including alcohol, lead, or particular neurotoxins; and

(viii) demyelinated lesions in which a portion of the nervous system is destroyed or injured by a demyelinating disease including but not limited to multiple sclerosis, human immunodeficiency virus-associated myelopathy, transverse myelopathy or various etiologies, progressive multifocal leukoencephalopathy, and central pontine myelinolysis.

Therapeutics which are useful according to the invention for treatment of a nervous system disorder may be selected by testing for biological activity in promoting the survival or differentiation of neurons. For example, and not by way of limitation, therapeutics which elicit any of the following effects may be useful according to the invention:

- (i) increased survival time of neurons in culture;
- (ii) increased sprouting of neurons in culture or *in vivo*;
- (iii) increased production of a neuron-associated molecule in culture or *in vivo*, e.g., choline acetyltransferase or acetylcholinesterase with respect to motor neurons; or
- (iv) decreased symptoms of neuron dysfunction *in vivo*.

Such effects may be measured by any method known in the art. In preferred, non-limiting embodiments, increased survival of neurons may be measured by the method set forth in Arakawa et al. (1990, J. Neurosci. 10:3507-3515); increased sprouting of neurons may be detected by methods set forth in Pestronk et al. (1980, Exp. Neurol. 70:65-82) or Brown et al. (1981, Ann. Rev. Neurosci. 4:17-42); increased production of neuron-associated molecules may be measured by bioassay, enzymatic assay, antibody binding, Northern blot assay, etc., depending on the molecule to be measured; and motor neuron dysfunction may be measured by assessing the physical manifestation of motor neuron disorder, e.g., weakness, motor neuron conduction velocity, or functional disability.

In specific embodiments, motor neuron disorders that may be treated according to the invention include but are not limited to disorders such as infarction, infection, exposure to toxin, trauma, surgical damage, degenerative disease or malignancy that may affect motor neurons as well as other components of the nervous system, as well as disorders that selectively affect neurons such as amyotrophic lateral sclerosis, and including but not limited to progressive spinal muscular atrophy, progressive bulbar palsy, primary lateral sclerosis, infantile and juvenile muscular atrophy, progressive bulbar paralysis of childhood (Fazio-Londe syndrome), poliomyelitis and the post polio syndrome, and Hereditary Motorsensory Neuropathy (Charcot-Marie-Tooth Disease).

4.10.18 OTHER ACTIVITIES

A polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape);

effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, co-factors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

4.10.19 IDENTIFICATION OF POLYMORPHISMS

The demonstration of polymorphisms makes possible the identification of such polymorphisms in human subjects and the pharmacogenetic use of this information for diagnosis and treatment. Such polymorphisms may be associated with, *e.g.*, differential predisposition or susceptibility to various disease states (such as disorders involving inflammation or immune response) or a differential response to drug administration, and this genetic information can be used to tailor preventive or therapeutic treatment appropriately. For example, the existence of a polymorphism associated with a predisposition to inflammation or autoimmune disease makes possible the diagnosis of this condition in humans by identifying the presence of the polymorphism.

Polymorphisms can be identified in a variety of ways known in the art which all generally involve obtaining a sample from a patient, analyzing DNA from the sample, optionally involving isolation or amplification of the DNA, and identifying the presence of the polymorphism in the DNA. For example, PCR may be used to amplify an appropriate fragment of genomic DNA which may then be sequenced. Alternatively, the DNA may be subjected to allele-specific oligonucleotide hybridization (in which appropriate oligonucleotides are hybridized to the DNA under conditions permitting detection of a single base mismatch) or to a single nucleotide extension assay (in which an oligonucleotide that hybridizes immediately adjacent to the position of the polymorphism is extended with one or more labeled nucleotides). In addition, traditional restriction fragment length polymorphism analysis (using restriction enzymes that provide differential digestion of the genomic DNA depending on the presence or

absence of the polymorphism) may be performed. Arrays with nucleotide sequences of the present invention can be used to detect polymorphisms. The array can comprise modified nucleotide sequences of the present invention in order to detect the nucleotide sequences of the present invention. In the alternative, any one of the nucleotide sequences of the present invention can be placed on the array to detect changes from those sequences.

Alternatively a polymorphism resulting in a change in the amino acid sequence could also be detected by detecting a corresponding change in amino acid sequence of the protein, e.g., by an antibody specific to the variant sequence.

4.10.20 ARTHRITIS AND INFLAMMATION

The immunosuppressive effects of the compositions of the invention against rheumatoid arthritis is determined in an experimental animal model system. The experimental model system is adjuvant induced arthritis in rats, and the protocol is described by J. Holoshitz, et al., 1983, Science, 219:56, or by B. Waksman et al., 1963, Int. Arch. Allergy Appl. Immunol., 23:129. Induction of the disease can be caused by a single injection, generally intradermally, of a suspension of killed Mycobacterium tuberculosis in complete Freund's adjuvant (CFA). The route of injection can vary, but rats may be injected at the base of the tail with an adjuvant mixture. The polypeptide is administered in phosphate buffered solution (PBS) at a dose of about 1-5 mg/kg. The control consists of administering PBS only.

The procedure for testing the effects of the test compound would consist of intradermally injecting killed Mycobacterium tuberculosis in CFA followed by immediately administering the test compound and subsequent treatment every other day until day 24. At 14, 15, 18, 20, 22, and 24 days after injection of Mycobacterium CFA, an overall arthritis score may be obtained as described by J. Holoskitz above. An analysis of the data would reveal that the test compound would have a dramatic affect on the swelling of the joints as measured by a decrease of the arthritis score.

4.11 THERAPEUTIC METHODS

The compositions (including polypeptide fragments, analogs, variants and antibodies or other binding partners or modulators including antisense polynucleotides) of the invention have numerous applications in a variety of therapeutic methods. Examples of therapeutic applications include, but are not limited to, those exemplified herein.

4.11.1 EXAMPLE

One embodiment of the invention is the administration of an effective amount of the polypeptides or other composition of the invention to individuals affected by a disease or disorder that can be modulated by regulating the peptides of the invention. While the mode of administration is not particularly important, parenteral administration is preferred. An exemplary mode of administration is to deliver an intravenous bolus. The dosage of the polypeptides or other composition of the invention will normally be determined by the prescribing physician. It is to be expected that the dosage will vary according to the age, weight, condition and response of the individual patient. Typically, the amount of polypeptide administered per dose will be in the range of about 0.01 $\mu\text{g/kg}$ to 100 mg/kg of body weight, with the preferred dose being about 0.1 $\mu\text{g/kg}$ to 10 mg/kg of patient body weight. For parenteral administration, polypeptides of the invention will be formulated in an injectable form combined with a pharmaceutically acceptable parenteral vehicle. Such vehicles are well known in the art and examples include water, saline, Ringer's solution, dextrose solution, and solutions consisting of small amounts of the human serum albumin. The vehicle may contain minor amounts of additives that maintain the isotonicity and stability of the polypeptide or other active ingredient. The preparation of such solutions is within the skill of the art.

4.12 PHARMACEUTICAL FORMULATIONS AND ROUTES OF ADMINISTRATION

A protein or other composition of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources and including antibodies and other binding partners of the polypeptides of the invention) may be administered to a patient in need, by itself, or in pharmaceutical compositions where it is mixed with suitable carriers or excipient(s) at doses to treat or ameliorate a variety of disorders. Such a composition may optionally contain (in addition to protein or other active ingredient and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the disease or disorder in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet-derived growth

factor (PDGF), transforming growth factors (TGF- α and TGF- β), insulin-like growth factor (IGF), as well as cytokines described herein.

The pharmaceutical composition may further contain other agents which either enhance
4 the activity of the protein or other active ingredient or complement its activity or use in
treatment. Such additional factors and/or agents may be included in the pharmaceutical
composition to produce a synergistic effect with protein or other active ingredient of the
invention, or to minimize side effects. Conversely, protein or other active ingredient of the
8 present invention may be included in formulations of the particular clotting factor, cytokine,
lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-
inflammatory agent to minimize side effects of the clotting factor, cytokine, lymphokine, other
hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent (such as
12 IL-1Ra, IL-1 Hy1, IL-1 Hy2, anti-TNF, corticosteroids, immunosuppressive agents). A protein
of the present invention may be active in multimers (*e.g.*, heterodimers or homodimers) or
complexes with itself or other proteins. As a result, pharmaceutical compositions of the
invention may comprise a protein of the invention in such multimeric or complexed form.

16 As an alternative to being included in a pharmaceutical composition of the invention
including a first protein, a second protein or a therapeutic agent may be concurrently
administered with the first protein (*e.g.*, at the same time, or at differing times provided that
therapeutic concentrations of the combination of agents is achieved at the treatment site).
20 Techniques for formulation and administration of the compounds of the instant application may
be found in "Remington's Pharmaceutical Sciences," Mack Publishing Co., Easton, PA, latest
edition. A therapeutically effective dose further refers to that amount of the compound sufficient
to result in amelioration of symptoms, *e.g.*, treatment, healing, prevention or amelioration of the
24 relevant medical condition, or an increase in rate of treatment, healing, prevention or
amelioration of such conditions. When applied to an individual active ingredient, administered
alone, a therapeutically effective dose refers to that ingredient alone. When applied to a
combination, a therapeutically effective dose refers to combined amounts of the active
28 ingredients that result in the therapeutic effect, whether administered in combination, serially or
simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically
effective amount of protein or other active ingredient of the present invention is administered to
32 a mammal having a condition to be treated. Protein or other active ingredient of the present
invention may be administered in accordance with the method of the invention either alone or in
combination with other therapies such as treatments employing cytokines, lymphokines or other
hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other

hematopoietic factors, protein or other active ingredient of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein or other active ingredient of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

4.12.1 ROUTES OF ADMINISTRATION

Suitable routes of administration may, for example, include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as intrathecal, direct intraventricular, intravenous, intraperitoneal, intranasal, or intraocular injections. Administration of protein or other active ingredient of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

Alternately, one may administer the compound in a local rather than systemic manner, for example, via injection of the compound directly into a arthritic joints or in fibrotic tissue, often in a depot or sustained release formulation. In order to prevent the scarring process frequently occurring as complication of glaucoma surgery, the compounds may be administered topically, for example, as eye drops. Furthermore, one may administer the drug in a targeted drug delivery system, for example, in a liposome coated with a specific antibody, targeting, for example, arthritic or fibrotic tissue. The liposomes will be targeted to and taken up selectively by the afflicted tissue.

The polypeptides of the invention are administered by any route that delivers an effective dosage to the desired site of action. The determination of a suitable route of administration and an effective dosage for a particular indication is within the level of skill in the art. Preferably for wound treatment, one administers the therapeutic compound directly to the site. Suitable dosage ranges for the polypeptides of the invention can be extrapolated from these dosages or from similar studies in appropriate animal models. Dosages can then be adjusted as necessary by the clinician to provide maximal therapeutic benefit.

4.12.2 COMPOSITIONS/FORMULATIONS

Pharmaceutical compositions for use in accordance with the present invention thus may be formulated in a conventional manner using one or more physiologically acceptable carriers

comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. These pharmaceutical compositions may be manufactured in a manner that is itself known, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. When a therapeutically effective amount of protein or other active ingredient of the present invention is administered orally, protein or other active ingredient of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein or other active ingredient of the present invention, and preferably from about 25 to 90% protein or other active ingredient of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein or other active ingredient of the present invention, and preferably from about 1 to 50% protein or other active ingredient of the present invention.

When a therapeutically effective amount of protein or other active ingredient of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein or other active ingredient of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein or other active ingredient solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein or other active ingredient of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. For transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

For oral administration, the compounds can be formulated readily by combining the active compounds with pharmaceutically acceptable carriers well known in the art. Such carriers enable the compounds of the invention to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral ingestion by a patient to be treated. Pharmaceutical preparations for oral use can be obtained from a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate. Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added. All formulations for oral administration should be in dosages suitable for such administration. For buccal administration, the compositions may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.*, gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch. The compounds may be formulated for parenteral

administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

A pharmaceutical carrier for the hydrophobic compounds of the invention is a co-solvent system comprising benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. The co-solvent system may be the VPD co-solvent system. VPD is a solution of 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant polysorbate 80, and 65% w/v polyethylene glycol 300, made up to volume in absolute ethanol. The VPD co-solvent system (VPD:5W) consists of VPD diluted 1:1 with a 5% dextrose in water solution. This co-solvent system dissolves hydrophobic compounds well, and itself produces low toxicity upon systemic administration. Naturally, the proportions of a co-solvent system may be varied considerably without destroying its solubility and toxicity characteristics. Furthermore, the identity of the co-solvent components may be varied: for example, other low-toxicity nonpolar surfactants may be used instead of polysorbate 80; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, *e.g.* polyvinyl pyrrolidone; and other

sugars or polysaccharides may substitute for dextrose. Alternatively, other delivery systems for hydrophobic pharmaceutical compounds may be employed. Liposomes and emulsions are well known examples of delivery vehicles or carriers for hydrophobic drugs. Certain organic solvents such as dimethylsulfoxide also may be employed, although usually at the cost of greater toxicity. Additionally, the compounds may be delivered using a sustained-release system, such as semipermeable matrices of solid hydrophobic polymers containing the therapeutic agent. Various types of sustained-release materials have been established and are well known by those skilled in the art. Sustained-release capsules may, depending on their chemical nature, release the compounds for a few weeks up to over 100 days. Depending on the chemical nature and the biological stability of the therapeutic reagent, additional strategies for protein or other active ingredient stabilization may be employed.

The pharmaceutical compositions also may comprise suitable solid or gel phase carriers or excipients. Examples of such carriers or excipients include but are not limited to calcium carbonate, calcium phosphate, various sugars, starches, cellulose derivatives, gelatin, and polymers such as polyethylene glycols. Many of the active ingredients of the invention may be provided as salts with pharmaceutically compatible counter ions. Such pharmaceutically acceptable base addition salts are those salts which retain the biological effectiveness and properties of the free acids and which are obtained by reaction with inorganic or organic bases such as sodium hydroxide, magnesium hydroxide, ammonia, trialkylamine, dialkylamine, monoalkylamine, dibasic amino acids, sodium acetate, potassium benzoate, triethanol amine and the like.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) or other active ingredient(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically

acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithins, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent Nos. 4,235,871; 4,501,728; 4,837,028; and 4,737,323, all of which are incorporated herein by reference.

8 The amount of protein or other active ingredient of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein or other active ingredient of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein or other active ingredient of the present invention and observe the patient's response. Larger doses of protein or other active ingredient of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 μ g to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein or other active ingredient of the present invention per kg body weight. For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein or other active ingredient of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing or other active ingredient-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalcium phosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalcium phosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability. Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt %, preferably 1-10 wt % based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells. In further compositions, proteins or other active ingredients of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired

patients for such treatment with proteins or other active ingredients of the present invention. The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, *e.g.*, amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (*e.g.*, bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA). Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

4.12.3 EFFECTIVE DOSAGE

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. More specifically, a therapeutically effective amount means an amount effective to prevent development of or to alleviate the existing symptoms of the subject being treated. Determination of the effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from appropriate *in vitro* assays. For example, a dose can be formulated in animal models to achieve a circulating concentration range that can be used to more accurately determine useful doses in humans. For example, a dose can be formulated in animal models to achieve a circulating concentration range that includes the IC_{50} as determined in cell culture (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of the protein's biological activity). Such information can be used to more accurately determine useful doses in humans.

A therapeutically effective dose refers to that amount of the compound that results in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio between LD₅₀ and ED₅₀. Compounds which exhibit high therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in human. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. See, e.g., Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p.1. Dosage amount and interval may be adjusted individually to provide plasma levels of the active moiety which are sufficient to maintain the desired effects, or minimal effective concentration (MEC). The MEC will vary for each compound but can be estimated from *in vitro* data. Dosages necessary to achieve the MEC will depend on individual characteristics and route of administration. However, HPLC assays or bioassays can be used to determine plasma concentrations. Dosage intervals can also be determined using MEC value. Compounds should be administered using a regimen which maintains plasma levels above the MEC for 10-90% of the time, preferably between 30-90% and most preferably between 50-90%. In cases of local administration or selective uptake, the effective local concentration of the drug may not be related to plasma concentration.

An exemplary dosage regimen for polypeptides or other compositions of the invention will be in the range of about 0.01 µg/kg to 100 mg/kg of body weight daily, with the preferred dose being about 0.1 µg/kg to 25 mg/kg of patient body weight daily, varying in adults and children. Dosing may be once daily, or equivalent doses may be delivered at longer or shorter intervals.

The amount of composition administered will, of course, be dependent on the subject being treated, on the subject's age and weight, the severity of the affliction, the manner of administration and the judgment of the prescribing physician.

4.12.4 PACKAGING

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may, for example, comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration. Compositions comprising a compound of the invention formulated in a compatible pharmaceutical carrier may also be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition.

4.13 ANTIBODIES

Also included in the invention are antibodies to proteins, or fragments of proteins of the invention. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} , F_{ab}' and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In general, an antibody molecule obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG₁, IgG₂, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to antibodies includes a reference to all such classes, subclasses and types of human antibody species.

An isolated related protein of the invention may be intended to serve as an antigen, or a portion or fragment thereof, and additionally can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, (for example the amino acid sequence shown in SEQ ID NO: 1351), and encompasses an epitope thereof such that an antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of related protein that is located on the surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human related protein sequence will

indicate which regions of a related protein are particularly hydrophilic and, therefore, are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, e.g., Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78: 3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each of which is incorporated herein by reference in its entirety.

Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (see, for example, *Antibodies: A Laboratory Manual*, Harlow E, and Lane D, 1988, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

5.13.1 Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable in humans such as Bacille Calmette-Guerin and *Corynebacterium parvum*, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (*The Scientist*, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

5.13.2 Monoclonal Antibodies

The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be immunized *in vitro*.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). Preferably, antibodies having a high degree of specificity and a high binding affinity for the target antigen are isolated.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for

example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13 (1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5.13.2 Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further comprise humanized antibodies or human antibodies. These antibodies are suitable for administration to humans without engendering an immune response by the human against the administered immunoglobulin. Humanized forms of antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that are principally comprised of the sequence of a human immunoglobulin, and contain minimal sequence derived from a non-human immunoglobulin. Humanization can be performed following the method of Winter and co-workers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies can also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., 1986; Riechmann et al., 1988; and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

5.13.3 Human Antibodies

Fully human antibodies relate to antibody molecules in which essentially the entire sequences of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein.

Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, et al., 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, et al., 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, et al., 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks et al. (Bio/Technology 10, 779-783 (1992)); Lonberg et al. (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al. (Nature Biotechnology 14, 845-51 (1996)); Neuberger (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The preferred embodiment of such a nonhuman animal is a mouse, and is termed the XenomouseTM as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the

immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

4 An example of a method of producing a nonhuman host, exemplified as a mouse, lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the
8 locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

12 A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another
16 mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

 In a further improvement on this procedure, a method for identifying a clinically relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds
20 immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

5.13.4 F_{ab} Fragments and Single Chain Antibodies

24 According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, et al., 1989 Science 246: 1275-1281) to allow rapid and effective identification of
28 monoclonal F_{ab} fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F_{(ab)²} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated
32 by reducing the disulfide bridges of an F_{(ab)²} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

5.13.5 Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, *Nature*, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, 1991 *EMBO J.*, 10:3655-3659.

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh *et al.*, *Methods in Enzymology*, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (*e.g.* F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan *et al.*, *Science* 229:81 (1985) describe a procedure

wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab' -TNB derivatives is then reconverted to the Fab' -thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab' -TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on

a leukocyte such as a T-cell receptor molecule (*e.g.* CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc R), such as Fc RI (CD64), Fc RII (CD32) and Fc RIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

5.13.6 Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention.

Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

5.13.7 Effector Function Engineering

It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., *J. Exp Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. *Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., *Anti-Cancer Drug Design*, 3: 219-230 (1989).

5.13.8 Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of

bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is in turn conjugated to a cytotoxic agent.

4.14 COMPUTER READABLE SEQUENCES

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled

artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. As used herein, "recorded" refers to a process for
4 storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a
8 computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer
12 readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring
16 formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing any of the nucleotide sequences SEQ ID NO: 1-13901 or a representative fragment thereof, or a nucleotide sequence at least 95% identical to any of the nucleotide
20 sequences of SEQ ID NO: 1-13901 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the
24 BLAST (Altschul et al., J. Mol. Biol. 215:403-410 (1990)) and BLAZE (Brutlag et al., Comp. Chem. 17:203-207 (1993)) search algorithms on a Sybase system is used to identify open reading frames (ORFs) within a nucleic acid sequence. Such ORFs may be protein encoding fragments and may be useful in producing commercially important proteins such as enzymes used in
28 fermentation reactions and in the production of commercially useful metabolites.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present
32 invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. As stated above, the computer-based systems of the present invention comprise a data storage means having stored

therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of a known sequence which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, Smith-Waterman, MacPattern (EMBL), BLASTN and BLASTA (NPOLYPEPTIDEIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems. As used herein, a "target sequence" can be any nucleic acid or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 300 amino acids, more preferably from about 30 to 100 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

4.15 TRIPLE HELIX FORMATION

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA.

Polynucleotides suitable for use in these methods are preferably 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 15241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Olmno, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

12 4.16 DIAGNOSTIC ASSAYS AND KITS

The present invention further provides methods to identify the presence or expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using a nucleic acid probe or antibodies of the present invention, optionally conjugated or otherwise associated with a suitable label.

In general, methods for detecting a polynucleotide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polynucleotide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polynucleotide of the invention is detected in the sample. Such methods can also comprise contacting a sample under stringent hybridization conditions with nucleic acid primers that anneal to a polynucleotide of the invention under such conditions, and amplifying annealed polynucleotides, so that if a polynucleotide is amplified, a polynucleotide of the invention is detected in the sample.

In general, methods for detecting a polypeptide of the invention can comprise contacting a sample with a compound that binds to and forms a complex with the polypeptide for a period sufficient to form the complex, and detecting the complex, so that if a complex is detected, a polypeptide of the invention is detected in the sample.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the nucleic acid probes of the present invention and assaying for binding of the nucleic acid probes or antibodies to components within the test sample.

Conditions for incubating a nucleic acid probe or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the nucleic acid probe or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization,

amplification or immunological assay formats can readily be adapted to employ the nucleic acid probes or antibodies of the present invention. Examples of such assays can be found in Chard, T., An Introduction to Radioimmunoassay and Related Techniques, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. et al., Techniques in Immunocytochemistry, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., Practice and Theory of immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology, Elsevier Science Publishers, Amsterdam, The Netherlands (1985). The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention. Specifically, the invention provides a compartment kit to receive, in close confinement; one or more containers which comprises: (a) a first container comprising one of the probes or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound probe or antibody.

In detail, a compartment kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or probe. Types of detection reagents include labeled nucleic acid probes, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the enzymatic, or antibody binding reagents which are capable of reacting with the labeled antibody. One skilled in the art will readily recognize that the disclosed probes and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

4.17 MEDICAL IMAGING

The novel polypeptides and binding partners of the invention are useful in medical imaging of sites expressing the molecules of the invention (*e.g.*, where the polypeptide of the invention is involved in the immune response, for imaging sites of inflammation or infection).

- 4 See, *e.g.*, Kunkel et al., U.S. Pat. NO. 5,413,778. Such methods involve chemical attachment of a labeling or imaging agent, administration of the labeled polypeptide to a subject in a pharmaceutically acceptable carrier, and imaging the labeled polypeptide *in vivo* at the target site.

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4.18 SCREENING ASSAYS

- Using the isolated proteins and polynucleotides of the invention, the present invention further provides methods of obtaining and identifying agents which bind to a polypeptide encoded by an ORF corresponding to any of the nucleotide sequences set forth in SEQ ID NO: 1-13901, or bind to a specific domain of the polypeptide encoded by the nucleic acid. In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by an ORF of the present invention, or nucleic acid of the invention; and
- (b) determining whether the agent binds to said protein or said nucleic acid.

- In general, therefore, such methods for identifying compounds that bind to a polynucleotide of the invention can comprise contacting a compound with a polynucleotide of the invention for a time sufficient to form a polynucleotide/compound complex, and detecting the complex, so that if a polynucleotide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

- Likewise, in general, therefore, such methods for identifying compounds that bind to a polypeptide of the invention can comprise contacting a compound with a polypeptide of the invention for a time sufficient to form a polypeptide/compound complex, and detecting the complex, so that if a polypeptide/compound complex is detected, a compound that binds to a polynucleotide of the invention is identified.

- Methods for identifying compounds that bind to a polypeptide of the invention can also comprise contacting a compound with a polypeptide of the invention in a cell for a time sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a receptor gene sequence in the cell, and detecting the complex by detecting reporter gene sequence expression, so that if a polypeptide/compound complex is detected, a compound that binds a polypeptide of the invention is identified.

Compounds identified via such methods can include compounds which modulate the activity of a polypeptide of the invention (that is, increase or decrease its activity, relative to

activity observed in the absence of the compound). Alternatively, compounds identified via such methods can include compounds which modulate the expression of a polynucleotide of the invention (that is, increase or decrease expression relative to expression levels observed in the absence of the compound). Compounds, such as compounds identified via the methods of the invention, can be tested using standard assays well known to those of skill in the art for their ability to modulate activity/expression.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention. Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like, capable of binding to a specific peptide sequence, in order to generate rationally designed antipeptide peptides, for example see Hurby et al., Application of Synthetic Peptides: Antisense Peptides," In Synthetic Peptides, A User's Guide, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak et al., Biochemistry 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control. One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods preferably contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription

from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition.

4.19 USE OF NUCLEIC ACIDS AS PROBES

Another aspect of the subject invention is to provide for polypeptide-specific nucleic acid hybridization probes capable of hybridizing with naturally occurring nucleotide sequences. The hybridization probes of the subject invention may be derived from any of the nucleotide sequences SEQ ID NOS: 1-13901. Because the corresponding gene is only expressed in a limited number of tissues, a hybridization probe derived from any of the nucleotide sequences SEQ ID NO: 1-13901 can be used as an indicator of the presence of RNA of cell type of such a tissue in a sample.

Any suitable hybridization technique can be employed, such as, for example, in situ hybridization. PCR as described in US Patents Nos. 4,683,195 and 4,965,188 provides additional uses for oligonucleotides based upon the nucleotide sequences. Such probes used in PCR may be of recombinant origin, may be chemically synthesized, or a mixture of both. The probe will comprise a discrete nucleotide sequence for the detection of identical sequences or a degenerate pool of possible sequences for identification of closely related genomic sequences.

Other means for producing specific hybridization probes for nucleic acids include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art and are commercially available and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerase as T7 or SP6 RNA polymerase and the appropriate radioactively labeled nucleotides. The nucleotide sequences may be used to construct hybridization probes for mapping their respective genomic sequences. The nucleotide sequence provided herein may be mapped to a chromosome or specific regions of a chromosome using well known genetic and/or chromosomal mapping techniques. These techniques include in situ hybridization, linkage analysis against known chromosomal markers, hybridization screening with libraries or flow-sorted chromosomal preparations specific to known chromosomes, and the like. The technique of fluorescent in situ hybridization of

chromosome spreads has been described, among other places, in Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York NY.

Fluorescent *in situ* hybridization of chromosomal preparations and other physical chromosome mapping techniques may be correlated with additional genetic map data. Examples of genetic map data can be found in the 1994 Genome Issue of Science (265:1981f). Correlation between the location of a nucleic acid on a physical chromosomal map and a specific disease (or predisposition to a specific disease) may help delimit the region of DNA associated with that genetic disease. The nucleotide sequences of the subject invention may be used to detect differences in gene sequences between normal, carrier or affected individuals.

4.20 PREPARATION OF SUPPORT BOUND OLIGONUCLEOTIDES

Oligonucleotides, *i.e.*, small nucleic acid segments, may be readily prepared by, for example, directly synthesizing the oligonucleotide by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer.

Support bound oligonucleotides may be prepared by any of the methods known to those of skill in the art using any suitable support such as glass, polystyrene or Teflon. One strategy is to precisely spot oligonucleotides synthesized by standard synthesizers. Immobilization can be achieved using passive adsorption (Inouye & Hondo, (1990) J. Clin. Microbiol. 28(6) 1469-72); using UV light (Nagata *et al.*, 1985; Dahlen *et al.*, 1987; Morrissey & Collins, (1989) Mol. Cell Probes 3(2) 189-207) or by covalent binding of base modified DNA (Keller *et al.*, 1988; 1989); all references being specifically incorporated herein.

Another strategy that may be employed is the use of the strong biotin-streptavidin interaction as a linker. For example, Broude *et al.* (1994) Proc. Natl. Acad. Sci. USA 91(8) 3072-6, describe the use of biotinylated probes, although these are duplex probes, that are immobilized on streptavidin-coated magnetic beads. Streptavidin-coated beads may be purchased from Dynal, Oslo. Of course, this same linking chemistry is applicable to coating any surface with streptavidin. Biotinylated probes may be purchased from various sources, such as, *e.g.*, Operon Technologies (Alameda, CA).

Nunc Laboratories (Naperville, IL) is also selling suitable material that could be used. Nunc Laboratories have developed a method by which DNA can be covalently bound to the microwell surface termed Covalink NH. CovaLink NH is a polystyrene surface grafted with secondary amino groups (>NH) that serve as bridge-heads for further covalent coupling. CovaLink Modules may be purchased from Nunc Laboratories. DNA molecules may be bound to CovaLink exclusively at the 5'-end by a phosphoramidate bond, allowing immobilization of more than 1 pmol of DNA (Rasmussen *et al.*, (1991) Anal. Biochem. 198(1) 138-42).

The use of CovaLink NH strips for covalent binding of DNA molecules at the 5'-end has been described (Rasmussen et al., (1991). In this technology, a phosphoramidate bond is employed (Chu et al., (1983) *Nucleic Acids Res.* 11(8) 6513-29). This is beneficial as immobilization using only a single covalent bond is preferred. The phosphoramidate bond joins the DNA to the CovaLink NH secondary amino groups that are positioned at the end of spacer arms covalently grafted onto the polystyrene surface through a 2 nm long spacer arm. To link an oligonucleotide to CovaLink NH via an phosphoramidate bond, the oligonucleotide terminus must have a 5'-end phosphate group. It is, perhaps, even possible for biotin to be covalently bound to CovaLink and then streptavidin used to bind the probes.

More specifically, the linkage method includes dissolving DNA in water (7.5 ng/ul) and denaturing for 10 min. at 95°C and cooling on ice for 10 min. Ice-cold 0.1 M 1-methylimidazole, pH 7.0 (1-MeIm₇), is then added to a final concentration of 10 mM 1-MeIm₇. A ss DNA solution is then dispensed into CovaLink NH strips (75 ul/well) standing on ice.

Carbodiimide 0.2 M 1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide (EDC), dissolved in 10 mM 1-MeIm₇, is made fresh and 25 ul added per well. The strips are incubated for 5 hours at 50°C. After incubation the strips are washed using, e.g., Nunc-Immuno Wash; first the wells are washed 3 times, then they are soaked with washing solution for 5 min., and finally they are washed 3 times (where in the washing solution is 0.4 N NaOH, 0.25% SDS heated to 50°C).

It is contemplated that a further suitable method for use with the present invention is that described in PCT Patent Application WO 90/03382 (Southern & Maskos), incorporated herein by reference. This method of preparing an oligonucleotide bound to a support involves attaching a nucleoside 3'-reagent through the phosphate group by a covalent phosphodiester link to aliphatic hydroxyl groups carried by the support. The oligonucleotide is then synthesized on the supported nucleoside and protecting groups removed from the synthetic oligonucleotide chain under standard conditions that do not cleave the oligonucleotide from the support. Suitable reagents include nucleoside phosphoramidite and nucleoside hydrogen phosphorate.

An on-chip strategy for the preparation of DNA probe for the preparation of DNA probe arrays may be employed. For example, addressable laser-activated photodeprotection may be employed in the chemical synthesis of oligonucleotides directly on a glass surface, as described by Fodor *et al.* (1991) *Science* 251(4995) 767-73, incorporated herein by reference. Probes may also be immobilized on nylon supports as described by Van Ness *et al.* (1991) *Nucleic Acids Res.* 19(12) 3345-50; or linked to Teflon using the method of Duncan & Cavalier (1988) *Anal. Biochem.* 169(1) 104-8; all references being specifically incorporated herein.

To link an oligonucleotide to a nylon support, as described by Van Ness *et al.* (1991), requires activation of the nylon surface via alkylation and selective activation of the 5'-amine of oligonucleotides with cyanuric chloride.

One particular way to prepare support bound oligonucleotides is to utilize the light-generated synthesis described by Pease *et al.*, (1994) PNAS USA 91(11) 5022-6, incorporated herein by reference). These authors used current photolithographic techniques to generate arrays of immobilized oligonucleotide probes (DNA chips). These methods, in which light is used to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays, utilize photolabile 5'-protected *N*-acyl-deoxynucleoside phosphoramidites, surface linker chemistry and versatile combinatorial synthesis strategies. A matrix of 256 spatially defined oligonucleotide probes may be generated in this manner.

4.21 PREPARATION OF NUCLEIC ACID FRAGMENTS

The nucleic acids may be obtained from any appropriate source, such as cDNAs, genomic DNA, chromosomal DNA, microdissected chromosome bands, cosmid or YAC inserts, and RNA, including mRNA without any amplification steps. For example, Sambrook *et al.* (1989) describes three protocols for the isolation of high molecular weight DNA from mammalian cells (p. 9.14-9.23).

DNA fragments may be prepared as clones in M13, plasmid or lambda vectors and/or prepared directly from genomic DNA or cDNA by PCR or other amplification methods. Samples may be prepared or dispensed in multiwell plates. About 100-1000 ng of DNA samples may be prepared in 2-500 ml of final volume.

The nucleic acids would then be fragmented by any of the methods known to those of skill in the art including, for example, using restriction enzymes as described at 9.24-9.28 of Sambrook *et al.* (1989), shearing by ultrasound and NaOH treatment.

Low pressure shearing is also appropriate, as described by Schrieffer *et al.* (1990) Nucleic Acids Res. 18(24) 7455-6, incorporated herein by reference). In this method, DNA samples are passed through a small French pressure cell at a variety of low to intermediate pressures. A lever device allows controlled application of low to intermediate pressures to the cell. The results of these studies indicate that low-pressure shearing is a useful alternative to sonic and enzymatic DNA fragmentation methods.

One particularly suitable way for fragmenting DNA is contemplated to be that using the two base recognition endonuclease, CviJI, described by Fitzgerald *et al.* (1992) Nucleic Acids Res. 20(14) 3753-62. These authors described an approach for the rapid fragmentation and fractionation

of DNA into particular sizes that they contemplated to be suitable for shotgun cloning and sequencing.

The restriction endonuclease *Cvi*JI normally cleaves the recognition sequence PuGCPy between the G and C to leave blunt ends. Atypical reaction conditions, which alter the specificity of this enzyme (*Cvi*JI**), yield a quasi-random distribution of DNA fragments from the small molecule pUC19 (2688 base pairs). Fitzgerald *et al.* (1992) quantitatively evaluated the randomness of this fragmentation strategy, using a *Cvi*JI** digest of pUC19 that was size fractionated by a rapid gel filtration method and directly ligated, without end repair, to a lac Z minus M13 cloning vector. Sequence analysis of 76 clones showed that *Cvi*JI** restricts pyGCPy and PuGCPu, in addition to PuGCPy sites, and that new sequence data is accumulated at a rate consistent with random fragmentation.

As reported in the literature, advantages of this approach compared to sonication and agarose gel fractionation include: smaller amounts of DNA are required (0.2-0.5 ug instead of 2-5 ug); and fewer steps are involved (no preligation, end repair, chemical extraction, or agarose gel electrophoresis and elution are needed).

Irrespective of the manner in which the nucleic acid fragments are obtained or prepared, it is important to denature the DNA to give single stranded pieces available for hybridization. This is achieved by incubating the DNA solution for 2-5 minutes at 80-90°C. The solution is then cooled quickly to 2°C to prevent renaturation of the DNA fragments before they are contacted with the chip. Phosphate groups must also be removed from genomic DNA by methods known in the art.

4.22 PREPARATION OF DNA ARRAYS

Arrays may be prepared by spotting DNA samples on a support such as a nylon membrane. Spotting may be performed by using arrays of metal pins (the positions of which correspond to an array of wells in a microtiter plate) to repeated by transfer of about 20 nl of a DNA solution to a nylon membrane. By offset printing, a density of dots higher than the density of the wells is achieved. One to 25 dots may be accommodated in 1 mm², depending on the type of label used. By avoiding spotting in some preselected number of rows and columns, separate subsets (subarrays) may be formed. Samples in one subarray may be the same genomic segment of DNA (or the same gene) from different individuals, or may be different, overlapped genomic clones. Each of the subarrays may represent replica spotting of the same samples. In one example, a selected gene segment may be amplified from 64 patients. For each patient, the amplified gene segment may be in one 96-well plate (all 96 wells containing the same sample). A plate for each of the 64 patients is prepared. By using a 96-pin device, all samples may be spotted on one 8 x 12 cm membrane.

Subarrays may contain 64 samples, one from each patient. Where the 96 subarrays are identical, the dot span may be 1 mm² and there may be a 1 mm space between subarrays.

Another approach is to use membranes or plates (available from NUNC, Naperville, Illinois) which may be partitioned by physical spacers *e.g.* a plastic grid molded over the membrane, the grid being similar to the sort of membrane applied to the bottom of multiwell plates, or hydrophobic strips. A fixed physical spacer is not preferred for imaging by exposure to flat phosphor-storage screens or x-ray films.

The present invention is illustrated in the following examples. Upon consideration of the present disclosure, one of skill in the art will appreciate that many other embodiments and variations may be made in the scope of the present invention. Accordingly, it is intended that the broader aspects of the present invention not be limited to the disclosure of the following examples. The present invention is not to be limited in scope by the exemplified embodiments which are intended as illustrations of single aspects of the invention, and compositions and methods which are functionally equivalent are within the scope of the invention. Indeed, numerous modifications and variations in the practice of the invention are expected to occur to those skilled in the art upon consideration of the present preferred embodiments. Consequently, the only limitations which should be placed upon the scope of the invention are those which appear in the appended claims.

All references cited within the body of the instant specification are hereby incorporated by reference in their entirety.

5.0 EXAMPLES

5.1 EXAMPLE 1

Novel Nucleic Acid Sequences Obtained From Various Libraries

A plurality of novel nucleic acids were obtained from cDNA libraries prepared from various human tissues and in some cases isolated from a genomic library derived from human chromosome using standard PCR, SBH sequence signature analysis and Sanger sequencing techniques. The inserts of the library were amplified with PCR using primers specific for the vector sequences which flank the inserts. Clones from cDNA libraries were spotted on nylon membrane filters and screened with oligonucleotide probes (*e.g.*, 7-mers) to obtain signature sequences. The clones were clustered into groups of similar or identical sequences. Representative clones were selected for sequencing.

In some cases, the 5' sequence of the amplified inserts was then deduced using a typical Sanger sequencing protocol. PCR products were purified and subjected to fluorescent dye terminator cycle sequencing. Single pass gel sequencing was done using a 377 Applied Biosystems

(ABI) sequencer to obtain the novel nucleic acid sequences. In some cases RACE (Random Amplification of cDNA Ends) was performed to further extend the sequence in the 5' direction.

4 5.2 EXAMPLE 2

Novel Contigs

The novel contigs of the invention were assembled from sequences that were obtained from a cDNA library by methods described in Example 1 above, and in some cases sequences obtained from one or more public databases. The sequences for the resulting nucleic acid contigs are designated as SEQ ID NO: 1-13901 and are provided in the attached Sequence Listing. The contigs were assembled using an EST sequence as a seed. Then a recursive algorithm was used to extend the seed EST into an extended assemblage, by pulling additional sequences from different databases (i.e., Hyseq's database containing EST sequences, dbEST version 114, gb pri 114, and UniGene version 101) that belong to this assemblage. The algorithm terminated when there was no additional sequences from the above databases that would extend the assemblage. Inclusion of component sequences into the assemblage was based on a BLASTN hit to the extending assemblage with BLAST score greater than 300 and percent identity greater than 95%.

Table 3 sets forth the novel predicted polypeptides (including proteins) encoded by the novel polynucleotides (SEQ ID NO: 1-13901) of the present invention, and their corresponding nucleotide locations to each of SEQ ID NO: 1-13901. Table 3 also indicates the method by which the polypeptide was predicted. Method A refers to a polypeptide obtained by using a software program called FASTY (available from <http://fasta.bioch.virginia.edu>) which selects a polypeptide based on a comparison of the translated novel polynucleotide to known polynucleotides (W.R. Pearson, Methods in Enzymology, 183:63-98 (1990), herein incorporated by reference). Method B refers to a polypeptide obtained by using a software program called GenScan for human/vertebrate sequences (available from Stanford University, Office of Technology Licensing) that predicts the polypeptide based on a probabilistic model of gene structure/compositional properties (C. Burge and S. Karlin, J. Mol. Biol., 268:78-94 (1997), incorporated herein by reference). Method C refers to a polypeptide obtained by using a Hyseq proprietary software program that translates the novel polynucleotide and its complementary strand into six possible amino acid sequences (forward and reverse frames) and chooses the polypeptide with the longest open reading frame.

The nearest neighbor results for SEQ ID NO: 1-13901 were obtained by a BLASTP version 2.0a1 19MP-WashU search against Genpept release 120 and Geneseq database release 200101 (Derwent), using BLAST algorithm. The nearest neighbor result showed the closest

homologue for SEQ ID NOS: 1-13901. The nearest neighbor results for SEQ ID NO: 1-13901 are shown in Table 2 below.

4 Tables 1, 2 and 3 follow. Table 1 shows the various tissue sources of SEQ ID NOS: 1-13901. Table 2 shows the nearest neighbor result for the assembled contig. The nearest neighbor result shows the closest homolog with an identifiable function for each assemblage. Table 3 contains the start and stop nucleotides for the translated amino acid sequence for which each assemblage encodes. Table 3 also provides a correlation between the amino acid sequences set forth
8 in the Sequence Listing, the nucleotide sequences set forth in the Sequence Listing and the SEQ ID NO. in USSN 09/515,126

TABLE 1

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
adult brain	GIBCO	AB3001	83 544 597-598 600-607 616 841 1004 1148 1346 1493 1974 2138 2141 2143 2161 2266 2345 2363 2511 2569 2876 2880 3001 3099-3101 3105-3106 3110-3111 3115-3117 3199 3272 3282 3284 3356 3425 3537 3634 3689 3709 3797 3810 3839 3899 4006 4021-4022 4025 4043 4194 4201 4253 4277 4297 4388 4399 4410 4667 4671 4722 4747-4748 4750 4755 4767 4845 4865 4940 5037 5075 5093 5118 5163 5171-5172 5268 5481 5523 5553 5656 5724 5894 5902 5938 6052 6170-6173 6176 6214 6307 6336 6369 6374 6793 6894-6897 6979 7058 7169 7455 7492-7493 7495-7499 7501 7504 7577 7586 7761 7792 7864 7870 8035 8065 8085 8110 8120 8140 8224 8226 8298 8372 8427 8452 8456 8535 8648 8672 8674-8679 8681- 8684 8816 8838-8839 8870 8898 9012 9041 9079 9128 9257 9264 9304 9317 9460 9503 9517 9567 9623 9734 9781 9792- 9798 9929 9964 9999 10296 10330 10469-10470 10578 10679 10778 10786 10895 10984-10986 11032 11052 11069 11130 11145 11239 11289 11402 11818 11862 11870-11876 11878- 11881 12017 12037 12127 12160 12294 12363 12375 12405 12424 12438 12467 12539 12570 12590 12615-12616 12618 12685 12688 12712 12739 12748 12830 12913 12916 12948- 12950 13002 13064 13073 13083 13141 13150 13153 13164- 13166 13257 13391 13456 13479 13489 13492 13494 13499 13501 13503 13560 13595-13596 13627 13645 13679 13782 13795 13861 13866 13869 13882
adult brain	GIBCO	ABD003	67 83 142 443 587 598 608-609 611 613-624 633 731 734 737- 742 760 799-800 809 1148 1152 1167-1184 1193 1346 1433- 1516 1552 1575 1671 1756 1774 1833 1974 2138 2145 2176- 2178 2237 2266 2299-2301 2303-2306 2343 2363 2412 2444 2449 2511 2516 2555 2569 2576 2614 2716 2809 2876 2911 2926 3001 3093 3114 3119 3121-3124 3126 3128-3130 3234 3254-3256 3258-3263 3265-3267 3270-3274 3276-3277 3280- 3281 3284 3286 3348 3356 3378 3435 3459 3484 3537 3548 3595 3605 3625 3627 3634 3686-3697 3700 3702 3709 3711 3720 3722 3737 3757 3797 3804 3810 3839 3856 4006 4019 4025 4040 4055 4057-4058 4060 4078 4194 4201 4246 4253 4277 4282 4390 4405 4412 4431 4620 4622 4641 4689 4751- 4764 4791 4808 4837 4845 4847-4849 4852-4858 4860-4862 4864-4869 4940 4957 4962 4972 4998 5021 5031 5037-5038 5040 5076 5093 5108 5118 5167 5169 5171-5172 5251-5261 5263-5265 5270 5364 5401 5481 5492 5521 5523 5535 5656 5674 5693 5766 5788 5817 5906-5909 5938 6005 6027 6057 6064 6147 6178 6180-6182 6189 6214 6229-6233 6254 6272 6369 6371 6421-6426 6555 6595 6598 6601 6799 6803 6825 6836 6886 6894 6913 6972 6995 7058 7104 7130 7133 7148 7164 7169 7339 7347 7386 7426 7455 7494 7502 7507 7509 7511-7512 7516 7520 7584-7587 7590-7596 7598-7601 7603- 7604 7608 7632 7677 7743 7748 7761 7768 7792 7797 7807 7815 7839 7849-7861 7864 7870 7930 7937 8035 8065 8067 8080 8087 8095 8110 8120 8139-8140 8209 8224 8226 8235 8246 8262 8285 8298 8320 8323 8336 8354 8361 8365 8370 8375 8387 8452 8456 8535 8556 8576-8577 8603 8630 8648 8674 8685-8686 8688-8690 8693 8695 8702 8712 8742 8760- 8761 8763-8764 8766-8769 8813 8815-8816 8830 8834 8838- 8839 8848 8863 8870 8898 8921 8943-8944 8951 8989 9010 9041 9050-9056 9058-9064 9076 9079 9092 9097 9128 9144- 9145 9257 9264 9271 9278-9279 9304 9315 9317 9455 9466 9472 9475 9480 9503 9511 9517 9525 9539 9689 9734 9773 9781 9791 9799-9802 9847 9852 9873 9928-9929 9964 9999-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			10001 10003-10004 10053 10175 10267 10276 10330 10349 10434 10449 10466 10471-10474 10492 10496 10509 10566 10578 10597-10599 10645 10679 10788 10891 10948 10988- 10990 11032 11039 11041-11043 11052 11065 11069 11105 11108 11130 11145 11167 11196 11203-11207 11209 11239 11399 11401-11402 11406 11459 11470 11604 11606 11642 11761 11818 11862 11877 11882-11884 11886 11889-11893 11944-11946 11981 11988 12016 12019 12022 12037 12083 12127 12143 12164-12165 12168-12171 12178 12195 12236 12265 12305 12327 12363 12375 12405 12423-12424 12430 12438 12546 12570 12590 12594 12612 12615-12618 12630 12670 12674 12685-12688 12693 12704 12706-12707 12748 12772 12830 12885 12904 12913 12916 12923 12933 12951 12956 12993 13001 13020-13021 13038 13047 13064 13072- 13073 13084-13085 13092 13117 13142 13167-13171 13191 13254 13257 13260 13295 13390-13391 13394 13456 13479 13483 13489 13497 13501 13503 13505-13507 13512 13516 13546 13551 13555 13575 13590 13592 13597 13613-13614 13645 13649 13659 13711 13782 13795 13838 13861 13869 13875 13882 13884-13885 13888 13892 13896
adult brain	Clontech	ABR001	142 858 1542 2174 2407 2483 2652 3272 3287 3460 3492 3535 3595 3737 3839 4005 4060 4282 4434 4791 4972 5040 5293 5523 5530 5535 5788 5906 6082 6601 6799 6980 7373 7577 7587 7759 7788 7851 8081-8082 8110 9167 9455 9466 9781 9928 10422 10774 10791 11069 11401 11406 11459 11604 11607 11791 11818 11865 11961 11979 12022 12122 12160 12327 12442 12594 12615 12640 12670 12705 12935 12957 12985 13047 13197 13257 13456 13511-13512 13546 13554 13646 13793 13885 13889 13893
adult brain	Clontech	ABR006	6 67 1004 1908 3272 3286 3548 4011 4282 4998 5923 5928 6374 6730 6815 6867 6890 7067 8365 9264 9729 9780 10776 11587 11618 12596 12601 12605 12704 12749 12754 12951 13047 13051 13090 13479 13488 13498-13499 13503 13512 13575 13882
adult brain	Clontech	ABR008	6 11 21 41 51 88 142 364 376 579 598 651 736 800 1050 1148 1184 1251-1265 1291 1346 1404 1479 1529 1543 1671-1674 1697 1699-1710 1820 1830 1832-1838 1840 1848-1849 1908 1914 1919 1927 1957 1964 1974 1976 1978-1979 2005-2006 2050 2081 2090 2110-2111 2129 2150 2174 2200 2310 2327 2342 2408-2410 2420 2444 2449 2461-2467 2484 2490 2499- 2506 2511 2553 2574 2576 2611 2652 2809 2827 2866 2894 3032 3207 3535 3591 3610 3634 3715 3722 3737 3766-3770 3819 4006-4007 4011 4025 4032 4060 4078 4095 4109 4128 4143-4155 4182 4194 4247-4257 4277 4282 4294 4296 4310 4330 4348 4355 4360 4381 4395 4399 4411 4431 4543 4641 4662 4694 4698 4767 4781 4791 4808 4833 4837 4985 5001 5022 5040 5075 5094 5108 5163 5303-5306 5308-5314 5320 5380 5523 5553 5615 5625-5626 5634 5638-5644 5701 5706 5711 5727-5742 5766 5772 5775 5783 5801 5814 5817 5820- 5821 5829 5837 5851 5855 5858 5864 5867 5874 5885 5890 5897 5901 5906 5923 6057 6125 6214 6223 6288 6302 6456- 6464 6545 6598 6601-6602 6624 6676-6685 6699 6726 6728 6746-6749 6765 6799 6805 6854 6860 6893-6894 7004-7007 7049 7076 7078 7081-7083 7105 7117 7119 7133 7153 7166 7431 7579 7708 7768 7849 7900-7905 8018 8083-8084 8095 8110 8196-8208 8262 8288 8312 8320 8331 8336 8356 8375 8452 8482 8633 8681 8710 8739 8777 8815 8817 8830 8839 8963 8965 8983 9010 9097 9100 9102-9108 9111 9128 9142 9257 9264 9313 9364 9378-9384 9401 9454-9455 9458 9460- 9464 9503 9509 9511 9515-9516 9522 9528-9529 9533 9539 9542 9544 9573 9577 9646 9773 9780 9924 10000 10025-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			10029 10097 10148 10209 10218-10223 10225-10229 10267 10275-10276 10284 10292 10296 10303 10313 10326 10329- 10331 10333-10334 10343 10346 10393 10430 10494 10496 10513 10542 10557 10613-10616 10679 10688 10691 10719- 10721 10729 10743 10758 10760 10776 10782 10786 10795 10895 11100 11114 11132 11195 11240 11242-11254 11401 11406 11437 11454 11459 11462 11466-11473 11475-11476 11519 11532-11535 11550 11553 11555-11556 11559 11588- 11589 11606 11615 11618 11621 11627-11628 11633 11761 11791 11807 11818 11932 11955 12006 12039 12041 12092 12212-12224 12231 12236 12305 12363 12368 12396-12399 12405 12424 12439 12442 12465-12466 12468 12477 12479- 12482 12490 12521 12546 12552-12553 12576-12577 12579 12582 12585 12590 12601 12609 12617-12618 12636 12658 12707 12725 12735-12736 12749 12754 12776-12779 12859 12868 12894 12905 12909 12940 12955 12959 12977 12980 12990 13002 13004-13005 13020 13035 13038 13042-13044 13047 13051-13052 13056 13062 13073 13082-13083 13196 13249 13280 13311-13312 13336 13387 13417 13421-13426 13436 13445 13456 13458 13479-13482 13488 13490 13494- 13495 13497-13500 13503 13507 13512 13516 13533 13546 13554-13555 13590 13613 13630 13649 13659 13670 13678 13713 13724 13769 13793-13794 13808 13827-13828 13838 13861 13867-13868 13875 13882 13884-13885 13888-13889 13893 13896 13898
adult brain	Clontech	ABR011	1006 1257 3797 4006 4025 5535 6057 7169 7870 8262 8937 8966 9257 10778 12736 13394 13679 13793 13861
adult brain	BioChain	ABR012	88 598 1007 1134 2597 3557 3590 3627 3797 4006 4192 4246 4282 4391 4940 5523 5535 6288 6338 7138 8110 8898 9076 9401 9455 9476 10772 11061 11114 12989 13394 13511 13866
adult brain	Invitrogen	ABR013	598 2614 3191 4355 4391 5523 5788 8085 8486 11513 12521 12989 13861
adult brain	Invitrogen	ABT004	40 51 598 1050-1057 1148 1777-1778 1947 1976 2270-2272 2327 2490 2617 3050 3600-3602 3722 3987 4390-4391 4434 4543 4689 5031 5157-5159 5167 5169 5466 5505 5682-5683 5701 5766 5778 5794 5902 6147 6367-6371 6459 6545 6709 6728 6783 6801 6971 7104 7175 7815 7839 7864 8139 8342 8345 8355 8363 8372 8452 8633 8963 8975-8976 9012 9133 9423-9424 9511 9515 9517 9528 9556 9827 9949 10260 10267 10275 10570-10571 10733 10767 11132 11159 11406 11459 11932 12009 12092 12109-12111 12127 12283 12428 12511 12579 12605 12725 12747 12830 12885-12886 12910 12913 12954 12987-12989 13051 13054 13062 13073 13090 13249- 13253 13438 13445 13456 13489 13500 13512 13516 13533 13546 13590 13622 13649 13683-13684 13713 13803 13838 13861 13866 13896
cultured preadipocytes	Stratagene	ADP001	1134 1346 2343 2614 3272 3426 3610 3720 3839 3885 4011 4277 4282 4297 4346 4388 4391 4405 4434 4641 4833 4940 4985 5018 5030 5040 5163 5167 5523 5581 5778 5788 5794 5895 5951 6082 6147 6272 6607 7067 7141 8093 8235 8285 8312 8363 8629 8648 8830 8839 9290 9401 9466 9503 9781 10346 10470 10776 10795 10971 11108 11170 11513 11818 12034 12037 12046 12093 12375 12387 12405 12424 12570 12636 12670 12674 12688 12735 12749 12913 12940 13126 13163 13295 13489 13494 13497 13499 13511 13516 13575 13652-13653 13866 13888-13889
adrenal gland	Clontech	ADR002	8 83 142 225 351 443 551 569 731 864 1134 1266-1271 1273- 1274 1276-1292 1294-1295 1381 1391 1544-1545 1658 1671 1908 1959 1983 2010 2023 2145 2175 2283 2310 2328-2334 2343 2444 2449 2510 2522 2576 3032 3069 3153 3166 3272

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			3378 3416 3548 3625 3709 3711 3771-3788 3790-3791 3797 3839 3870 3899 3985 4019 4054 4060 4109 4173 4192 4194 4201 4253 4277 4282 4389 4391 4395-4396 4431 4667 4687 4694 4783 4957 4966 4985 4998 5037 5108 5293 5316-5323 5325-5336 5481 5505 5527 5531-5533 5560 5628 5656 5701 5766 5865 5874 5902 5939 5979 6020 6052 6057 6227 6288 6354 6405 6449 6465-6482 6521 6603 6726 6894 6979 7008- 7011 7155-7156 7204 7604 7634 7845 7871 7906-7912 7915- 7918 7920-7930 8022 8067 8085-8086 8095 8110 8116 8224 8262 8363 8365 8412 8520 8535 8554 8699 8742 8831 8870 8950-8951 9002 9010 9012 9097 9109-9119 9121-9127 9190 9264 9280 9304 9317 9455 9457 9495 9503 9553 9556 9586 9709 9780-9781 9895 9927 10007 10030-10032 10034-10035 10037-10045 10119 10277 10284 10346 10595 10617-10620 10623-10627 10645 10675 10679 10760-10761 10766 10774 10782 11108 11194 11255 11258-11270 11289 11400 11406 11457 11519 11588 11600 11621 11626 11818 11952 12080 12159 12225 12227-12230 12232-12237 12239-12240 12242- 12249 12251 12305 12363 12375 12404-12405 12424 12439 12577 12599 12601 12630 12636 12657-12658 12663 12688 12693 12706 12713 12715 12735 12749 12754 12780-12787 12848 12863 12909 12913 12923 12957 12990 13006-13007 13020-13021 13064 13095 13104 13295 13313 13315 13388- 13389 13391 13456 13473 13494 13507 13515 13546 13613 13631 13679 13725-13733 13858 13866 13872 13883-13884 13888-13889
adult heart	GIBCO	AHR001	51 83 88 94 221 239 360 366-367 404 410-411 413 415 458- 459 461 465-468 471 473-478 486 545-546 559 567 616 625- 630 743-744 799 802-806 808 810-835 837-842 959 1004 1066- 1085 1134 1178 1184-1193 1346 1512 1516 1546-1547 1556 1575 1671 1727 1774 1829 1959 1976-1977 2090 2096 2108 2110 2128 2138 2145-2147 2161 2179 2195-2198 2257 2276 2278-2281 2302 2307-2309 2363 2398-2399 2409 2411-2412 2444 2449 2497 2516 2529 2563 2569 2575-2576 2597 2605 2614 2617 2762 2809 2816 2879-2880 2911-2924 2926 2961 2978-2980 2985-2986 2993 2995-3002 3032 3042 3051 3058 3069 3081 3091-3094 3109 3114 3132-3133 3135 3137-3138 3141 3191 3196 3199 3215 3263 3272 3282-3286 3317 3349- 3350 3353-3359 3361-3362 3364-3367 3370-3393 3396-3399 3403 3406 3425 3451 3465-3466 3479 3500 3503 3537-3538 3544 3548 3550 3555 3557 3590-3591 3595 3604 3606-3612 3614-3621 3623-3627 3634 3689 3697-3698 3701-3709 3711- 3713 3720 3722 3737 3757 3797 3839 3885 3898 3988-3989 3996 4005-4006 4008 4010-4011 4019 4021-4022 4025 4040 4043 4054-4055 4058-4060 4078 4183 4192 4194 4201 4246 4253 4269 4277 4282 4341 4351 4391 4403 4405 4434 4517 4543 4553 4590 4615 4622 4631 4633-4634 4641 4654 4664 4666-4667 4672-4675 4688-4689 4693-4694 4738 4740 4755 4783 4828 4870-4871 4905-4906 4909-4915 4917-4919 4921- 4924 4926-4927 4940 4957 4972 4985 4991 4998 5001 5030 5037-5038 5040 5076 5118 5163 5171-5175 5177-5178 5180- 5182 5266-5268 5380 5422 5481 5490 5492 5506-5507 5523 5534-5535 5581 5656 5682 5711 5740 5766 5788 5895 5908 5923-5924 5938 6047 6057 6083 6085 6104 6110-6111 6117 6147 6184-6185 6189 6195 6215 6255-6257 6259-6266 6268 6272 6288 6307 6336 6375-6379 6382 6427-6429 6458 6555 6588 6595 6607 6629 6665 6689 6765 6767 6799 6815 6871- 6873 6879 6881-6882 6898 6926-6928 6975-6978 6987 7058 7090 7148 7313-7314 7341 7343-7344 7346-7347 7350 7354 7359 7362 7373 7380 7394 7402 7407-7408 7410 7413 7415- 7416 7418-7419 7426 7431 7468 7473 7480 7494 7505 7513-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			7516 7520 7544 7561 7584 7587 7599 7601-7604 7635 7638- 7643 7645-7649 7651-7655 7657 7659-7662 7733 7735 7743 7748 7783-7796 7815 7852 7857 7862-7863 7865-7870 7930 7933 7983 8062-8065 8067 8087-8088 8093 8095 8110 8116 8120 8139-8140 8224 8226 8235 8262 8298 8336 8344-8345 8354 8356 8363 8368 8372 8378 8387 8410 8427 8452 8456 8531-8532 8534-8535 8563-8569 8572 8576-8577 8592-8593 8597 8603 8606 8610 8613-8614 8616-8617 8646 8648 8670 8681 8691 8698-8699 8702 8712 8742 8756 8760 8763 8795 8807-8809 8811-8814 8816-8819 8821-8833 8835-8839 8858 8863 8870 8898 8921 8927 8936 8939 8943 8946 8950-8951 8966 8988-8992 8994-8995 9010 9049 9059 9065-9067 9070- 9072 9076 9097-9098 9167 9190 9257-9260 9262 9269 9281 9287 9301 9304 9315 9317 9401 9454-9455 9466 9476 9480 9484 9556 9577 9612 9689 9698 9720-9721 9734 9741-9743 9747-9750 9758 9781 9791 9804 9871-9882 9884-9885 9928 9939 9942 9954-9960 9999-10000 10005 10175 10179 10275 10284 10292 10296 10329-10331 10346 10400 10422 10430- 10431 10437 10442 10444-10447 10475 10511-10512 10514- 10521 10557 10576-10577 10616 10645 10679 10691 10729 10742 10744 10772 10774 10777-10778 10782 10788 10839 10891 10894-10895 10902 10917-10920 10937 10942 10946 10948 10969-10970 10992 11032 11044-11045 11061 11066- 11074 11108 11114 11132 11145 11153 11165-11170 11173 11205 11208 11210-11215 11283 11289 11386 11388 11401- 11402 11406 11462 11559 11565 11576 11596 11606 11615 11620 11744 11788-11789 11793 11818 11823-11825 11831- 11832 11869 11894 11947 11961 11982-11989 12000 12006 12009 12011 12019-12020 12028 12037 12044 12078 12081 12093 12119-12122 12143 12160 12166 12172-12175 12177- 12179 12197 12305 12335 12363 12375-12376 12383 12387 12400 12402 12405 12424 12428 12438 12479 12521 12523 12546 12560 12564 12570 12590 12599 12601 12605 12609 12611 12616-12618 12653 12662-12663 12670 12674 12688 12717-12720 12734 12752 12754 12772 12905 12907 12914 12916-12917 12923 12925 12940 12961 12963-12965 12989 12991 12993 13020-13021 13033 13035 13072-13073 13082- 13083 13104 13117 13126 13132 13136 13141-13142 13148 13169 13203-13210 13212 13260-13261 13293 13295 13326 13377 13394 13413 13442 13456 13477 13480 13488 13490 13494-13496 13501-13503 13506-13507 13511 13516 13533 13568 13570-13571 13575 13582 13592 13613 13624-13630 13632 13644 13646 13659-13660 13678-13679 13689 13701 13711-13713 13775 13782 13795 13797 13866-13869 13872 13882 13884-13885 13893
adult kidney	GIBCO	AKD001	49 67 83-84 142 354 405-407 415-429 431-432 445 460 462 479-484 486 488 492-493 524 548-549 598 616 631-638 744 787 809 841 1004 1068 1086 1160 1163-1166 1171 1184 1193 1346 1359 1449 1479 1516 1552 1556 1671 1724 1727 1774 1826 1858 1914 1974 1976 1978-1979 2081 2097-2099 2111- 2113 2117-2118 2129-2130 2138 2145 2148-2150 2161 2186 2218 2266 2268 2302 2310 2327 2343 2363 2409 2412 2444 2449 2468 2483 2523 2569 2576 2614 2617 2827 2845 2876 2910 2915 2926-2931 2933-2934 2938-2943 2945-2947 2955- 2956 2976 2981 2983-2984 3001-3016 3018 3053 3109 3114 3140 3142-3146 3149-3150 3199 3254 3265 3272 3283-3284 3286 3333 3350 3356 3378 3406 3435 3445 3460 3492 3503 3535 3537 3544 3548 3590-3591 3598 3625 3627 3634 3676- 3677 3679-3685 3689 3697 3709 3711 3720 3722 3737 3757 3797 3808 3810 3839 3885 3989 4005-4006 4011 4019 4022 4025 4040 4043 4054-4055 4060 4078 4109 4192 4194 4201

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			4246 4253 4269 4277 4341 4354 4387-4388 4390 4398 4402 4405 4410 4434 4473 4540 4543 4583 4591-4592 4607 4637 4640-4641 4649 4654 4665 4668 4676-4677 4680-4685 4688- 4689 4711-4712 4751 4758 4766-4768 4783 4808 4833 4836- 4837 4845 4874 4904 4940 4957 4962-4963 4972 4983 4991 4998 5022 5037 5040 5076 5093 5118 5143 5163 5171-5172 5246-5249 5281 5362 5364 5380 5422 5481 5521 5523 5526- 5527 5535 5656 5693 5726 5740 5766 5769 5778 5788 5794 5894 5902 5908 5911 5916-5917 5923 5928 5938 5990 6005 6049-6051 6057 6078 6082 6086 6088 6105-6107 6112-6117 6120-6122 6147 6159 6186-6189 6215 6257 6272 6288 6369 6418 6423 6430 6555 6595 6598 6738 6743 6765 6767 6793 6799 6805 6815 6836 6857 6867-6870 6872-6873 6878 6884 6886 6893 6899-6900 6931 6947 6976 6979 6988 7024 7045 7058 7104 7118 7155 7275 7281 7306 7312 7338 7347-7348 7351-7352 7355 7357 7359-7363 7366 7369 7371-7373 7381 7383 7386 7400 7402 7404-7406 7408 7420 7422 7424 7426- 7428 7430-7431 7433-7435 7439 7455 7465-7468 7494 7502 7506 7517-7521 7579 7587 7604 7634 7639 7642 7733 7735 7743 7748 7792 7797 7839 7842-7846 7848 7852 7857 7862 7864 7870 7930 7933 8065 8077 8084 8087 8093 8095 8105 8110 8116 8120 8139-8140 8156 8224 8226 8235 8262 8320 8336 8345 8351 8354 8359 8364 8368 8370 8372 8375 8377 8387 8427 8452 8456 8461 8486 8518 8520 8527 8535 8563- 8564 8566 8572-8573 8575-8577 8580-8583 8585 8588-8589 8597 8603 8618-8621 8623 8625-8626 8628 8630 8634 8647- 8650 8664 8674 8677-8678 8691 8694 8701-8704 8706 8711 8722 8740 8742 8763 8792 8798 8806 8812-8813 8816 8830 8838-8839 8848 8853 8863 8876 8898 8921 8935 8943-8944 8948 8951 8966 8989 9012 9041 9047-9049 9076 9092 9128 9137 9167 9218 9244 9249 9257 9264 9287 9304 9315 9317 9424 9455-9457 9466 9472 9475 9484 9503 9511 9517 9529 9536 9542 9544 9558 9612 9683 9699 9703 9722-9723 9725 9734 9744 9752-9755 9758 9772-9773 9780-9781 9805-9807 9841 9843 9927-9929 9939 9942 9969 9998-10000 10007 10175 10275 10284 10287 10292 10319 10346 10376 10423- 10424-10431 10442 10446 10448 10450 10475 10480 10496 10542 10557 10645 10679 10774 10778 10782 10788 10895 10921-10928 10947 10949-10953 10986 10994-10996 11032 11052 11061 11069 11114 11130 11132 11143 11145 11197- 11202 11205 11208 11212 11239 11289 11401-11402 11406 11459 11513 11586 11596 11604 11607 11618 11620 11695 11711 11759 11761 11790-11791 11793-11794 11818 11820- 11822 11834-11836 11857 11865 11869 11895-11899 11950 11970 12006 12022 12041 12078 12143 12159-12160 12178 12195 12197 12256 12265 12305 12327 12359 12363 12375 12387 12405 12424 12428 12438 12442 12467 12511 12521 12523 12535 12539 12546 12564 12570 12590 12599 12601 12609-12611 12616 12618 12630 12653 12656 12664 12666- 12667 12670 12674 12688-12689 12691 12739 12754 12830 12834 12904 12913-12914 12916-12917 12923 12940-12941 12951-12952 12956 12972 12976-12977 12993 12999 13002 13052 13062 13064 13066 13072-13073 13082-13083 13095 13104 13127 13131 13133 13136 13141 13143-13146 13148 13154-13155 13169 13172 13184 13195-13196 13249 13254 13260 13263 13280 13295 13307 13319 13394 13442 13456 13477 13479-13480 13488-13490 13492 13494-13495 13497- 13503 13506-13507 13512 13515-13516 13546 13551 13554- 13556 13572-13574 13590 13592 13613 13627 13631 13644- 13645 13656 13659-13660 13665 13670 13710 13713 13776 13782 13795 13859-13860 13864 13866-13868 13872 13882-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			13885 13888 13891-13892
adult kidney	Invitrogen	AKT002	67 142 550-552 598 639-641 1004 1015 1493 1516 1947 2215 2299 2343 2363 2449 2618 3054-3055 3152-3153 3155-3157 3434 3535 3590 3709 3797 3808 3839 3885 4011 4022 4025 4040 4253 4277 4391 4405 4671 4759 4767 4769 4837 4949 4972 5001 5035 5037 5052 5108 5526 5581 5615 5726 5788 5895 6062 6139 6190-6191 6803 6900 6947 6975 7468-7469 7473 7733 8095 8110 8139 8262 8323 8361 8363 8375 8520 8539 8648 8711 8798 8912 8950 8966 8983 9076 9264 9368 9510 9517 9665 9703 9734 10175 10476 10791 10989 10997 11132 11618 11745 11900 12006 12039 12160 12363 12375 12405 12424 12685 12702 12707 12904 13035 13060 13104 13136 13295 13394 13456 13488 13495 13501 13512 13533 13554 13583 13644 13670 13679 13696 13713 13795 13866 13888 13891
adult lung	GIBCO	ALG001	83-84 553 598 642-644 650 747 975 1004 1009 1015-1022 1449 1516 1816 2161 2186 2215 2343 2444 2968 3056 3158 3160-3162 3345 3466 3503 3519 3566 3568-3573 3595 3709 3797 3810 3839 3885 4025 4039 4059 4194 4405 4622 4755 4767 4770 4797 4865 4940 4949 4963 4972 4987 4991 4998 5001 5117-5129 5171-5172 5233 5401 5481 5581 5724 5788 5938 5960 6123 6125 6140 6215 6322 6336 6343-6348 6371 6886 6966-6967 7024 7143 7275 7441 7444 7502 7522-7523 7749-7752 8093 8110 8140 8336 8345 8375 8378 8449 8535 8612 8622 8635 8648 8651 8674 8702 8707-8708 8838-8839 8898 8941-8942 8944 8948 8951 9076 9128 9457 9466 9475 9497 9503 9544 9567 9703 9756 9758 9808-9810 9843 9873 9926 9999 10161 10175 10275 10329 10344 10400 10458 10554-10555 10796 10998 11032 11046 11069 11132 11144- 11145 11483 11627 11818 11837 11901 12006 12028 12039 12041 12087-12092 12146 12363 12375 12424 12438 12539 12570 12601 12617 12661 12670 12674 12688 12738 12749 12754 12904 12940 12974 13062 13173 13195 13232 13234 13260 13295 13307 13456 13472 13477 13490 13494 13497- 13498 13569 13584 13592 13660 13663-13666 13670 13743 13776 13882 13885 13889 13891
lymph node	Clontech	ALN001	83 142 364 487 495-497 554 629 645-646 648-650 716 938-951 953-962 1134 1516 1549 1671 1774 1976 2138 2225-2232 2234-2235 2340 2879 3019-3020 3057 3103 3163-3165 3272 3356 3498-3505 3507-3513 3515-3516 3538 3548 3628 3697 4194 4201 4253 4405 4641 4687-4688 4771-4772 4783 4808 4845 4963 4972 4987 4998 5042-5065 5076 5163 5504 5523 5835 5895 5917 6027 6142 6192 6272 6288 6308-6311 6313- 6314 6765 6805 6871 6949-6951 7700-7705 7707-7709 8085 8088 8091 8110 8235 8375 8387 8432 8629 8631 8633 8648 8677 8709 8713-8715 8830 8863 8887-8889 8891-8896 8943- 8944 8966 9010 9076 9111 9128 9142 9222 9455 9472 9520 9544 9734 9774 9780 9811 9905-9907 9928 9939 9999 10027 10129 10296 10439 10452 10501 10543-10545 10679 10777- 10778 10788 10891 10999-11000 11111-11113 11115 11130 11145 11344 11406 11513 11584 11885 12006 12028 12050- 12056 12143 12256 12363 12405 12442 12570 12674 12690 12913 12917 12940 12968-12970 13173 13220-13221 13394 13400 13492 13503 13511 13533 13630 13642 13645 13713 13868 13885 13889 13891
young liver	GIBCO	ALV001	211 498 598 651-653 1008-1014 1193 1264 1575 1976-1977 2131 2161 2254-2255 2269 2363 2568 2617 2627 2633 2636 2961 3021 3059 3093 3166 3215 3272 3356 3378 3426 3479 3559-3565 3590 3597 3627 3634 3673 3709 3797 3810 3885 3993 4006 4011 4019 4025 4194 4246 4253 4277 4422 4426 4431 4434 4437-4438 4634 4654 4687 4714 4722 4755 4773-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			4774 4808 4957 5001 5037 5052 5113-5115 5163 5167 5171 5508 5510 5526 5581 5616 5693 5726 5757 5772 5788 5928 6125 6141-6142 6193 6288 6340-6342 6589 6765 6815 6886 6901 7024 7118 7141 7442 7524 7735 7747-7748 7792 7852 7870 7924 7930 8066 8110 8120 8262 8375 8378 8518 8520 8648 8652 8691 8702 8716-8718 8816 8838-8839 8938-8940 9097 9119 9263-9264 9301 9317 9424 9454-9455 9544 9689 9703 9734 9758 9775 9925 9947 10393 10477 10769 10774 11001 11132 11140-11142 11173 11208 11318 11406 11587- 11588 11725 11804 11902 12081-12086 12118 12160 12178 12375 12377 12405 12424 12479 12511 12570 12599 12601 12618 12670 12674 12688 12737 12830 12913 12916 12933 12953 12977 12993 13047 13062 13073 13126 13169 13174 13230-13231 13295 13488-13489 13494 13498-13499 13502 13506-13507 13575 13592 13646 13660-13662 13670 13866 13868-13869 13882 13888 13901
adult liver	Invitrogen	ALV002	6 25 60 142 598 1004 1213 1296-1301 1381 1493 1513-1514 1977 2139 2161 2269 2310 2335 2342 2400 2413 2449 2458 2497 2568-2569 2576 2636 2809 2827 2880 2926 3471 3484 3503 3597 3722 3792-3796 3885 3994-3995 4025 4060 4201 4326 4422 4426 4618 4689 4767 4786 4985 4998 5093 5163 5337-5339 5511 5526 5581 5693 5701 5724 5726 5757 5895 5922-5923 5979 6020 6027 6083 6125 6192 6195 6253 6333 6346 6483-6485 6716 6765 6797 6975 7169 7422 7468 7614 7642 7807 7932 8089 8110 8140 8262 8323 8378 8633 8677 8711 8740 8759 8786 8834 8839 8944 9002 9128-9129 9264- 9265 9282 9466 9484-9485 9517 9677 9700 9773 10007 10046- 10047 10135 10616 10669 10777 11032 11114 11132 11142 11194 11271 11389 11462 11502 11560 11587 11602 11818 11980 11989 12086 12160 12195 12253-12254 12316 12327 12363 12378-12379 12411 12424 12511 12570 12630 12693 12706 12788-12789 12840 12863 12913-12914 13047 13062 13072-13073 13090 13242 13256 13378-13379 13389 13479 13487 13489 13497 13555 13734-13738 13859 13864 13889
adult liver	Clontech	ALV003	346 2529 3548 3797 3885 4438 4940 5101 5801 5902 9597 10769 10778 11587 11927 12086
adult ovary	Invitrogen	AOV001	6 13 40 67 83 88 142 196 444 522 555-560 577 579 598 609 654-657 659-665 667-668 708 740 745-749 751-754 756-761 806 841 871 1004 1023 1028-1034 1036-1039 1041-1047 1055 1087-1115 1119 1151-1162 1298 1346 1359 1456 1493 1507 1516 1658 1697 1752 1774 1812 1826 1848 1914 1974 1976- 1977 1979 1983 2099 2111 2138 2153-2155 2161 2175 2180- 2181 2186 2258-2267 2284-2286 2288-2290 2298-2299 2342- 2343 2449 2483 2523 2529 2555 2569 2576 2591 2597 2618 2708 2750 2783 2818 2839 2926 2961-2962 2988 3007 3022 3031 3060-3061 3063 3069 3166-3172 3174-3175 3177-3189 3226 3272 3286 3288-3289 3291-3293 3295-3299 3435 3450 3460 3479 3486 3503 3535 3577-3589 3612 3627 3629 3631- 3643 3673 3675 3720 3722 3737 3797 3806 3810 3812-3813 3839 3885 3985 4006 4012-4014 4023 4025 4040 4043 4060 4078 4133 4192 4194 4201 4246 4269 4277 4282 4341 4362 4381 4383 4385 4388 4390-4391 4396 4399 4402 4405 4410 4434 4465 4473 4515 4543 4582 4610 4654 4689 4694 4715- 4717 4722 4759 4767 4775-4782 4836-4837 4873-4878 4880 4940 4944 4957 4960 4962-4964 4972 4975 4981 4985 4998 5001-5002 5018 5030 5037 5040 5045 5075-5076 5093 5108 5135-5136 5138-5146 5148 5163 5191-5209 5213 5238-5245 5262 5374 5380 5451 5455 5490 5503 5505 5521 5523 5527 5560 5581 5674 5701 5724 5757 5778 5783 5788 5794 5817 5874 5894-5895 5902 5906 5908-5909 5916-5917 5923 5932 5938 5979 5989-5990 6005 6027 6048 6054 6057 6061 6078

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			6082 6086 6125 6140 6143-6144 6165 6171 6192 6194-6200 6215 6235-6239 6241 6270 6288 6307 6333 6336 6354-6360 6362-6364 6374 6385-6392 6410 6412 6415-6417 6458 6461 6508 6555 6583 6595 6598 6604 6607 6624 6626 6629 6708 6765 6767 6793 6797 6799 6801 6805 6825 6860 6870-6871 6873 6886 6888 6900 6902-6904 6915-6917 6947 6969-6970 6975 6980-6987 6998 7054 7058 7104 7109 7118 7133 7137 7141 7155 7166 7169 7171 7191 7204 7281 7386 7408 7431 7443 7468 7471-7472 7494 7507 7525-7528 7604-7609 7614 7642 7687 7716 7729 7762-7763 7765-7767 7769-7771 7773- 7775 7788 7802-7818 7829-7835 7838-7841 7864 7905 7937 7977 8007 8035 8077 8088 8093 8095 8110 8120 8134 8139- 8140 8143 8156 8235 8246 8262 8292 8320 8336 8345 8355 8358 8363 8365 8368 8370 8372 8375 8387 8444 8452 8456 8486 8520 8593 8610 8633-8634 8653 8719-8724 8773-8777 8779 8781-8782 8792 8798 8813 8830 8839 8853 8863 8870 8876 8898 8928 8944 8950 8956-8961 8963-8971 8989 9004- 9007 9009-9019 9042-9046 9055 9076 9097 9128 9134 9185 9264 9283-9284 9291 9313 9358 9424 9445 9454-9455 9457 9460 9466 9471-9472 9475 9480 9511 9517 9533 9539 9542 9544 9553 9565 9577 9586 9612 9626 9677 9694 9703 9722 9734 9757-9758 9773 9776-9778 9791 9812-9819 9827 9838 9843 9848-9853 9922 9927-9940 9942 9962-9970 9989-9992 9994-9997 10007 10027 10097 10149-10152 10249 10252 10275 10298 10333-10334 10346 10349 10351 10383 10386 10417 10438-10439 10452 10459 10470 10478-10480 10493- 10498 10557-10562 10564-10565 10580-10586 10594-10596 10645 10658 10676 10679 10767 10772 10774 10778 10782 10788 10791 10954 10971-10972 11002-11004 11032 11047- 11052 11061 11069 11083 11108 11130 11132 11151-11153 11155 11157-11158 11167 11170 11172-11176 11193-11196 11274 11343 11369 11406 11411 11431 11588 11596 11600 11604 11606-11607 11618 11620-11621 11629 11668 11814 11860 11865 11876 11903-11909 11932 11949-11954 11980 11985 12000 12006 12017 12022 12033 12039 12080 12083 12092-12093 12095-12104 12127-12129 12131-12142 12146 12159-12160 12162-12163 12178 12213 12216 12236 12256 12260 12305 12327 12363 12368 12371 12375 12379 12387 12401-12402 12405 12424 12430 12467 12520 12522 12546 12570 12576 12590 12594 12599 12605 12609 12611 12615 12617-12618 12630 12636 12643 12657-12658 12663 12670 12674 12685 12688 12691 12693 12702 12705-12707 12713 12724 12729 12735 12740-12745 12749 12754-12760 12765- 12770 12777 12842 12848 12875 12904 12906 12910 12913 12916-12917 12935 12940 12955 12957 12963 12972 12977- 12980 12982-12984 12992-12994 12997-13000 13020 13034 13047 13051 13054 13056 13060 13062 13066 13070 13072- 13073 13075 13082 13090 13092-13093 13104 13126 13136 13141 13175-13177 13179-13180 13193-13194 13196-13197 13202 13236-13241 13243 13245 13249 13254 13263-13275 13277 13286-13292 13295 13319 13351 13377 13389-13391 13394 13420 13436 13456 13477 13479 13488 13492 13494- 13495 13497-13499 13502-13503 13506 13512 13516 13533 13546 13549 13554-13555 13575 13590 13597 13600-13601 13613 13616-13620 13627 13631 13644-13645 13649 13659- 13660 13670 13674-13679 13693-13699 13707-13709 13713 13782 13803 13864 13866 13868-13869 13872 13875 13882- 13885 13888-13889 13892
adult placenta	Clontech	APL001	669-671 1006 1134 1184 1551 2053 2090 2156-2158 2342 2490 2716 3001 3064-3065 3190 3272 3625 3670 4019 4055 4194 4201 4246 4641 4718 4720-4721 4783-4786 4957 5523

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			5536 5581 5788 5895 6145-6146 6201-6202 6358 6803 7049 7204 7529 8367 8375 8609 8611 8630 8725-8727 9097 9480 9734 9820 10319 10460 10579 10795 10895 11519 11723 11737 11776 11827-11828 11959 12403 12546 12570-12663 12848 12875 12913 13051 13394 13782 13869 13889
placenta	Invitrogen	APL002	142 561 1023 1551 1976 2449 2569 2614 3191 3340 3592 3668 4060 4346 4767 4787-4789 4892 4985 5536 5674 5693 5757 5772 5794 5906 6147 6203 6215 6598 6788 6799 6979 7158 7530-7531 8139 8361 8611 8863 9457 9484 9517 9563 9703 9758 9821 9927 9939 9942 10481 10557 10778 10802 10973 11006-11011 11723 11731 11737 11776 11807 11866 11910- 11916 11959 12379 12403 12590 12685 13020 13054 13392 13489 13533 13554-13555 13867 13882 13888 13891
adult spleen	GIBCO	ASP001	463 499 562-563 598 672 990-993 995 1004 1020 1346 1515- 1516 1556 1774 1877 1914 1977 2159 2161 2215 2248 2257 2363 2529 2569 2614 2617 2812 2827 3093 3192 3195 3199 3272 3286 3350 3356 3434 3470 3503 3537 3544-3546 3548 3604 3634 3689 3709 3720 3722 3796-3798 3812 3839 3885 4006 4011 4022 4025 4043 4194 4201 4246 4253 4277 4388 4391 4396 4405 4434 4641 4689-4690 4781 4957 4987 4998 5001 5017 5030 5037 5052 5076 5118 5512-5513 5523 5526 5701 5740 5778 5788 5796 5801 5895 5938 6005 6064 6125 6140 6147 6192 6204 6272 6329 6458 6551 6590 6607 6873 6886 6931 6958 7018 7058 7109 7118 7133 7171 7233 7506 7532-7533 7561 7586 7733 7736 7807 7842 7845 7933 8065 8085 8093 8095 8110 8116 8139-8140 8226 8235 8262 8323 8359 8363 8365 8368 8372 8456 8535 8648 8702 8792 8816 8838-8839 8858 8863 8865 8876 8923-8928 8943 8950-8951 9128 9257 9264 9317 9455 9457 9466 9474 9544 9560 9773 9781 9919-9920 9927 9939 9942 10000 10048-10049 10155 10175 10267 10275 10296 10331 10549 10566 10774 10777 10828 10944 11032 11061 11108 11113 11132 11173 11272 11401 11406 11620-11621 11804 11818 11861 11917 12006 12039 12041 12073-12074 12078 12118 12127 12236 12327 12375 12387 12402 12405 12424 12426 12511 12546 12560 12570 12601 12617-12618 12670 12674 12734-12735 12749 12772 12790 12913 12916-12917 12972 12977 13002 13021 13066 13082 13084-13085 13169 13228-13229 13256 13260 13295 13316-13317 13394 13456 13488-13489 13494 13497 13512 13516 13546 13645 13649 13651 13659 13679 13739 13776 13864 13866-13867 13888
testis	GIBCO	ATS001	50 142 500-502 564-565 598 673-678 963-968 1193 1346 1556 1671 1826 1968 1977 2160-2161 2236-2237 2555 2590 2597 3024 3093 3196-3202 3284 3378 3517-3522 3524 3720 3797 3839 3885 4006 4025 4055 4109 4253 4354 4377 4388 4405 4434 4473 4480 4543 4688 4792 4940 4957 4962 4964 4975 5001 5018 5030 5037 5067-5072 5076 5118 5171 5481 5525 5535 5740 5757 5788 5907 5924 6125 6147 6257 6316-6322 6324 6607 6886 6952 7058 7141 7288 7445 7484 7534-7540 7677 7710-7711 7713-7717 7735 7792 7815 8087 8110 8120 8262 8368 8370 8375 8535 8577 8648 8655 8702 8729 8838- 8839 8848 8898-8906 8936 8939 8966 9076 9087 9244 9264 9304 9455 9466 9485 9542 9567 9703 9758 9822-9825 9908- 9910 9928 10462 10475 10478 10482 10551 10583 10679 10772 10778 10795 10955 10974 11108 11113 11116 11118- 11120 11132 11173 11239 11425 11606 11620 11629 11695 11807 11862 11918-11919 12000 12006 12017 12033 12057- 12061 12375 12405 12424 12570 12577 12599 12601 12605 12609 12668 12692 12730-12731 12748 12904 12917 12923 12929 12935 12940 12956 12971 13047 13051 13073 13090 13169 13222-13225 13249 13394 13442 13456 13479 13494

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			13497 13502-13503 13506 13512 13515 13533 13549 13555 13575 13613 13616 13627 13644-13646 13660 13866 13875 13882 13889
Genomic DNA from BAC 63I18	Research Genetics (CITB BAC Library)	BAC001	8711
adult bladder	Invitrogen	BLD001	731 1710 1779-1791 2076 2367 2479-2481 4067 4208-4214 4681 4767 4775 5163 5169 5553 5560 5581 5674 5684-5688 5794 6082 6244 6716 6718-6721 6799 6931 7045 7094-7097 7967 8110 8226 8249-8258 8364 8648 8737 9012 9097 9425- 9428 9430 9626 9703 9928 10007 10261 10557 10734-10735 11459 11504-11506 12000 12212 12512-12513 12515-12517 12670 12735 12914 13085 13439 13512 13687 13838-13841 13866
bone marrow	Clontech	BMD001	11 70 83 85 142 150 162-184 186-198 200-210 230-243 245- 277 279-281 306 370 373-387 389 433-435 438-440 457 483 503-510 566 568-569 595-596 598 609 616 679-683 740 770 843-857 859 861 864 867-876 880-884 886-890 892-893 896 900 902-920 1000 1004 1116-1120 1122-1126 1128-1134 1184 1211 1346 1359 1516 1552-1554 1575 1583 1671 1724 1774 1877 1894 1927 1974 1976 1983 2012-2024 2031 2033-2038 2040 2043-2044 2084-2088 2111 2120-2121 2132-2133 2137- 2138 2161 2163-2164 2186 2189 2199-2200 2202-2203 2205- 2210 2213-2218 2266 2291-2295 2342-2343 2414-2416 2444 2529 2555 2566 2569 2575-2576 2591 2597 2652 2681-2709 2711-2716 2735-2738 2740-2744 2746-2748 2750-2756 2758- 2759 2761-2764 2766-2768 2770 2772-2781 2783-2787 2806 2812-2813 2816 2873 2875 2880-2881 2883-2885 2887-2897 2899 2901 2926 2948 2954 2958 2977 2984 3026-3029 3032 3068-3069 3071 3081 3093 3096-3097 3139 3203-3205 3207 3238 3257 3272 3282-3283 3286 3317 3345 3356 3404-3418 3422-3434 3437-3438 3440 3442 3447 3449-3450 3456-3459 3461-3464 3466-3473 3483 3497 3535 3538 3548 3557 3572 3588 3593 3600 3604-3605 3610 3612 3625-3627 3634 3644- 3647 3649-3651 3653-3657 3709 3711 3722 3725 3727 3737 3797 3804 3808 3810 3839 3899 4005-4006 4011 4015-4019 4023 4025 4040 4043 4058 4060 4129 4132 4192 4194 4201 4246 4253 4277 4282 4367 4403 4466-4472 4474-4477 4479- 4484 4486-4490 4492-4497 4509 4512-4540 4582 4595 4597- 4606 4608-4615 4622 4642 4648 4650 4654 4667 4691-4695 4723 4741-4742 4759 4767 4783 4794-4796 4808 4836 4928- 4929 4931-4934 4938 4940 4942 4944-4948 4950-4953 4955- 4960 4962-4964 4967-4971 4973 4976-4979 4985-4987 4992- 4998 5000 5004-5016 5030 5037 5052 5075-5076 5093 5143 5149-5151 5163 5169 5210-5215 5217-5226 5262 5317 5357 5503 5523 5535 5537-5540 5560 5604 5695 5740 5748 5766 5788 5796 5801 5862 5874 5895 5906 5908 5938 5965-5967 5969-5979 5991-5994 5996-6005 6007-6009 6027 6047 6057 6065 6067-6068 6071-6072 6082 6086 6089-6091 6112 6125- 6127 6148-6152 6195 6214 6233 6257 6269-6276 6278-6280 6282-6283 6285-6289 6292-6300 6321 6374 6393-6403 6508 6555 6605 6607 6722 6730 6788 6815-6822 6826-6832 6836 6859-6861 6867 6870-6871 6873-6874 6905 6915 6929 6933- 6937 6940-6942 6944-6945 6988-6992 7051 7126 7155 7166 7169 7199-7210 7212-7219 7226 7233-7253 7256-7264 7275 7317-7318 7320 7322-7326 7347 7349 7373-7374 7379 7382 7446-7448 7473-7474 7491 7502 7542 7544 7569 7577 7579 7663-7671 7674 7677-7678 7680-7684 7686 7689-7696 7742 7768 7791 7815 7819-7824 7847 7864 7930 7995 8065 8085

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			8088 8090-8093 8095 8110 8120 8134 8139 8224 8226 8235 8241 8246 8262 8336 8354 8359 8363 8365 8368 8375 8421- 8427 8429-8440 8444 8452 8456-8460 8463-8465 8467-8476 8478-8489 8538-8539 8542-8551 8563 8566 8577 8593-8595 8597 8603 8633 8635-8637 8648 8656-8657 8671 8677 8679 8701 8792 8796 8817 8830 8840-8845 8847-8849 8852 8855- 8860 8863-8868 8870 8873 8875 8879-8881 8898 8935 8944 8963 8965 8995 9010 9012 9020-9031 9049 9051 9066 9076 9092 9097-9098 9128 9257 9264 9285-9288 9304 9317 9339 9381 9399 9401 9454-9455 9466 9471-9472 9474-9476 9516- 9517 9519 9529 9544 9622 9630-9643 9646 9650-9665 9689 9705-9712 9730 9734 9740 9758 9779-9781 9826 9885-9889 9892-9902 9928-9929 9939 9942 9972-9976 9978-9982 9999- 10000 10068 10153 10175 10249 10275 10277 10284 10287 10296 10319 10321 10343-10344 10346 10364-10374 10379- 10382 10385-10394 10414 10416 10426 10429 10439 10447 10452 10467-10468 10475 10483 10520 10522-10526 10528- 10529 10531-10535 10587-10590 10595 10616 10677-10679 10691 10750 10760 10767 10772 10778 10788 10794-10795 10828 10831-10837 10846-10847 10849-10851 10853-10858 10891 10895 10897 10899-10903 10905-10907 10931-10933 10956-10959 10975-10976 11012 11032 11046 11057 11059 11061 11077-11082 11085-11086 11088-11098 11108 11113 11132 11145 11177-11181 11194 11208 11289 11344 11401- 11402 11513 11618 11620 11631 11673-11675 11677-11690 11695 11697-11704 11706 11708-11715 11736 11742 11762- 11772 11774 11795-11796 11802-11804 11817-11818 11829 11839-11842 11863 11920 11946 11992-12002 12004-12008 12010 12012-12013 12015-12019 12022-12029 12033 12041 12081 12142-12149 12160 12178 12195 12200 12231 12236 12283 12305 12308 12316 12327 12363 12368 12404-12405 12424 12426 12430 12439 12527 12546 12570 12576 12590 12608 12610 12616 12634-12636 12641-12645 12654-12655 12657-12659 12669-12670 12674 12721-12724 12754 12761 12834 12840 12842 12904-12905 12910-12911 12913 12916- 12917 12922-12923 12925-12928 12933 12938 12956 12966 12977 12989-12990 12993 12995 13020 13033 13047 13060 13062 13064 13066 13095 13098 13103-13105 13107 13111- 13113 13129 13135 13137 13141 13150 13163 13173 13181 13213-13217 13234 13276-13278 13280 13391 13394 13400 13456 13472 13477 13490 13492 13494 13498 13501-13502 13506-13507 13511 13516 13528 13530-13534 13538 13540 13546 13551-13552 13554-13555 13560 13585-13586 13594 13613 13630 13633-13639 13644-13646 13649 13659-13660 13670 13673 13679 13713 13775 13795 13866 13872 13875 13882-13885 13889 13891 13893
bone marrow	Clontech	BMD002	51 242 442 654 1004 1134 1841-1904 1908 1927 2023 2107 2215 2342 2408 2507-2529 2576 2597 2806 2866 3286 3434 3722 3736-3737 3817 3823 3839 4060 4246 4258-4290 4389 4396 4411 4618 4641 4828 4836 4957 4987 5030 5037 5052 5108 5163 5526 5711 5743-5772 5774-5804 5813 5895 5939 6131 6236 6266 6287 6306-6307 6333 6655 6675 6728 6730 6750-6762 6764-6769 6788 7049 7106-7117 7137 7156 7738 8068 8085 8134 8156 8290-8297 8299-8305 8307-8312 8323 8368 8482 8499 8858 8863 8865 8928 8935 9076 9111 9128 9465-9502 9626 9700 9703 9923 9928-9929 9942 10277-10280 10282-10284 10286-10297 10396 10434 10515 10551 10645 10675 10691 10744-10753 10772 10778 11057 11098 11108 11132 11232 11252 11519 11536-11553 11606 11620 12033 12039 12146 12260 12305 12387 12402 12405 12500 12554- 12578 12594 12599 12608 12674 12754 12777 12839 12895-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			12904 12916 12923 13020-13021 13043 13057-13064 13169 13249 13446-13454 13479 13492 13494 13513 13533 13555 13659 13713 13775 13803 13863-13875 13877-13887 13889 13891
bone marrow	Clontech	BMD004	2249 2529 3286 3494 3548 3551 3797 3839 4025 4058 4201 4277 4282 5052 5108 6545 6961 8262 8898 9474 10000 11098 11818 13021 13893
bone marrow	Clontech	BMD007	8539 9780 9927 13021
adult colon	Invitrogen	CLN001	319 346 487 731 799 1792 1848 2050 2161 2449 2482-2483 3431 3901 4215-4217 4940 4957 4987 5163 5239 5560 5689-5695 5865 5911 5923 6722 6765 7098 7815 7864 7880 8110 8259-8262 8486 8597 8951 9484 9529 9542 9556 10376 11507-11508 11617 11869 12127 12236 12424 12518-12523 12601 12610 12777 12976 13062 13073 13367 13440 13507 13512 13630 13713 13843-13844 13864 13868-13869 13888
Mixture of 16 tissues – mRNAs*	Various Vendors*	CTL016	6815 10776 12977 13064 13512
Mixture of 16 tissues – mRNAs*	Various Vendors*	CTL021	1671 6738 8432 8648 8863 8944 9511 10769 13021 13062 13064
adult cervix	BioChain	CVX001	50 67 142 158 308 332 346 475 598 654 895 1004 1086 1286 1449 1516 1671 1698 1701 1711-1756 1758-1776 1828 1848 1959 2134 2186 2257 2267 2343 2408 2414 2468-2474 2476-2478 2608 2716 3002 3136 3166 3191 3199 3529 3535 3554 3572 3627 3722 3737 3777 3797 3839 3985 4158-4176 4178-4195 4197 4199-4207 4246 4277 4391 4396 4434 4641 4667 4759 4783 4828 4885 4940 4957 4963 4987 4998 5001 5038 5075 5108 5163 5293-5294 5455 5481 5523 5552 5581 5646-5652 5654-5659 5661-5671 5673-5681 5687 5701 5711 5723 5740 5788 5794 5848 5902 5908 5923-5924 5964 6020 6052 6057 6062 6091 6106 6112 6125 6129 6181 6350 6371 6374 6410 6446 6458 6504 6508 6512 6551 6598 6686-6687 6689-6705 6707-6715 6788 6873 6893 6917 6998 7008 7045 7078 7084-7093 7095 7130 7141 7148 7169 7204 7507 7579 7608 7675 7733 7768 7815 7871 7880 7893 8078 8138 8209-8215 8217-8236 8238-8242 8244-8248 8298 8345 8370 8444 8456 8486 8499 8535 8558 8592 8633 8635 8648 8669 8679 8742 8853 8863 8870 8898 8921 8939 8948 9012 9061 9098 9107 9128 9137 9153 9304 9308 9317-9318 9355 9385-9391 9393-9403 9405-9406 9408-9418 9420-9422 9457 9466 9475 9510 9539 9612 9734 9773 9927-9928 9939 9947 9960 10110 10175 10230-10256 10258-10259 10267 10274 10319 10329 10344 10491 10496 10540 10616 10660 10691 10722-10732 10778 10782 11055 11145 11217 11376 11462 11477-11489 11491-11503 11519 11584 11604 11695 11853 11869 11891 11980 12006 12066 12081 12127 12160 12195 12216 12240 12266 12308 12363 12379 12402 12405 12424 12438 12483-12494 12496-12510 12579 12605 12610-12611 12617-12618 12643 12653 12670 12674 12688 12691 12703 12707 12735 12740 12754 12830 12840 12866 12870-12881 12883-12884 12905

* The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphoblastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			12913-12914 12917 12923 12951 12955 12957 12965 12989-12990 12993 13002 13020 13035 13045-13050 13062 13064 13072 13092 13136 13141 13174 13197 13254 13283 13307 13391 13428 13430-13437 13442 13473 13479 13492 13494-13495 13497-13498 13502 13532 13554-13555 13575 13590 13597 13613 13616 13627 13644 13679 13713 13775 13829-13837 13866 13868-13869 13872 13884 13888 13891
diaphragm	BioChain	DIA002	731 1346 3548 3711 3885 4282 4654 5895 6873 8120 8931 8936 9455 11132 11818 12405 12609
endothelial cells	Stratagene	EDT001	21 51 67 83 332 569 598 609 762 796 1004 1024-1026 1086 1561 1848 1928 1959 1976-1977 1983 2138 2161 2166 2257 2282-2283 2417 2483 2490 2555 2569 2614 2926 3042 3189 3191 3272 3300-3303 3426 3494 3503 3548 3574-3576 3605 3627-3628 3673 3709 3720 3722 3737 3797 3839 3885 4005 4011 4019 4055 4133 4192 4246 4269 4282 4340 4354 4365 4384 4388 4399 4405 4410-4411 4434 4543 4641 4654 4767 4797-4799 4802 4881-4882 4885-4886 4888 4940 4957 4964 4972 4985 4998 5002 5017 5030 5076 5103-5104 5132-5133 5163 5167 5183-5185 5187-5190 5380 5523 5527 5535 5541-5542 5544 5674 5684 5693 5724 5766 5778 5788 5794 5796 5874 5895 5916 5923 5928 5938 6005 6048 6057 6068 6082 6165 6205 6215 6240-6241 6307 6321-6322 6349-6353 6383 6458 6595 6598 6606-6607 6765 6799 6805 6815 6860 6871 6873 6890 6918 6968 6972 6976 6979-6980 6998 7058 7067 7104 7113 7116 7137 7139 7169 7275 7468 7613 7716 7755-7757 7759-7760 7797 7799-7801 7930 8077 8084 8093-8095 8120 8139 8235 8262 8320 8323 8335-8336 8345 8354 8358 8363-8364 8370 8372 8375 8387 8452 8592 8648 8786 8788 8792 8813 8863 8898 8944-8955 8965 8996-9001 9051 9076 9097 9128 9264 9289-9291 9304 9315 9414 9455-9456 9466 9472-9473 9475 9484 9504 9517 9529 9542 9563 9570 9626 9703 9780-9781 9843 9927 9939 9961 10000 10027 10154 10267 10285 10321 10330-10331 10342 10344 10349 10496 10500 10550 10556-10557 10579 10679 10772 10776 10778 10788 10795 10802 11013 11132 11136 11146-11149 11406 11483 11565 11588 11600 11606-11607 11615 11626 11807 11818 11932 11955 12006 12034 12037 12041 12044 12078 12092-12094 12123-12126 12150 12213 12375 12381 12387 12405 12411 12424 12426 12522 12570 12576 12590 12601 12610 12612 12615 12617-12618 12663 12670 12674 12707 12729 12739 12749 12753-12754 12777 12830 12842 12913-12914 12916-12918 12929 12940 12972 12975-12977 13002 13024 13047 13051 13054 13062 13064 13082-13084 13090 13092 13094 13123 13126 13136 13195 13235 13263 13380 13389 13392 13394 13400 13456 13479 13488-13489 13492 13494-13499 13502 13506-13507 13514 13516 13546 13555 13568 13575 13590 13592 13613 13616 13621 13630 13649 13659-13660 13667-13668 13670-13673 13678-13679 13690-13692 13713 13796-13797 13838 13866-13869 13872 13882 13884 13888 13893
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM001	150 2023 2327 2490 4109 4783 5503 5560 10267 10760 12017 12160 12557 12582 12923 13020 13514
Genomic clones from the short arm of chromosome	Genomic DNA from Genetic Research	EPM003	5560 12017 12146

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
8			
Genomic clones from the short arm of chromosome 8	Genomic DNA from Genetic Research	EPM004	4783 4798 5560 10817 11926 12017 12160
esophagus	BioChain	ESO002	999-1000 2449 3272 3315 3548 3550 3634 3697 3796 4011 4025 4058 4201 4282 5106 5163 5553 6082 6873 7739 9304 10296 11133 11818 12033 12570 13869
fetal brain	Clontech	FBR001	51 142 1184 3664 4060 4109 4940 5021 5270 5523 5553 6112 6805 6908 7294 8558 9457 10376 11059 11985 12006 12122 12160 12754 13438 13507 13888
fetal brain	Clontech	FBR004	60 2704 3711 4025 4109 4783 5001 6082 7597 9010 9504 9949 11837 12033 12039 12363 12705 12905 13020 13503 13512 13891
fetal brain	Clontech	FBR006	6 60 67 598 800 932 1004 1170 1793-1794 1796-1797 1799-1805 1905-1914 1916-1958 1974 1976 1979 1983 2057 2129 2174 2221 2407 2444 2449 2484-2492 2530-2554 2556-2561 2563 2576 2857 3064 3207 3479 3556 3673 3709 3722 4060 4078 4157 4218-4221 4223-4224 4277 4291-4334 4338 4355 4364 4369 4431 4957 5001 5109 5270 5380 5553 5634 5696-5706 5711 5724 5766 5788 5794 5801 5805-5832 5834-5879 5882-5901 5936 5990 6057 6723-6732 6765 6770-6791 6797 6805 6894 7049-7050 7100-7102 7105 7118-7123 7125 7127 7169 7905 8263-8265 8267-8273 8294 8312-8333 8359 8361 8375 8452 8633 8664 8740 8757 8884 9010 9111 9432-9436 9503-9516 9518-9545 9547-9551 9556 9570 9577 9780 9895 9923-9924 9928 9942 10007 10027 10202 10263-10268 10276 10284 10298-10310 10329 10331 10496 10542 10595 10621 10736-10737 10755-10761 10772 10774 10795 11108 11132 11406 11483 11509-11523 11555-11582 11589-11590 11600 11606 11621 11713 11729 11807 11837 12006 12039 12044 12092 12113 12218 12231 12236 12327 12363 12398 12405 12465 12511 12524-12530 12576-12577 12579-12601 12729 12735 12754 12863 12869 12889 12906-12910 12914 12954 12973 13020-13021 13051-13052 13054 13065 13082-13083 13427 13445 13455-13470 13488 13490 13496 13498-13501 13507 13516 13560 13613 13630 13649 13708 13713 13769 13831 13845-13855 13868 13872 13882 13884 13888-13894 13896-13900
fetal brain	Clontech	FBRs03	1005 4405 5111 6337 6964 7742 13084 13864 13891
fetal brain	Invitrogen	FBT002	51 83 142 321 430 746 932 1054 1058-1065 1493 1833 1947 2273-2275 2299 2444 2449 2926 3479 3492 3885 4347 4354 4391 4405 4410 4434 4530 4804 4985 4998 5075 5160-5169 5380 5428 5466 5750 5788 5801 5895 6132 6215 6371-6374 6458 6598 6973-6974 7067 7096 7776-7778 7780-7782 7937 8143 8323 8361 8364 8372 8377 8452 8633 8977-8984 8986 9010 9142 9264 9332 9457 9474 9503 9511 9517 9539 9582 9827 9848 9927 9950-9953 10027 10161 10329 10430 10492 10573-10575 11014 11160-11164 11406 11628 11742 11814 11830 11985 12092 12112-12114 12116-12117 12127 12424 12511 12521 12570 12576 12643 12696 12735 12748-12751 12754 12830 12835 12913 12957 12977 12990 13002 13020 13062 13072 13083 13117 13254-13259 13377 13486 13489 13496 13499 13507 13590 13649 13685-13688 13713 13867 13888 13891 13893
fetal heart	Invitrogen	FHR001	1001 1004 2250 4025 6334 6765 7740 8933 8935 9457 9544 10000 11132 12599 12609 13021 13568 13656 13866
fetal kidney	Clontech	FKD001	142 346 364 511-517 570-572 574 598 685-690 969-970 972-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			981 983-987 1134 1346 2123 2167-2169 2238-2246 2342 2444 2483 2516 2555 2617 2728 2843 2876 3032 3049 3072 3206 3208 3282-3283 3525-3531 3533-3543 3548 3591 3709 3722 3797 3839 3878 4015 4019 4043 4246 4277 4367 4405 4696- 4698 4725 4767 4805-4810 4940 4947 4957 4986 4998 5037 5056 5073-5080 5082-5091 5099-5100 5108 5258 5504 5523 5560 5923 6005 6207-6208 6225 6272 6288 6325-6332 6478 6603 6702 6793 6815 6906 6953-6959 7045 7058 7204 7355 7426 7449-7450 7520 7543-7546 7561 7587 7718-7732 7930 8077 8097 8262 8375 8387 8452 8520 8638 8658 8736-8737 8834 8863 8898 8907-8918 8922 8950 9010 9134 9257 9401 9457 9544 9597 9760 9781 9791 9828-9830 9912 9914-9918 10296 10440 10484 10546-10548 10772 11108 11121-11129 11131-11132 11170 11513 11638 11695 11923-11924 12006 12033 12062-12070 12072 12160 12405 12522 12570 12594 12599 12605 12626 12663 12670 12732-12733 12749 12848 12904 12914 12940-12941 12990 13020 13083 13188 13226- 13227 13234 13263 13277 13280 13351 13391 13394 13491 13501 13512 13590 13644 13647-13650 13713 13782 13867- 13868 13872 13875
fetal kidney	Clontech	FKD002	3286 5030 5037 5105 11108 12033 12490 12570 13494 13866
fetal kidney	Invitrogen	FKD007	3272 3806 4025 4253 4277 4654 5112 5535 5788 5801 8863 8935 9401 9466 10553 11628 11818 13494 13646 13866
fetal lung	Clontech	FLG001	79 2367 2395 3010 3460 3885 4828 4948 4962 5001 5723 5748 5902 5908 6186 6738 7051 7067 7677 7759 9264 9553 9700 10007 10478 11098 12017 12383 12417 12424 12749 12917 13020 13169 13472 13554 13644 13782 13835
fetal lung	Invitrogen	FLG003	142 319 364 629 1671 1806-1814 1816-1819 1877 2129 2161 2169 2367 2449 2493 2529 3191 3503 3610 4109 4225-4234 4367 4434 4957 5108 5380 5421 5581 5707-5710 5712 5714 5788 5801 6057 6733-6741 7034 7103 8274-8278 8365 8597 8948 9264 9327 9437-9442 9444 9466 9510 9525 9530 9539 9677 9773 9841 10007 10190 10198 10269-10271 10329 11519 11524-11527 11927 12531-12539 12848 12890 12904 13021 13072 13249 13445 13472 13489 13551 13575 13649 13670 13679 13856-13857
fetal lung	Clontech	FLG004	1003-1004 2597 5110 6963 9924 10552 11138-11139 12080 12990 13659
fetal liver-spleen	Columbia University	FLS001	-2 4-14 16-22 24 26 28-31 33-46 48-49 51-61 63-68 71-91 93- 102 104-110 112-124 126-156 158-162 282-283 285-290 292- 299 301-304 307-312 314-326 328-338 340-344 346-353 355- 365 369 390-400 402 436 441 483 557 567 575-585 595 598 629 673 678 691-699 701-702 708 731 736 763-767 769-776 778-786 788-791 793-794 796 925 975 1004 1015 1023 1038 1068 1104 1134 1144 1184 1192 1216 1264 1298 1346 1482 1493 1516 1518-1521 1551 1556 1575 1583 1594 1636 1641 1707 1724 1774 1826-1829 1841 1858 1927 1959 1962-1965 1967-1972 1974-1979 1981-1998 2000-2009 2011 2045-2051 2053-2055 2057-2058 2060-2063 2065-2083 2089-2094 2100- 2101 2161 2170 2174 2184-2194 2215 2222 2269 2290 2310 2342 2409 2411 2414 2444 2449 2458 2483 2490 2497-2498 2510 2516 2523 2529 2555 2562 2566-2576 2578-2586 2588- 2591 2593-2601 2604 2607-2608 2611-2612 2614-2618 2620 2622-2642 2644 2646-2653 2655-2664 2666 2668 2670-2680 2696 2750 2788-2793 2795-2811 2814-2826 2828-2835 2837- 2842 2844 2846-2848 2851-2858 2860 2862-2871 2876 2878 2893 2900-2905 2907-2909 2926 2929 2949 2952-2953 2959- 2960 2984 2992 3032 3058 3069 3073-3076 3078-3080 3082 3093 3166 3194 3196 3207 3210-3211 3213-3214 3217-3225 3249 3257 3272 3282 3286-3287 3304-3307 3310-3311 3314-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			3317 3319 3321-3332 3334-3346 3356 3419 3426 3434 3446 3450 3455 3468 3470 3479 3484 3494 3503 3535 3537 3548 3552 3557 3572 3590 3594 3597 3604-3605 3610 3612 3625 3627 3634 3668 3670 3709 3711 3720 3722 3729 3737 3777 3797 3806 3808 3810 3813 3839 3885 3926 3990 3996-3997 4006 4009 4011 4019-4022 4025 4040 4043 4060 4078 4095 4109 4129 4192 4194 4201 4245-4246 4253 4261 4277 4282 4297 4335-4338 4340-4357 4359-4361 4364 4366-4367 4370- 4372 4374-4377 4379-4382 4384-4386 4388-4392 4395-4396 4398-4414 4417-4424 4426-4455 4457-4458 4460-4465 4542- 4543 4545 4547-4553 4555-4562 4565-4575 4577 4579 4581- 4582 4585-4588 4593 4596 4607 4616-4629 4644-4645 4647 4654 4671 4676 4687 4689 4694 4721 4726-4729 4759 4767 4775 4783-4784 4788 4790-4791 4811-4819 4830 4837 4845 4862 4874 4889-4902 4930 4940 4948-4949 4957 4962-4965 4972 4985 4998 5022 5029-5030 5037 5040 5075-5076 5092 5108 5132 5152 5163 5167 5171-5172 5335 5380 5398 5473 5503 5514 5516 5523 5526-5527 5535-5536 5553 5581 5598 5604 5616 5674 5684 5691 5693 5711 5715 5724 5726 5748 5750 5757 5778 5788 5794 5801 5817 5865 5874 5894-5895 5902-5914 5916-5919 5921-5928 5930-5949 5951-5954 5956- 5964 5966 5979 6005 6010 6013-6015 6017-6018 6020-6022 6024-6025 6028-6032 6034-6048 6052-6062 6064 6068 6073- 6081 6086 6092-6094 6104 6112 6125 6135 6140 6147 6149 6153-6157 6165 6186 6195 6209-6211 6240-6241 6243-6248 6250-6253 6272 6276 6287-6288 6307 6313 6338 6371 6374 6419 6430 6446 6451 6458 6478 6496 6508 6545 6579 6595 6598 6607 6611 6624 6629 6642 6658 6695 6726 6728 6730 6738 6745 6754 6765 6767 6788 6793-6797 6799-6808 6810- 6815 6833-6843 6845-6847 6850-6856 6858 6860 6862-6865 6870-6871 6875 6877 6891 6893-6894 6900 6907-6908 6917 6919-6925 6950 6979 7049 7058 7067 7077 7096 7109 7116 7118 7128-7131 7133-7135 7137-7141 7144-7147 7149-7150 7152-7153 7155-7179 7181-7192 7194-7198 7265-7271 7273- 7280 7282-7305 7307-7312 7316 7327-7336 7375-7376 7383 7386 7451 7455 7468 7473 7475-7477 7479 7484 7548-7553 7555-7558 7561 7608 7617-7618 7620-7631 7642 7675 7687 7695 7716 7768 7809 7811 7839 7842 7864 7883 7933 7977 8069 8093 8095 8105 8110 8116 8139 8224 8226 8235 8241 8262 8323 8334-8340 8342-8350 8352-8355 8357-8359 8361- 8408 8410-8411 8414-8419 8452 8456 8490-8498 8500-8502 8504-8526 8529-8530 8537 8540-8541 8553-8560 8563 8566 8568 8577 8592 8611 8639 8648 8659-8661 8664 8668-8669 8710 8738-8739 8741 8777 8792-8804 8830 8834 8839 8853 8858 8863 8865 8876 8898 8926 8935 8939 8950-8951 8957 8963 9010 9012 9076 9092 9097 9112 9119 9128 9257 9264 9266 9284 9291 9301 9304 9313 9318 9352 9375 9399 9414 9424 9445 9455 9457 9466 9473-9474 9476 9480 9484-9485 9511 9517 9528-9529 9536 9539 9542 9544 9552-9557 9559 9561-9564 9566-9572 9574-9577 9579-9630 9646 9655 9666- 9667 9669-9671 9673 9675-9697 9700-9701 9703-9704 9713- 9715 9718-9719 9722 9726-9729 9734 9752 9758 9761 9777 9780-9784 9813 9831 9854-9867 9869 9906 9927 9929 9939 9942-9943 9969 9983 10000 10007 10205 10267 10284 10296 10305 10311 10313-10316 10318-10325 10327 10329-10331 10333-10354 10356-10363 10395-10397 10400-10403 10405- 10410 10413 10417-10422 10427 10446-10447 10463 10470 10485 10496 10502-10507 10515 10542 10557 10565-10566 10645 10679 10688 10691 10729 10750 10760 10762 10764- 10769 10772-10774 10776-10782 10784 10786-10795 10797- 10815 10817-10830 10859 10861-10869 10871-10879 10881-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			10893 10908-10916 10929 10934 10943 10948 10968 10971 10975 10977-10983 11005 11009 11011 11015-11018 11028 11031 11054-11063 11094 11108 11114 11132 11136 11142 11194 11208 11213 11246 11390-11391 11401 11406 11411 11414 11459 11462 11483 11508 11513 11521 11534 11559- 11560 11565 11573 11585-11603 11606-11610 11612-11616 11618-11638 11640 11642-11657 11659-11667 11669-11670 11672 11699 11716-11718 11720-11722 11724-11741 11743- 11758 11760-11761 11775-11787 11797 11799-11801 11818 11830 11862 11864-11866 11869 11876-11889 11911 11925- 11928 11958-11961 11963-11976 11979-11980 12000 12006 12017 12019 12028 12033-12034 12041 12078 12086 12092 12122 12127 12159-12160 12178 12216 12218 12236 12245 12256 12260 12289 12303 12305 12308 12327 12330 12363 12375 12382 12387 12402-12405 12424 12426 12439 12442 12465 12470 12476 12511 12522-12523 12546 12551 12560 12570 12576 12590 12601-12602 12604-12619 12621-12633 12636 12639 12646-12653 12670-12671 12674 12682-12683 12688 12693 12696 12706 12709-12715 12735 12749-12750 12772 12790 12823 12830-12832 12835 12842 12849 12855 12863 12904-12905 12910-12911 12913-12916 12918-12924 12929 12931-12932 12934-12937 12939-12940 12954-12955 12965 12973 12976-12977 12989-12990 12993 12999 13020- 13021 13035 13051 13054-13055 13060 13062 13066-13067 13069-13087 13089-13095 13097-13102 13114-13117 13119- 13120 13122-13126 13134-13136 13141 13147 13156 13174 13193 13195-13196 13198-13201 13254 13260 13264 13277 13280 13295 13351 13368 13377 13391 13394 13400 13409 13412 13420 13456 13472-13477 13479-13484 13486-13492 13494-13496 13498-13499 13501-13510 13512-13516 13518- 13527 13533 13541-13544 13546-13551 13553-13555 13560 13575 13587-13589 13597 13603-13604 13613 13616 13622- 13623 13630-13631 13644-13646 13649 13659 13670 13679 13713 13743 13748 13769 13775 13782 13793 13803 13808 13818-13819 13858-13860 13864 13866-13869 13872 13882 13884 13888-13889 13891 13893 13901
fetal liver-spleen	Columbia University	FLS002	6 16 24 30-31 63 67 81 83 89 95 103 115 117 126 140 142 147 150-151 158 162 211 225 287 308 332 356 358 390-391 438- 439 483 551 556 641 654 694 701 708 731 788 997 1006 1012 1047 1082 1151 1154 1178 1184 1208 1212 1356 1480 1507 1551 1556 1623-1647 1649-1667 1669-1671 1675 1677-1698 1828-1829 1858 1877 1885 1889 1914 1927 1947 1961 1997 1999 2028 2057 2070 2092 2098 2138-2139 2154 2161 2174- 2175 2189 2191 2257 2282 2327 2342 2363 2399 2403 2409 2440-2441 2443-2450 2452-2459 2490 2498 2522-2523 2544 2555 2568 2575-2576 2592 2597 2605 2619 2623 2659 2806 2809 2812 2860 2869 2879 2903 2926 2932 2988 3031 3066 3075 3089 3188-3189 3286-3287 3319 3343-3344 3356 3426 3535 3548 3552 3554-3555 3583 3591 3610 3625 3634 3673 3709 3711 3720 3722 3839 3899 3926 3985 4005-4006 4011 4020 4025 4055 4058 4060 4078 4091-4116 4118-4126 4128- 4142 4172 4194 4201 4253 4277 4282 4347 4350 4353-4355 4362 4367 4374 4379 4386 4391 4394 4396 4402 4426 4431 4435 4437-4439 4512 4553 4578 4586 4607 4622 4644 4654 4671 4758 4767 4783 4798 4836 4845 4899 4940 4948 4962- 4963 4985 4991 4998 5001 5037 5108 5167 5171 5177 5198 5237 5293-5294 5380 5400 5523 5535-5536 5581-5591 5593- 5599 5601-5613 5615-5624 5627-5637 5653 5674 5691 5693 5711 5724 5726 5733 5748 5757 5772 5778 5794 5817 5874 5894 5902 5904 5906-5907 5909 5911 5916-5919 5923-5924 5927 5929 5932 5938 5941 5948 5957 5959-5960 5962 5964

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			5979 6005 6020 6027 6037-6038 6052 6054 6057 6060-6062 6064 6068 6112 6140 6195 6225 6246 6287-6288 6306-6307 6336 6354 6371 6374 6423 6430 6451 6458 6461 6469 6478 6496 6508 6538 6545 6563 6580 6583 6595 6598 6607 6629 6638 6641-6643 6645-6675 6709 6726 6730 6765-6766 6788 6792-6793 6795 6797-6798 6800-6801 6808 6812 6836 6843 6850-6851 6855 6860 6864 6870 6875 6888 6908 6924 6950 6958 6968 6998 7003 7018 7045 7049 7056 7071-7079 7095- 7096 7109 7116 7118 7126 7133 7135 7137-7139 7155-7156 7166-7167 7169 7175 7178 7275 7291 7294 7329 7422 7426 7478 7608 7627 7687 7695 7716 7815 7839 7871 7893 7914 7937 7977 8022 8095 8120 8133-8134 8148-8149 8151-8167 8169-8182 8184 8186-8192 8194-8196 8241 8246 8276 8289 8298 8336 8339 8343 8345 8349 8355-8356 8361 8363 8365 8367-8368 8370 8373 8375-8378 8385 8388 8417 8496 8518 8520 8543 8558 8561 8563 8646 8667 8710 8738-8740 8786 8803 8813 8865 8926 8946 8948 8963 8970 9010 9049 9119 9128 9142 9164 9222 9264 9289 9296 9301 9317-9318 9320 9322 9335-9341 9343-9362 9365-9368 9370 9372-9373 9375- 9377 9399 9455 9457 9466 9472 9475 9480 9483 9495 9526 9533 9536 9553 9556 9558 9560 9563 9567 9570 9582 9597 9601 9630 9646 9655 9671 9683 9695 9700 9703 9715 9722 9729 9733 9752 9758 9783 9843 9848 9855 9880 9936 9942 9983 10007 10027 10103 10142 10186-10217 10274 10284 10287 10296 10313-10314 10329 10331 10349 10352 10354 10400 10405 10430 10439 10496 10500 10507 10542 10621 10709-10710 10712-10717 10750 10760 10776-10779 10782 10794 10809 10816 10837 10885 10891 10895 10913 10960 10971 10975 11057 11071 11098 11142-11143 11148 11194 11246 11401 11406 11430-11453 11455-11464 11483 11504 11508 11556 11560 11589 11596 11615 11618 11626 11631 11714 11729 11830 11833 11865 11988 12000 12006 12017 12019-12020 12041 12044 12081 12092 12178 12195 12245 12256 12277 12297 12327 12363 12383 12402-12403 12405 12426-12427 12444-12455 12457-12465 12467-12473 12475- 12476 12520 12546 12576 12599 12607 12611 12614-12615 12617-12618 12622 12627 12630-12632 12636 12647-12648 12650 12685 12688 12691 12693 12696 12703 12739-12740 12743 12763 12808 12830 12834 12842 12849-12858 12860- 12866 12885 12895 12906 12910 12913 12915 12917 12920 12922 12929 12933 12940-12941 12954-12955 12957 12965 12977 12990 12993 12999 13021 13039-13040 13047 13051 13054-13055 13060 13062 13072-13073 13077 13082-13083 13085 13092-13095 13098 13117 13123 13136 13173 13195- 13197 13202 13249 13254 13362 13377 13391 13394 13406- 13409 13411-13415 13417-13420 13456 13473-13474 13477 13480 13484 13486 13488-13489 13496-13498 13500 13502 13504 13506-13507 13511-13512 13515 13521 13546 13551 13554-13555 13560 13575 13590 13597 13613 13616-13617 13622 13630 13659-13660 13670 13678-13679 13695-13696 13701 13708 13713 13726 13748 13775 13795-13796 13815- 13826 13835 13838 13859-13860 13864 13867 13869 13872 13882-13885 13888-13889 13891 13893
fetal liver-spleen	Columbia University	FLS003	525 2269 2529 2627 2636 3552 3554-3555 3597 4201 4246 4253 4422 4426 4434 4438 5536 5801 8935 9536 11136 11142 11519 11626 11927 12028 12077-12079 12086 12305 12403 12424 13021 13472
fetal liver	Invitrogen	FLV001	40 51 60 598 731 1023 1048-1049 1820 1976 2111 2268-2269 2449 2483 2529 2568 2576 2614 2809 3207 3220 3468 3595- 3599 3885 4020 4346 4390 4422 4434 4543 4615 4767 4833 5092 5152-5155 5270 5505 5526 5553 5581 5715 5724 5726

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			5750 5766 5788 5794 5801 5902 6125 6147 6458 6598 6624 6645 6765 6799 6805 6862 7104 7856 8070 8156 8359 8361 8432 8740 8928 8935 8972-8974 9012 9041 9128 9264 9445 9474 9485 9511 9536 9593 9597 9703 9780 9927 9943 9945- 9946 9948 10007 10137 10275 10334 10529 10557 10566- 10569 10776 10828 11142 11560 11587 11618 11927 12070 12086 12105-12108 12127 12218 12236 12327 12424 12511 12541-12542 12605 12746 12916 12977 12985-12986 13020- 13021 13060 13064 13135 13246-13247 13472 13479 13488- 13489 13497 13533 13554 13590 13659 13680-13682 13859- 13860 13882 13888-13889
fetal liver	Clontech	FLV002	360 996 1134 3226 5102 9401
fetal liver	Clontech	FLV004	998 1927 2449 2627 4025 4043 4426 4438 4834 5030 5726 6730 9474 9942 10769 11142 11587 12590 12608 13889
fetal muscle	Invitrogen	FMS001	40 150 731 894 1264 1555 1613 1821-1822 1883 1959 2161 2343 2494-2496 2555 3203 4235-4237 4434 4671 4694 4783 4885 4940 4985 5037 5045 5481 5716-5718 5724 5788 5902 5932 6624 6742-6743 6825 7054 7104 7141 7632 7800 8279- 8281 8863 8935 9204 9264 9446-9449 9451 9474 9511 9536 9556 9722 9780-9781 10097 10273-10274 10330 10738-10739 10750 11098 11406 11528-11530 11560 12305 12544-12546 12590 12609 12618 12663 12670-12702 12735 12891-12892 12916 13051 13053 13195 13441-13442 13479 13613 13782
fetal muscle	Invitrogen	FMS002	3378 4348 4434 8932 11132 12033 12570 13782
fetal skin	Invitrogen	FSK001	60 142 235 319 641 683 800 1015 1050 1346 1774 1823-1825 2044 2099 2111 2161 2215 2223 2280 2367 2401 2408 2513 2516 2614 2812 2871 2926 3207 3356 3468 3490 3503 3548 3599 3720 3722 3885 4020 4032 4060 4109 4238 4240-4244 4246 4253 4277 4340 4353 4355 4388-4389 4391 4405 4434 4543 4562 4568 4654 4667 4671 4767 4940 4944 4947 5030 5037 5075 5163 5198 5296 5380 5481 5514 5581 5656 5674 5691 5719-5724 5748 5757 5801 5894 5902 5923 6057 6076 6078 6125 6147 6215 6336 6374 6409 6437-6438 6551 6563 6744 6783 6803 6805 6815 6873 6900 6908 6917 6985 6987 7037 7054 7058 7067 7075 7275 7355 7431 7484 7507 7587 7627 7642 7653 7687 7871 7977 8110 8134 8186 8226 8235 8251 8262 8282-8287 8298 8356 8365 8368 8452 8455-8456 8539 8597 8648 8679 8813 8863 8898 8921 8935 8939 8948 8951 8957 8983 9002 9041 9061 9122 9128 9257 9285 9414 9452-9453 9466 9474 9484 9503 9517 9529 9553 9563 9671 9677 9703 9714 9781 9841 9927 10007 10175 10296 10343 10491 10741-10742 10778 10795 10907 10948 11239 11513 11531 11573 11606 11626 11807 11869 11952 12000 12006 12160 12190 12218 12256 12327 12363 12371 12375 12378 12426 12438 12465 12470 12488 12549-12550 12570 12604 12615 12617 12663 12670 12735 12749 12754 12830 12893 12904 12910 12916-12917 12976-12977 13038 13084 13090 13116 13249 13254 13367 13389 13391 13443-13445 13456 13472 13479-13480 13494 13496 13499 13505 13512 13516 13551 13554-13555 13575 13590 13613 13630-13631 13644 13670 13713 13782 13784 13793 13803 13858 13866 13869 13882 13891
fetal skin	Invitrogen	FSK002	1004 3544 4834 5523 9922 9942 11134-11135 12570 13495 13499 13793 13884 13889
fetal spleen	BioChain	FSP001	997 5030 9466 11108 12033 12749 13590
umbilical cord	BioChain	FUC001	60 83 89 142 166 567 609 760 997 1302-1304 1306-1307 1309 1671 1697 1724 1848 1917 1978 2111 2154 2161 2207 2215 2315 2343 2444 2569 2576 2591 2597 2652 2866 2926 3468 3526 3599 3602 3625 3697 3722 3799-3805 3813 3839 3885 4025 4060 4173 4197 4246 4277 4340 4364 4387 4391 4395-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			4396 4405 4410 4434 4543 4589 4667 4694 4767 4834 4865 4940 4957 4963 4985 5030 5093 5096 5108 5163 5171 5213 5313 5340 5342-5344 5380 5481 5521 5526 5627 5656 5674 5714 5743 5750 5757 5801 5895 5902 5912 5938 6027 6061 6082 6125 6186 6195 6218 6241 6313 6321 6410 6458 6486- 6495 6595 6607-6608 6668 6745 6825 6860 6870 6979 7054 7141 7260-7261 7275 7329 7355 7373 7383 7444 7579 7586 7677 7716 7807 7930 7935-7936 7995 8077 8093 8226 8246 8262 8298 8343 8345 8358 8387 8452 8535 8563 8635 8669 8711 8819 8858 8863 8921 8935 8943-8944 8948 8963 9001- 9002 9012 9097 9130 9132 9134-9138 9264 9303-9304 9313 9332 9401 9424 9466 9472 9474 9544 9597 9665 9677 9700 9722 9734 9758 9834 9841 9848 10050 10175 10183 10267 10277 10311 10337 10446 10470 10508 10529 10566 10691 10772 10828 10961 11108 11132 11145 11239 11241 11273- 11276 11293 11408 11484 11513 11596 11604 11607 11620 11695 11823 11909 11927 11942 12000 12077 12160 12245 12255-12256 12292 12305 12308 12363 12383 12404-12405 12426 12438 12511 12570 12601 12605 12630 12700 12706 12754 12875 12913 12916 12935 12957 12993 13002 13009 13020-13021 13062 13135-13136 13141 13254 13283 13318- 13319 13336 13394 13400 13472 13479 13481 13488-13489 13495-13496 13499 13507 13511-13512 13516 13551 13555 13568 13575 13590 13613 13630 13644 13713 13740-13742 13866-13867 13882 13884 13888
fetal brain	GIBCO	HFB001	51 70 211-213 215-222 224-229 445 586-588 598 608 703-710 712-716 1068 1148 1178 1184 1193 1308 1516 1556 1774 1778 1957 1974 1976-1977 2010 2025-2029 2134-2135 2145 2161 2171 2174 2220 2223 2257 2266 2283 2444 2449 2510 2555 2563 2569 2590 2597 2614 2617 2717 2719-2723 2726 2729- 2734 2809 2997 3002 3081 3083 3086 3109 3226-3237 3239 3257 3272 3278 3282-3283 3286 3356 3419 3460 3479 3492 3495 3544 3548 3557 3590 3604-3605 3625 3627 3634 3673 3689 3697 3709 3722 3797 3810 3839 3885 4006 4011 4019 4022 4025 4040 4054 4059 4095 4194 4201 4253 4277 4282 4355 4364 4383 4399 4405 4410 4412 4434 4473 4480 4498- 4504 4507-4508 4517 4543 4654 4689 4694 4730-4733 4735 4755 4783 4820-4823 4825-4830 4845 4885 4940 4949 4957 4962 4972 4985 5017 5019 5022 5031 5037 5108 5132 5167 5171-5172 5262 5380 5481 5521 5523 5527 5553 5616 5656 5711 5740 5788 5801 5894 5902 5906 5908 5923 5938 5979- 5989 6057 6082 6096 6125 6147 6159 6161-6163 6165 6207 6212-6213 6215-6222 6241 6257 6288 6336 6369 6374 6419 6422 6512 6551 6555 6595 6598 6607 6711 6767 6788 6823- 6825 6860 6871 6879 6892-6894 6900 6909-6910 7058 7118- 7119 7169 7220 7222 7224-7225 7228-7229 7231-7233 7275 7426 7431 7444 7481-7483 7485-7488 7560-7567 7569 7608 7743 7768 7792 7814 7845 7864 7930 7977 7995 8093 8095 8110 8140 8226 8235 8262 8345 8358 8361 8370 8372 8387 8441-8443 8445 8447 8450-8455 8520 8535 8558 8597 8603 8648 8663-8666 8677 8702 8742-8749 8811 8838-8839 8943 8951 9010 9092 9134 9137 9257 9287 9304 9317 9455 9457 9466 9472 9475 9484 9510 9515 9533 9553 9567 9644-9645 9647-9649 9734 9758 9781 9785-9786 9791 9832-9837 9927- 9928 9939 9942 9970 10053 10175 10275 10277 10296 10329 10375-10378 10434 10464 10486 10496 10645 10679 10691 10778 10782 10791 10838-10844 10928 11019-11025 11027 11032 11055 11061 11108 11132 11145 11153 11208 11239 11343 11483 11513 11588 11596 11604 11606 11620-11621 11668 11691-11695 11818 11867 11869 11929-11930 12006 12033 12039 12041 12044 12047 12066 12078 12197 12218

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			12327 12375 12405 12411 12424 12438 12521-12522 12564 12570 12576 12582 12590 12599 12601 12604 12611 12626 12630 12637-12640 12670 12674 12688 12694-12695 12703 12734 12748 12754 12785 12835 12840 12913 12916-12917 12929-12930 12935 12940 12946 12959 12989 12993 13020 13051-13052 13054 13073 13083 13090 13108-13110 13117 13131 13136 13148 13158 13160 13169 13184-13186 13254 13263 13277 13295 13389 13394 13438 13456 13477 13479- 13481 13489-13490 13494-13500 13502-13503 13506 13512 13516 13535-13536 13555 13575 13590 13592 13605-13606 13613 13616 13627 13630 13644-13645 13660 13670 13679 13687 13713 13793 13803 13838 13861 13866 13868-13869 13875 13888 13891 13896
macrophage	Invitrogen	HMP001	1002 2253 3548 4011 4058 4201 4246 4282 5526 8093 8262 11137 12039 12426 12511 12521 13888
infant brain	Columbia University	IB2002	6 89 142 211 276 307 518 589-590 598 644 717-718 720-721 773 841 921-924 926-932 937 1023 1091 1147-1150 1289 1493 1522-1525 1557-1564 1724 1778 1928 1947 1976 1978 2097 2111 2138 2172 2218-2223 2257 2283 2401 2418-2419 2444 2449 2516 2555 2563 2569 2575 2597 2627 2809 2818 2880 2932 3087 3166 3226 3241-3245 3272 3435 3474 3476-3477 3481 3483-3486 3488-3489 3492 3494-3495 3497 3538 3544 3548 3572 3595 3597 3669 3671-3672 3709 3720 3722 3737 3797 3817 3885 3985 3997-3999 4006 4011 4022-4031 4040 4095 4201 4246 4253 4277 4297 4355 4405 4410 4434 4676 4689 4767 4775 4831-4834 4837 4885 4962 4983 4998 5017- 5019 5021-5031 5035-5037 5040 5095 5143 5164 5167 5169 5233-5236 5380 5505 5517-5519 5523 5536 5546-5548 5691 5695 5724 5750 5766 5788 5801 5895 6027 6048 6082 6095 6111 6119 6132 6135 6147 6223 6301-6303 6305-6307 6374 6411 6459 6555 6563 6591-6595 6601 6606-6607 6609-6611 6613-6614 6624 6711 6767 6799 6805 6909 6946 7018 7052 7067 7118 7133 7166 7168-7169 7386 7464 7469 7473 7571- 7573 7697-7698 7716 7814 7827-7828 7905 7934 7977 8071- 8073 8084 8098-8104 8235 8320 8331 8351 8354-8356 8364- 8365 8370 8372 8376 8452 8520 8572 8667-8668 8750-8752 8813 8830 8863 8883-8885 8950 8958 8963 9040-9041 9251 9257 9267 9293-9298 9313 9424 9454 9456-9457 9466 9510 9514-9515 9533 9542 9556 9576-9577 9597 9626 9646 9722 9758 9787 9903-9904 9988 10027 10138-10139 10155-10160 10284 10296 10319 10346 10496 10536-10542 10557 10670- 10672 10680 10682 10778 10791 10897 10971 11028-11030 11052 11100-11109 11122 11132 11192 11392 11403-11404 11447 11513 11568 11595 11606 11626 11638 11818 11927 11931-11933 12028 12030-12031 12033-12034 12036-12039 12041 12047 12049 12146 12155-12157 12160 12327 12344 12363 12383-12385 12402 12405-12408 12424 12439 12521- 12522 12570 12590 12601 12611 12615-12616 12626 12639 12684-12685 12688 12696-12697 12707 12725-12727 12729 12748-12749 12754 12763-12764 12830 12904 12913 12916- 12917 12923 12929 12959 12977 12990 12996 13000 13047 13051 13054 13062 13073 13082-13084 13117 13141 13187- 13188 13196 13218-13219 13249 13257 13277 13284-13285 13351 13389 13394-13395 13456 13458 13479-13481 13488 13494-13495 13499 13503 13512 13516 13530 13535 13575 13607-13608 13613 13616 13641 13649 13659 13679 13705- 13706 13708 13713 13793 13798-13801 13803 13861 13869 13872 13875 13883-13884 13888 13891-13893 13896
infant brain	Columbia University	IB2003	6 46 746 1914 1947 1959 1994 2111 2220 2257 2516 2962 3166 3226 3272 3435 3572 3885 4277 4377 4410 4833 4837 5029-5030 5040 5147 5259 5851 6147 6423 6595 6598 6611

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			7145 7169 7716 8262 8354-8355 8364 8452 8863 9264 9457 9515 9556 9577 9626 9646 9715 9781 9928 9970 10027 10329 10376 10557 10791 11083 11289 11406 11459 11513 11663 11933 12039 12405 12546 12570 12601 12616 12685 12754 12913 12916 12954 12977 12990 13000 13056 13062 13195 13257 13392 13456 13458 13480-13481 13488 13497 13499 13506-13507 13511-13512 13514 13516 13549 13616-13617 13649 13793 13861 13884 13888 13891 13896
infant brain	Columbia University	IBM002	1564-1565 1976 2218 2420 3166 4391 5788 6147 6302 10329 11108 11513 12039 12729 12830 13062 13257 13512 13617 13803 13859 13861
infant brain	Columbia University	IBS001	927 931 1564 2915 3166 3737 3885 5029 5044 5095 5143 5701 5894-5895 6135 6307 7018 8452 8963 9424 9556 9626 10296 10542 11083 11100 11108 11167 12383 12611 12785 13257 13280 13479 13495 13506 13617 13679 13713 13896
lung, fibroblast	Stratagene	LFB001	67 235 552 641 746 1346 2090 2186 2343 2770 2812 2871 3203 3537 3548 3634 3812 3839 4073 4253 4434 4654 4783 4786 4821 4940 4957 4963 4985 5163 5172 5492 5523 5788 5911 5938 6027 6048 6057 6223 6272 6322 6599 6873 6886 6997 7204 7759 7815 7933 7977 8226 8235 8262 8354 8452 8648 8742 8791 8830 8863 8898 8944 8948 8951 9000 9076 9097 9128 9290 9304 9414 9455 9466 9472 9476 9503 9544 9563 9671 10000 10050 10342 10376 10434 10447 10679 10760 10857 11055 11094 11289 11402 11607 11818 11837 12000 12006 12178 12363 12405 12462 12582 12617 12636 12670 12754 12913 12916-12917 12925 12940 13126 13377 13394 13446 13456 13494 13497 13499 13502 13575 13613 13670 13679 13691 13795 13797 13867-13868 13882
lung tumor	Invitrogen	LGT002	51 69 88 142 158 211 444 598 608 722-723 733 795-797 799 1004 1023 1135-1145 1308 1338 1346 1493 1526-1533 1535 1566-1569 1626 1654 1816 1841 1848 1860 1976 1983 2090 2150 2161 2173 2223 2257 2266 2296-2297 2342 2402 2449 2483 2555 2569 2576 2591 2611 2623 2724 2809 2868 2880 2926 3088 3166 3272 3347 3571 3658-3666 3673 3722 3737 3797 3839 3885 4000-4002 4006 4011 4025 4032-4034 4060 4133 4201 4246 4253 4277 4282 4340-4341 4384 4388 4391 4399 4402 4405 4434 4543 4622 4671 4686 4767 4783 4791 4833-4834 4836 4885 4903 4940 4957 4987 4998 5001 5017- 5018 5030 5037 5052 5108 5163 5210 5227-5232 5422 5451 5520-5528 5581 5627 5637 5674 5693 5713 5724 5748 5766 5772 5788 5894-5895 5902 5907 5917 5938 5990 6005 6020 6094 6129 6147 6171 6224-6225 6239 6241 6253 6322 6336 6404-6410 6461 6508 6595-6598 6624 6765 6793 6798 6851 6870 6873 6994 7003 7008 7045-7047 7053-7055 7067 7085 7109 7116 7139 7141 7158 7169 7187 7468 7517 7524 7579 7608 7676 7687 7716 7761 7825-7826 8074-8078 8105-8106 8139 8235 8298 8323 8335 8345 8354 8359 8363 8365 8370 8372 8375 8456 8563 8633 8648 8678 8741 8792 8798 8805 8831 8863 8870 8989 9002 9010 9012 9032-9037 9039 9051 9076 9080 9092 9128 9257 9269-9271 9273-9274 9276 9299- 9301 9399 9414 9424 9457 9466 9472 9480 9484-9485 9517 9533 9536 9539 9544 9567 9612 9626 9665 9677 9689 9700 9703 9758 9773 9784 9788 9838-9841 9870 9928-9929 9942 9970 9983-9986 10140-10143 10149 10161 10175 10275 10296 10319 10330 10346 10349 10386 10496 10508 10561 10591- 10593 10673-10674 10742 10774 10778 10782 10788 10802 10836 10971 11031-11033 11064 11108 11132 11182-11191 11393-11395 11406 11459 11462 11560 11565 11588 11596 11604 11606-11607 11615 11618 11629 11821 11823 11845 11869 11932 11934 11961 11978-11980 12000 12006 12017 12022 12033 12078 12080 12127 12150-12154 12178 12236

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			12327 12363 12371 12379 12386-12393 12409 12424 12521 12570 12590 12616-12618 12630 12637 12674 12691 12693 12698-12699 12716 12749 12754 12760 12762 12830 12832- 12833 12842 12904 12907 12913 12917 12923 12993 13020 13031-13032 13035 13060 13062 13064 13072 13083 13090 13136 13150 13193 13197 13202 13234 13277 13279 13281- 13282 13295-13296 13381-13383 13385-13386 13394 13400 13456 13477 13479-13480 13484 13488-13489 13492 13494 13496-13497 13499 13503 13506-13507 13511 13554 13575 13597 13616 13630 13646 13649 13659-13660 13670 13701- 13704 13713 13743 13782 13788-13789 13791-13792 13802- 13803 13864 13867-13868 13872 13882-13884 13888 13892
lymphocytes	ATCC	LPC001	142 316 1034 1977 2161 2342 2367 2483 2513 2529 2932 2962 3272 3711 3722 3839 4006 4277 4282 4405 4434 4836 4970 5037 5239 5451 5706 5796 5924 5941 6048 6147 6301 6765 6793 6805 6815 7133 7171 7275 7320 7687 7815 8033 8093 8095 8105 8110 8246 8262 8345 8365 8368 8370 8535 8664 8674 8722 8834 8858 8898 8919 8963 9012 9257 9456-9457 9484 9539 9544 9560 9758 9928 9939 10175 10201 10284 10333 10496 10520 10529 10679 10744 10766 11032 11108 11508 11513 11519 11853 11862 12033 12160 12363 12387 12402 12424 12438 12520 12560 12570 12663 12830 12913 12923 12968 13021 13066 13072 13085 13140 13147-13148 13394 13479 13488 13495 13499 13507 13575 13867 13869 13888
leukocyte	GIBCO	LUC001	21 49 51 67 83 88 94 142 211 316 326 340 368 371 403 438 443-455 464 485 518-523 525-530 532-535 591-592 616 724- 726 744 800 841 889 943 1004 1346 1556 1570-1572 1826 1914 1916 1927 1959 1976-1977 2095 2103-2107 2124-2127 2134 2138 2145 2161 2163 2175 2215 2223 2237 2266 2343 2363 2412 2421 2449 2483 2529 2555 2569 2575 2597 2617- 2618 2695-2696 2827 2876-2877 2899 2903 2961 2965-2975 3002 3035-3038 3040-3046 3109 3132 3166 3199 3203 3207 3246-3251 3265 3272 3286-3287 3312 3344 3356 3361 3378 3400 3434 3451 3468 3479 3484 3494 3503 3552 3590 3610 3627 3634 3704 3709 3720 3722 3725 3757 3797 3804 3810 3839 3885 3985 3996 4006 4009-4011 4019 4022-4023 4025 4035-4037 4058 4060 4194 4253 4269 4277 4297 4341 4362 4388 4390-4391 4396 4399-4400 4402 4405 4410 4412 4431 4434 4534 4543 4594 4615 4630 4641 4651-4663 4670 4688- 4689 4694 4699-4706 4736 4755 4758-4759 4767 4775 4783 4791 4798 4828 4835-4840 4845 4865 4930 4940 4947-4948 4957 4962 4964 4972 4976 4985 4991 4998 5001 5003 5017 5022 5030 5037 5040 5075-5076 5108 5118 5143 5163 5171- 5172 5313 5481 5503 5505 5521 5523 5526 5535 5549 5552 5656 5691 5724 5726 5740 5750 5766 5772 5788 5794 5796 5801 5865 5874 5894-5895 5906 5908 5923-5924 5928 5938 5989 6027 6042 6057 6063-6064 6082 6094-6103 6125 6130- 6137 6142 6147 6166-6167 6171 6181 6214 6226 6239 6253 6301 6307 6371 6374 6418 6512 6662 6716 6730 6788 6792 6799 6815 6836 6860 6873 6876-6877 6886-6887 6945 6975 6979 7018 7037 7056 7058 7067 7116 7118 7137 7155 7158 7171 7275 7315 7384-7385 7387-7389 7391-7393 7395-7398 7452-7463 7468 7494 7608 7671 7676 7687 7714 7733 7792 7815 7845 7864 7870 7905 7930 8093 8107 8110 8120 8139- 8140 8224 8226 8262 8276 8320 8363-8365 8368 8375 8387 8432 8452 8456 8520 8535-8536 8539 8562-8563 8577 8579 8597 8599-8601 8603-8605 8608 8640-8646 8648 8664 8669 8674 8677 8691 8702 8722 8753 8755 8798 8815-8816 8830 8838-8839 8858 8863 8870 8876 8898 8943-8944 8948 8951 9001 9010 9012 9061 9076 9092 9097 9128 9257 9304 9454-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
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leukocyte	Clontech	LUC003	536 539 541-543 593 728 1552 1927 1974 3089 3252-3253 3434 3548 3709 3711 3722 3797 4011 4019 4040 4060 4194 4201 4277 4282 4622 4707 4791 4841-4842 4949 4998 5001 5030 5345 5895 6052 6138 6227 6419 6595 6754 6765 6767 6788 6911-6912 7049 7139 7171 7464 7575-7577 8093 8110 8116 8365 8370 8375 8592 8648 8830 8863 8944 9466 9544 9612 9758 9771 9773 9790 9929 10326 10346 10679 10779 10961 11035-11036 11132 11401 11513 11853 11940 12160 12256 12405 12670 12674 12681 12840 12904 12906 13020 13051 13162 13280 13400 13488 13511 13516 13554 13670 13679 13860 13869 13883 13889
melanoma from cell line ATCC #CRL 1424	Clontech	MEL004	83 142 360 447 841 1061 1346 1516 1573 1724 1959 1963 2159 2175 2343 2367 2513 2652 2812 2876 2961 3001 3272 3345 3604 3627 3722 3754 3839-3840 3985 3988 4040 4194 4246 4341 4515 4568 4641 4667 4862 4940 5075 5132 5163 5481 5492 5523 5740 5788 6008 6112 6119 6147 6189 6195 6272 6287 6418 6423 6508 6563 6726 6860 6870 7134 7166 7169 7275 7294 7579 7677 7748 7831 7852 7980 8110 8116 8226 8235 8262 8320 8345 8363 8370 8456 8563-8564 8633 8838 9001-9002 9128 9296 9304 9313 9484 9542 9544 9646 9703 9758 9780-9781 9808 9999 10007 10027 10296 10346 10470 11145 11239 11289 11401 11406 11508 11596 11606 11620 11823 11899 11950 12019 12107 12160 12292 12329 12363 12405 12436 12523 12599 12658 12670 12749 12754 12774 12842 12930 13020 13296 13394 13458 13489 13498 13501 13507 13551 13554 13575 13613 13616 13649 13660 13743 13775 13868
mammary gland	Invitrogen	MMG001	51 67 142 449 594 598 616 708 729-733 1004 1060 1194-1196 1310-1315 1329 1536-1541 1826 1848 1858 1914 1947 1974 1976-1978 2174-2175 2283 2299 2310 2336 2343 2403-2406 2449 2483 2555 2563 2576 2597 2611 2614 2617 2812 2827

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			2926 3191 3207 3490 3503 3673 3714-3715 3722 3737 3777 3796 3807-3819 3885 4003-4004 4060 4330 4346 4355 4391 4399 4434 4543 4671 4767 4791 4836-4837 4843 4940 4964 4975 4985 4998 5001 5017 5019 5022 5052 5108 5155 5163 5168-5169 5269 5345-5347 5466 5526-5527 5529 5581 5615 5724 5772 5778 5788 5794 5894-5895 5902 5907 5911 5917 5923-5924 6048 6057 6064 6094 6109 6125 6147 6156-6157 6215 6228 6321 6430 6458 6496-6499 6545 6579 6598-6599 6607 6711 6765 6780 6793 6797 6799 6805 6880 6931 6979 6987 6996 7012-7013 7048 7054 7057 7104 7141 7158 7169 7517 7578-7581 7583 7872 7937-7940 8110 8139 8156 8224 8262 8292 8298 8336 8359 8363 8365 8372 8452 8619 8628 8646 8648 8722 8758-8759 8782 8813 8815 8863 8882 8939 8963 8983 9012 9097 9111 9139-9141 9143 9157 9164 9264 9313 9327 9347 9466 9484 9511 9517 9544 9553 9563 9577 9646 9700 9703 9734 9746 9780 9791 9844-9846 9927-9928 9942 10006-10007 10051-10055 10144 10146-10147 10162 10285 10330 10346 10439 10490-10491 10496 10542 10557 10600 10628 10645 10691 10729 10772 10796 10983 11038 11108 11132 11216-11217 11277-11279 11396-11397 11406 11459 11513 11596 11606-11607 11626 11628 11823 11830 11833 11902 11941-11943 11979 12000 12009 12037 12047 12078 12093 12146 12160 12181 12258-12263 12281 12327 12371 12383 12387 12395 12424 12426 12438 12442 12484 12511 12564 12570 12590 12594 12601 12605 12609 12615- 12616 12618 12621 12653 12670 12691 12699 12702-12703 12749 12771 12791-12794 12834-12835 12885 12898 12905 12913 12916-12917 12920 12923 12955 12976-12977 13002 13020 13035 13047 13062 13064 13066 13072-13073 13084 13090 13092 13127 13135 13169 13190 13193 13195 13249 13254 13296 13320-13322 13392 13456 13477 13479-13480 13488-13489 13494 13497-13499 13505-13507 13512 13514 13516 13546 13551 13554-13555 13590 13611-13612 13631 13649 13670 13713 13743-13745 13838 13864 13866-13867 13869 13872 13875 13882-13885 13888 13891
induced neuron cells	Stratgene	NTD001	88 1493 1552 1561 2034 2090 2510 2522 2570 2576 2623 3226 3272 3839 4006 4058 4282 4384 4694 4783 4888 5103-5104 5172 5523 5541-5542 5684 5766 5788 5794 5938 6082 6195 6418 6449 6607 6960 6972 7058 7494 7815 7937 8370 8929- 8930 8996 9000 9003 9128 9157 9289-9291 9472 9928 10275 10550 10729 10760 11607 11736 11818 12039 12075 12094 12256 12363 12381 12423 12522 12707 12735 12863 12906 12958-12959 12963 13020 13052 13054 13196 13202 13310 13368 13378 13438 13479 13486 13506-13507 13546 13616 13654 13659 13691 13795 13891
retinoid acid induced neuronal cells	Stratgene	NTR001	1552 3839 3885 4282 4434 5030 9308 9466 11108 11132 12034 12039 12405 12424 12570 12905 13047
neuronal cells	Stratgene	NTU001	88 708 1552 1561 1947 2223 2490 2614 3272 3610 3625 3627 4032 4201 4253 4297 4337 4434 4543 4622 4641 5104 5163 5523 5541 5684 5788 6094 6147 6307 6601 6862 7755 8648 8740 8996 9097 9128 9289 9308 9466 9511 9544 10333 10779 10963 11032 11108 11132 12034 12039 12075 12405 12424 12570 12590 12706 12749 12830 12905 12917 12963 13035 13073 13280 13490 13507 13613 13616
pituitary gland	Clontech	PIT004	1148 5674 6068 6371 7759 8093 10430 12605 12636 12658 12916 13021 13082 13875
placenta	Clontech	PLA003	3885 4025 5030 5536 5711 5923 8349 8367 9921 12033 12076 12403 12511 13655 13885
prostate	Clontech	PRT001	67 83 142 225 235 379 486 572 616 1286 1316-1329 1538

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			2023 2139 2147 2161 2266 2290 2337-2344 2346 2367 2422 2444 2511 2631 2809 3001-3002 3084 3419 3563 3625 3627 3797 3810 3821-3827 3829-3835 4019 4022 4173 4282 4332 4434 4667 4755 4791 4862 4865 4998 5001 5066 5171 5349 5352-5356 5358-5361 5363-5364 5481 5581 5656 5674 5723 5740 5902 6027 6047 6125 6321 6371 6374 6427 6458 6463 6500-6507 6509 6563 6598 6643 6793 6803 6871 7014-7015 7058 7104 7275 7320 7608 7635 7733 7842 7852 7864 7941- 7943 7946-7951 7953-7954 8077 8087 8093 8110 8224 8226 8452 8487 8520 8558 8635 8677 8863 8950 8963 8983 8997 9012 9145-9148 9150-9154 9269 9302 9317 9466 9503 9528 9646 9703 9780 10000 10027 10056-10060 10491 10629 10691 10777 10891 11145 11200 11239 11281 11283-11295 11344 11406 11761 11837 11862 12006 12166 12264-12278 12305 12363 12368 12411-12412 12438 12467 12685 12691 12729 12734 12795-12798 12800 12830 12863 12904 13010-13011 13104 13146 13295 13323-13326 13377 13394 13456 13473 13477 13489 13516 13533 13550 13611 13678-13679 13746 13866-13867 13884 13889
rectum	Invitrogen	REC001	6 67 142 683 731 997 1178 1909 1959 2005 2023 2596 2611 2614 2809 2926 3314 3333 3455 3722 3780 3870 4173 4355 4837 4949 4987 5526 5580 5615 5674 5691 5724 5788 5895 5909 5924 6057 6112 6195 6765 6805 7815 7833 8095 8664 8863 9517 9539 9544 9884 9927 10400 10666 11401 11513 11606 11985 12160 12327 12428 12693 12848 12910 12977 13051 13064 13072 13420 13494 13497 13507 13512 13515- 13516 13866 13869 13884 13888
salivary gland	Clontech	SAL001	67 731 800 997 1054 1914 2267 2395 2529 3136 3595 3627 4011 4192 4246 4330 4434 4641 4957 4987 5040 5052 5163 5451 5481 5706 5723 5788 5895 6219 6621 6801 6900 6975 7045 7733 8110 8372 8535 8563 8635 8830 8951 9000 9010 9051 9313 9472 9475 9671 9724 9758 9927 10027 11145 11695 11725 12017 12284 12363 12424 12427 12570 12609 12670 12674 12693 12977 13035 13307 13554 13617 13867 13872 13889 13891
salivary gland	Clontech	SALs03	1516 1724 1858 5030 6186 13657 13864
skin fibroblast	ATCC	SFB001	2251-2252 5788 6068 12511
skin fibroblast	ATCC	SFB002	6068 8951 12511
skin fibroblast	ATCC	SFB003	4025 5895 7741
small intestine	Clontech	SIN001	142 319 627 654 1034 1063 1197-1198 1330-1338 1340-1359 1575 1646 1774 1814 1978 2161 2347-2354 2409 2876 3046 3419 3460 3605 3716-3718 3737 3797 3837-3839 3841-3843 3845-3857 3885 3986 4060 4201 4301 4351 4385 4568 4689 4694 5076 5163 5270-5273 5304 5326 5365 5367-5372 5374 5503 5550 5701 5772 6064 6094 6171 6288 6427 6430-6432 6438 6510-6522 6598 6615 6793 6815 6997-6998 7016-7018 7054 7058 7072 7309 7450 7604 7769 7811 7873-7876 7955 7957 7959-7962 7964 8120 8298 8350 8452 8830 8863 8950- 8951 8966 9010 9073-9075 9119 9126 9128 9155-9166 9303 9544 9560 9780 9884 9928-9929 10008-10010 10061-10068 10097 10262 10330 10351 10601 10630-10634 10760 10983 11061 11219 11296-11308 11310-11313 11513 11620 11693 12182-12183 12280-12287 12327 12363 12488 12707 12799- 12801 12922 12991 13012-13014 13035 13051 13064 13297 13307 13328-13332 13335 13382 13499 13506 13554 13560 13575 13631 13695 13714 13747-13749 13751 13882 13884
skeletal muscle	Clontech	SKM001	1104 1346 2363 2367 2495 2555 2876 2880 3555 3634 3722 4011 4022 4194 4201 4253 4277 4282 4434 4641 4940 4972 4998 5343 5481 5523 5801 6005 6336 6873 7408 7995 8110 8120 8235 8262 8292 8345 8372 8576 8740 8830 8936 8951

Tissue Origin	RNA Source TM	Library Name	SEQ ID NOS:
			9303 9689 10616 10679 11132 11145 11825 11869 11927 12387 12442 12467 12570 12663 12735 12916 13280 13503 13872 13885
skeletal muscle	Clontech	SKM002	8535
skeletal muscle	Clontech	SKMs03	6336 6962 8936
skeletal muscle	Clontech	SKMs04	770 1724 3797 4277 6336 12405 13658
spinal cord	Clontech	SPC001	83 142 390 415 598 668 708 731 1184 1199-1207 1360-1375 1377-1396 1516 1574-1576 1595-1596 1849 1927 2070 2129 2161 2311-2314 2345 2355-2368 2423-2424 2430 2484 2529 2569 2576 2876 3215 3249 3272 3283 3532 3584 3627 3634 3711 3719-3722 3737 3839 3860-3884 4011 4025 4038-4039 4043 4055-4056 4173 4246 4282 4354 4375 4391 4434 4681 4767 4781 4808 4964 4985 4998 5037 5163 5233 5274-5277 5375-5392 5394-5402 5523 5569-5570 5581 5615 5723 5788 5835 5902 5928 5936 6047 6078 6082 6211 6288 6374 6433- 6435 6512 6523-6531 6534 6595 6616 6625-6626 6788 6894 6979 6999 7018-7026 7126 7166 7359 7473 7642 7653 7807 7814 7877-7879 7965-7968 7970 7972-7980 8105 8108-8110 8139 8246 8298 8345 8363 8368 8482 8603 8646 8884 8898 8981 9010 9012 9076-9078 9098 9167-9179 9184-9189 9264 9302 9304 9319-9320 9455 9466 9520 9530 9544 9556 9567 9781 9895 9901 9928 9942 9947 9969 9999 10007 10069- 10077 10079-10085 10177 10296 10326 10346 10376 10422 10566 10602 10635-10638 10679 10685-10686 10729 10776 11132 11220 11246 11314-11323 11325-11330 11417-11418 11459 11513 11818 12000 12011 12017 12033 12039 12160 12184-12185 12288-12292 12295-12299 12301-12305 12363 12375 12383 12387 12402 12413 12442 12468 12527 12605 12617 12636 12657-12658 12739-12740 12754 12772 12802- 12809 12830 12835 12841-12842 12905 12923 12940 12976 13003 13015 13017-13021 13051-13052 13117 13126 13136 13260 13277 13283 13295 13336-13343 13367 13442 13456 13473 13477 13481 13495 13497 13499-13500 13507 13516 13659 13670 13713 13715-13716 13748 13752-13759 13803 13869 13872 13884-13885 13888 13893 13896
adult spleen	Clontech	SPLc01	800 1927 4032 4834 6064 6135 6195 6446 6788 6873 7166 7455 8966 9929 10744 12402 12564 12590 12691 12904 12933 13082 13500 13506-13507 13516 13575 13864 13869 13883 13889
stomach	Clontech	STO001	21 83 142 1004 1208-1215 1217-1219 1397 1399-1405 1671 2315-2316 2345 2369-2373 2375 2575-2576 2809 2846 2984 3136 3166 3537 3610 3698 3723-3725 3839 3885-3897 4057- 4059 4173 4277 4410 4480 4667 4791 4808 4940 4987 5262 5278-5281 5283-5284 5403-5405 5407-5424 5481 5656 5674 5796 5904 6418 6436-6440 6535-6540 6563 6627-6629 6765 6940 7000-7001 7027-7030 7064 7135 7509 7604 7880-7885 7981-7990 8087 8110 8120 8143 8226 8452 8535 9010 9079- 9081 9191 9193-9196 9304-9306 9313 9317 9321 9715 10007 10011-10013 10086-10093 10178-10179 10603-10605 10640- 10642 11069 11167 11221-11222 11331-11337 11339-11343 11419 11513 11818 12186-12190 12307-12314 12327 12363 12425-12427 12438 12617 12773-12774 12810-12811 12834 13082 13103 13298-13299 13344-13349 13592 13630 13670 13717 13760-13764 13782 13888
thalamus	Clontech	THA002	579 598 616 1065 1148 1220-1221 1223-1226 1407-1432 1597 2266 2317-2319 2340 2342 2376-2378 2380 2431 2444 2555 3093 3230 3286 3537 3722 3726-3732 3737 3898-3902 3904-

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			3918 3920-3922 4060-4062 4173 4201 4282 4360 4391 5270 5285-5288 5425-5438 5440-5449 5701 5902 5938 6137 6437 6458 6461 6541-6544 6546-6550 6630 6755 7031 7095 7119 7166 7484 7579 7815 7849 7905 7977 7991-8000 8002-8005 8126-8128 8134 8363 8558 8664 8786 8890 8930 8963 9082- 9085 9128 9197-9199 9201-9216 9251 9264 9308 9503 9515 9556 9646 9703 9928 10014-10017 10027 10094-10100 10102 10267 10496 10606-10608 10643-10650 10696 10891 11145 11223-11225 11344-11355 11406-11407 11420 11513 11604 11695 11791 11950 12022 12107 12191-12199 12315-12331 12363 12375 12405 12428-12430 12688 12706 12735 12748 12754 12812-12813 12815 12835 12914 12959 13020 13023- 13025 13060 13073 13300 13351-13358 13402-13403 13489 13496 13506 13512 13719-13720 13765-13768 13770 13872 13883
thymus	Clontech	THM001	51 142 150 332 346 360 438 546 731 760 895 1004 1104 1227- 1234 1264 1391 1516 1577-1585 1812 1860 1877 2129 2174 2215 2263 2321-2322 2408 2414 2425 2449 2490 2555 2569 2575 2611 2847 2880 3435 3530 3722 3727 3733 3735-3742 3839 3870 4006 4041 4043-4046 4060 4109 4375 4396 4399 4434 4667 4671 4759 4791 4885 4976 4987 5108 5289-5290 5466 5481 5526 5553-5554 5796 5956 5979 6020 6186 6253 6336 6371 6411 6438 6441-6447 6617-6621 6765 6788 6797 6870 6886 6908 6972 6994 7059-7060 7126 7141 7166 7168 7310 7383 7450 7494 7632 7716 7779 7887 7889-7891 8087 8111-8114 8117-8120 8139 8226 8343 8368 8370 8452 8456 8633 8830 8898 8921 8963 9010 9076 9086-9087 9128 9134 9264 9304 9307-9313 9401 9466 9497 9544 9563 9582 9612 9626 9646 9758 9781 9927 9937 9969 10018 10065 10163- 10166 10175 10284 10329 10414 10557 10609-10610 10617 10679 10687-10691 10742 10760 10772 10776 10778 10881 10891 11187 11194 11226-11229 11274 11406 11408-11410 11412 11459 11513 11676 11695 11830 11865 11942 12000 12006 12016 12022 12092 12160 12186 12200-12204 12327 12363 12414-12417 12427 12462 12470 12490 12564 12693 12706 12735 12740 12835 12840 12898 12905 12910 12913- 12914 12916 12977 13020 13036 13051 13062 13111 13126 13141 13295 13301-13305 13326 13351 13391 13396-13397 13456 13484 13498 13505 13507 13512 13516 13546 13713 13803 13805 13808 13866 13869 13885 13888
thymus	Clontech	THMc02	16 27 51 67 142 390 598 1233 1493 1508 1586-1588 1598-1603 1724 1841 1918 1927 1959 1976 1979 1989 2057 2107 2161 2223 2290 2407 2426-2428 2432-2433 2444 2487 2569 2617 3537 3664 3711 3720 3722 3737 3780 3817 4021 4025 4047- 4049 4060 4063-4068 4246 4277 4377 4405 4688 4694 4759 4791 4837 4949 4957 4992 4998 5037 5052 5108 5505 5553 5555-5564 5571-5572 5683 5766 5772 5788 5796 5894 5911 6048 6186 6225 6288 6306 6333 6621 6728 6730-6765 6767 6780 6788 6815 6867 6873 6979 7049 7061-7062 7166 7169 7676 7687 7809 8084 8121 8129-8130 8179 8262 8354 8363 8365 8375 8482 8597 8654 8740 8786 8791 8963 9076 9157 9257 9264 9314 9323-9324 9401 9454 9466 9519 9529 9536 9637 9700 9703 9927-9929 9940 10004 10007 10070 10167 10169-10172 10180 10182 10267 10284 10326 10331 10383 10439 10452 10542 10605 10691 10693-10694 10697 10744 10775 10778 10795 11046 11098 11274 11413-11415 11462 11519 11576 11592 11606 11618 11621 11627-11628 11693 11807 11814 12022 12034 12044 12080-12081 12086 12160 12236 12256 12327 12335 12363 12368 12387 12418-12419 12424 12433 12556 12560 12564 12570 12577 12594 12599 12612 12663 12735 12754 12836-12839 12844 12905 12913

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
			12955 12977 13020 13035 13037 13051 13062 13072 13087 13193 13280 13295 13398 13404 13456 13488 13499-13500 13503 13507 13516 13533 13535 13546 13611 13613 13630 13646 13649 13659 13670 13678-13679 13713 13769 13775 13803 13806-13808 13810-13811 13869 13872 13882-13883 13885 13888-13889
thyroid gland	Clontech	THR001	49 115 142 360 641 698 800 1004 1134 1193 1233 1235 1237- 1241 1329 1433-1471 1473-1476 1478-1479 1481 1589-1591 1593-1594 1604 1606-1612 1614-1615 1639 1671 1906 1927 1959 1976 1994 2090 2099 2134 2150 2161 2174 2186 2215 2343 2367 2381-2387 2429 2434-2437 2449 2490 2510 2529 2555 2569 2662 2827 2901 2961 2997 3001 3109 3265 3286 3425 3490 3503 3560 3643 3698 3722 3737 3743-3747 3797 3839 3885 3923-3941 3943-3954 3956-3961 4009 4050-4053 4060 4069-4082 4109 4173 4194 4253 4277 4282 4348 4354- 4355 4376 4391 4396 4412 4434 4641 4689 4694 4755 4759 4783 4791 4834 4957 4972 4985 4987 5018 5037 5052 5075- 5076 5108 5147 5163 5171 5270 5292-5294 5317 5380 5450- 5461 5464-5481 5503 5523 5565-5568 5573-5574 5693 5711 5724 5757 5772 5788 5894-5895 5917 5923 5938 5959 5966 6005 6013 6027 6047-6048 6061 6064 6125 6135 6139 6189 6215 6240 6336 6371 6374 6448-6449 6458 6508 6538 6551- 6554 6556-6561 6563-6572 6595 6598 6607 6622-6623 6631- 6636 6793 6803 6815 6873 6899 6955 6958 7032-7038 7040 7043 7063 7066-7067 7079 7116 7155 7233 7275 7455 7669 7743 7792 7839 7845 7857 7892-7893 7910 7930 7989 8006- 8008 8010-8033 8053 8067 8087 8092-8093 8110 8116 8120 8122-8124 8131-8143 8196 8226 8235 8262 8345 8365 8368 8370 8372 8375 8452 8520 8535 8543 8597 8646 8711 8760 8816 8839 8863 8898 8930 8948 8951 8963 8966 9010 9055 9088-9091 9142 9157 9217-9220 9222-9227 9229-9242 9244 9257 9264 9304 9315-9316 9325-9330 9368 9401 9455 9466 9484 9525 9542 9544 9563 9646 9695 9703 9780-9781 9855 9928 9942 9947 10000 10019 10027 10103-10117 10119-10120 10173-10175 10183-10185 10346 10376 10440 10470 10496 10611 10651-10657 10666 10679 10695 10698-10704 10760 10772 10778 10782 10788 10891 11033 11051-11052 11061 11063 11112 11231 11256 11356-11357 11359-11360 11362- 11367 11369-11372 11376 11385 11406 11416 11421-11425 11462 11513 11588 11605-11607 11620 11833 11869 11932 11980 11985 12006 12017 12033 12143 12160 12193 12195 12205 12207-12208 12292 12332-12336 12338-12345 12347 12349-12356 12358-12360 12363 12368 12405 12420 12422 12424 12428 12434-12439 12465 12523 12601 12605 12609- 12611 12617 12636 12645 12670 12691 12707 12740 12749 12754 12768 12775 12777 12817-12824 12830 12840 12845- 12848 12863 12911 12940 12955 12977 13020 13026-13028 13038 13047 13051 13062 13072-13073 13090 13104 13117 13126 13195 13202 13254 13295-13296 13360-13371 13389 13391 13399 13412 13479 13488-13489 13492 13494 13498 13500 13503-13504 13506-13507 13511-13512 13516 13533 13551 13554 13590 13613 13627 13644 13646 13656 13659- 13660 13670 13713 13721 13743 13771-13774 13782 13803 13809 13812-13814 13860 13866-13867 13869 13872 13882 13884-13885 13888 13891 13893
trachea	Clontech	TRC001	83 438 483 858 1006 1034 1242-1245 1359 1483-1494 1616- 1619 1621 1671 2266 2324 2388-2391 2409 2438-2439 2444 2575 3001 3136 3272 3425 3460 3535 3548 3748-3756 3810 3962-3967 4083-4086 4530 4755 4758 4949 4957 4987 5075 5213 5295-5299 5481-5482 5484 5486-5488 5490-5491 5535 5576-5580 5656 5941 6091 6450-6453 6574-6578 6637 6797

Tissue Origin	RNA Source	Library Name	SEQ ID NOS:
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uterus	Clontech	UTR001	1036 1134 1246-1250 1324 1493 1495-1511 1622 1671 1928 2145 2266 2310 2326 2343 2367 2392-2397 2555 3281 3479 3720 3757-3760 3762 3969-3986 4088-4090 4192 4201 4246 4277 4390-4391 4434 4515 4998 5002 5184 5300-5301 5481 5492-5504 5656 5695 5712 5794 5936 6116 6475 6579-6587 6595 6870 7002 7043-7044 7311 7484 7895-7899 8046-8055 8057-8059 8061 8110 8146-8147 8152 8226 8262 8622 8677 9008 9092 9137 9252-9257 9334 9370 9414 9466 9539 9703 10023-10024 10128-10134 10346 10595 10660-10668 10706- 10708 11145 11239 11289 11377 11379-11385 11695 11830 12367-12369 12371-12374 12442-12443 12570 12670 12693 12827-12829 12914 13002 13047 13073 13083-13084 13131 13260 13277 13309-13310 13374-13376 13394 13489 13512 13713 13782 13784-13787 13866 13869

TABLE 2

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1	M36501	Homo sapiens	alpha-2-macroglobulin	118	69
2	AF118090	Homo sapiens	PRO2044	247	59
3	X01683	Homo sapiens	alpha 1-antitrypsin	544	78
4	L27428	Homo sapiens	reverse transcriptase	79	27
5	M22332	Homo sapiens	unknown protein	89	40
6	AF015539	Mytilus edulis	precollagen P	113	33
7	X03325	Homo sapiens	apolipoprotein B fragment	540	83
8	AB019280	Mus musculus	sprouty-4	91	35
9	D88152	Homo sapiens	acetyl-coenzyme A transporter	625	87
10	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	124	58
11	AL049569	Homo sapiens	dJ37C10.5 (KIAA0445)	182	82
12	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	85	37
13	L27428	Homo sapiens	reverse transcriptase	135	61
14	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	266	72
15	U93569	Homo sapiens	putative p150	135	37
16	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	132	67
17	X53581	Rattus norvegicus	ORF4	124	34
18	AF183961	Homo sapiens	carbon catabolite repression 4 protein homolog	431	75
19	AJ002190	Homo sapiens	dihydroxyacetone phosphate acyltransferase	551	88
20	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	127	45
21	AK001269	Homo sapiens	unnamed protein product	1643	99
22	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	275	58
23	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	123	75
24	AF156550	Mus musculus	putative E1-E2 ATPase	168	58
25	AF119856	Homo sapiens	PRO1851	585	83
26	U49974	Homo sapiens	mariner transposase	187	46
27	G00901	Homo sapiens	Human secreted protein, SEQ ID NO: 4982.	86	30
28	AF295773	Homo sapiens	ral guanine nucleotide dissociation stimulator	126	74
29	AF113685	Homo sapiens	PRO0974	92	73
30	U83303	Homo sapiens	line-1 reverse transcriptase	102	50
31	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	279	75
32	AF003535	Homo sapiens	ORF2-like protein	114	47
33	M15386	Homo sapiens	gamma-globin	370	84
34	M19419	Mus musculus	proline-rich salivary protein	110	35
35	AF211943	Homo sapiens	WW domain-containing protein WWOX	586	83
36	X13885	Nicotiana tabacum	extensin (AA 1-620)	103	35
37	U93563	Homo sapiens	putative p150	127	58
38	U93564	Homo sapiens	putative p150	103	77
39	AF069732	Homo sapiens	ADA2-like protein	524	88
40	X61046	Hydra sp.	mini-collagen	101	34
41	AK000322	Homo sapiens	unnamed protein product	566	80
42	G03646	Homo sapiens	Human secreted protein, SEQ ID NO:	103	57

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7727.		
43	AF071081	Mycobacterium tuberculosis	proline-rich mucin homolog	104	41
44	AF092135	Homo sapiens	PTD014	228	41
45	Y73353	Homo sapiens	HTRM clone 1870914 protein sequence.	295	56
46	AF118082	Homo sapiens	PRO1902	119	44
47	X78926	Homo sapiens	zinc finger protein	442	52
48	X54326	Homo sapiens	glutamyl-tRNA synthetase	542	81
49	D50645	Homo sapiens	SDF2	321	95
50	M92439	Homo sapiens	leucine-rich protein	344	80
51	U28963	Homo sapiens	Gps2	593	82
52	U41806	Homo sapiens	p60	660	81
53	AF181490	Homo sapiens	prenylcysteine lyase	461	78
54	U93570	Homo sapiens	putative p150	147	36
55	W73499	Homo sapiens	Von Willebrand factor.	529	76
56	AF119851	Homo sapiens	PRO1722	126	57
57	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	115	61
58	AL021939	Homo sapiens	dJ352A20.2 (aldehyde dehydrogenase family protein)	422	90
59	L24158	Homo sapiens	integrin alpha 9 protein	117	71
60	Y32157	Homo sapiens	Human SH3D1A protein.	530	91
61	X61296	Rattus norvegicus	open reading frame 2	117	31
62	AK002064	Homo sapiens	unnamed protein product	330	80
63	AB012223	Canis familiaris	ORF2	80	56
64	U93570	Homo sapiens	putative p150	113	37
65	U15647	Mus musculus	reverse transcriptase	152	55
66	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	126	54
67	Y48359	Homo sapiens	Human prostate cancer-associated protein 56.	590	99
68	W74879	Homo sapiens	Human secreted protein encoded by gene 151 clone HTLEF62.	368	98
69	AF104921	Homo sapiens	succinyl-CoA synthetase alpha subunit	604	93
70	AF175265	Homo sapiens	vacuolar sorting protein 35	632	88
71	U93571	Homo sapiens	p40	106	33
72	X15324	Homo sapiens	angiotensinogen	330	84
73	Z98204	Hordeum vulgare	extensin	111	38
74	Y30713	Homo sapiens	Amino acid sequence of a human secreted protein.	232	61
75	AF118092	Homo sapiens	PRO2061	453	79
76	M63175	Homo sapiens	autocrine motility factor receptor	190	85
77	M26361	Mus musculus	LINE/Ig H-chain fusion protein	153	38
78	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	171	58
79	X78926	Homo sapiens	zinc finger protein	199	37
80	M77381	Homo sapiens	acrosin	98	54
81	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	129	44
82	U93569	Homo sapiens	putative p150	94	38
83	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	100
84	AF255446	Cryptocodinium cohnii	Dip1-associated protein C	129	34
85	R59837	Homo sapiens	Sequence of human microtubule-	82	48

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			associated protein tau.		
86	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	157	76
87	AF116712	Homo sapiens	PRO2738	91	58
88	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	77	44
89	Y82742	Homo sapiens	DNA replication and repair associated protein (DRASP).	315	79
90	M16961	Homo sapiens	alpha-2-HS-glycoprotein	138	74
91	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	250	56
92	AF220656	Homo sapiens	apoptosis-associated nuclear protein PHLDA1	62	69
93	U65928	Homo sapiens	Jun activation domain binding protein	188	75
94	U93568	Homo sapiens	putative p150	102	48
95	S80119	Rattus sp.	reverse transcriptase homolog	130	53
96	U93563	Homo sapiens	putative p150	242	50
97	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	105	46
98	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	132	62
99	X74045	Equus caballus	preproalbumin	289	65
100	AF118090	Homo sapiens	PRO2044	269	90
101	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	198	51
102	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	88	53
103	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	225	82
104	AF003535	Homo sapiens	ORF2-like protein	114	47
105	AF130079	Homo sapiens	PRO2852	133	56
106	AF130089	Homo sapiens	PRO2550	107	71
107	M63473	Homo sapiens	alpha-5 type IV collagen	131	45
108	AF116661	Homo sapiens	PRO1438	112	54
109	X92485	Plasmodium vivax	pval	101	41
110	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	113	80
111	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	199	69
112	AF194537	Homo sapiens	NAG13	104	44
113	L27428	Homo sapiens	reverse transcriptase	160	34
114	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	137	56
115	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	191	67
116	AF130052	Homo sapiens	PRO0956	163	47
117	L27428	Homo sapiens	reverse transcriptase	117	36
118	U93569	Homo sapiens	putative p150	104	66
119	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	96	66
120	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	81	57
121	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	78	51
122	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	95	80
123	X61296	Rattus norvegicus	open reading frame 2	94	36
124	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	131	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
125	AF119900	Homo sapiens	PRO2822	168	68
126	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	209	58
127	L27428	Homo sapiens	reverse transcriptase	102	35
128	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	99	63
129	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	113	73
130	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	170	36
131	U93572	Homo sapiens	putative p150	168	38
132	U37263	Homo sapiens	KRAB zinc finger protein; Method: conceptual translation supplied by author	155	57
133	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	137	92
134	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:75.	58	61
135	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	128	66
136	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	102	38
137	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	230	55
138	AK000496	Homo sapiens	unnamed protein product	127	46
139	X53581	Rattus norvegicus	ORF4	136	38
140	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	158	48
141	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	162	65
142	AF090930	Homo sapiens	PRO0478	127	65
143	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	141	58
144	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	98	65
145	AJ238588	Sciurus vulgaris	cytochrome c oxidase subunit III	417	72
146	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	139	76
147	Y36156	Homo sapiens	Human secreted protein #28.	91	40
148	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	121	70
149	Y76184	Homo sapiens	Human secreted protein encoded by gene 61.	214	85
150	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	95	57
151	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	126	66
152	G00262	Homo sapiens	Human secreted protein, SEQ ID NO: 4343.	105	51
153	AF119900	Homo sapiens	PRO2822	116	62
154	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	149	66
155	AB009993	Mus musculus	collagen a1(V)	105	36
156	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	155	69
157	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	348	71
158	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	146	54
159	AF247705	Oryctolagus cuniculus	alpha 1 type X collagen	102	42

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
160	R95913	Homo sapiens	Neural thread protein.	99	56
161	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	112	52
162	X71442	Rattus norvegicus	ORF 1; putative	96	47
163	U93570	Homo sapiens	putative p150	118	38
164	U23515	Caenorhabditis elegans	weak similarity to adenylyl cyclase-associated protein (CAP) and to P. chabaudi adami major merozoite surface antigen protein (PIR:A32555). Final exon overlaps gene predicted on other strand.	93	37
165	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	143	66
166	AF130079	Homo sapiens	PRO2852	143	90
167	L27428	Homo sapiens	reverse transcriptase	200	53
168	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	92	51
169	R95913	Homo sapiens	Neural thread protein.	116	54
170	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	324	85
171	U83303	Homo sapiens	line-1 reverse transcriptase	111	50
172	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	111	69
173	AF130089	Homo sapiens	PRO2550	126	59
174	S80119	Rattus sp.	reverse transcriptase homolog	151	46
175	G02451	Homo sapiens	Human secreted protein, SEQ ID NO: 6532.	113	53
176	U15647	Mus musculus	reverse transcriptase	104	46
177	M24732	Homo sapiens	lamin-like protein	112	42
178	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	137	38
179	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	143	58
180	AF194537	Homo sapiens	NAG13	92	90
181	U93564	Homo sapiens	putative p150	131	53
182	U93574	Homo sapiens	putative p150	86	46
183	Y14166	Gallus gallus	attachment region binding protein	91	40
184	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	104	64
185	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	183	73
186	U93572	Homo sapiens	putative p150	139	64
187	M22332	Homo sapiens	unknown protein	79	41
188	Y87202	Homo sapiens	Human secreted protein sequence SEQ ID NO:241.	75	71
189	U70935	Peromyscus maniculatus	reverse transcriptase	132	37
190	S80119	Rattus sp.	reverse transcriptase homolog	172	43
191	AF194537	Homo sapiens	NAG13	81	75
192	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	112	64
193	X92485	Plasmodium vivax	pval	96	40
194	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	112	45
195	L27428	Homo sapiens	reverse transcriptase	141	37
196	U93570	Homo sapiens	putative p150	201	41
197	X92485	Plasmodium vivax	pval	120	48
198	AF130089	Homo sapiens	PRO2550	137	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
199	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	377	84
200	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	119	52
201	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	151	68
202	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	247	78
203	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	126	56
204	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	362	80
205	R59842	Homo sapiens	ApoE4L1 protease.	100	82
206	AF161356	Homo sapiens	HSPC093	78	62
207	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	111	48
208	U83280	Leishmania donovani	39 kDa antigen	121	53
209	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	84	80
210	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	146	72
211	M69197	Homo sapiens	haptoglobin-related protein	344	92
212	AF034611	Homo sapiens	intrinsic factor-B12 receptor precursor; cubilin	123	37
213	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	129	65
214	V00662	Homo sapiens	cytochrome oxidase I	485	87
215	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	124	80
216	U35312	Mus musculus	nuclear receptor co-repressor	115	47
217	L26953	Homo sapiens	chromosomal protein	143	77
218	U12690	Homo sapiens	cytochrome oxidase subunit II	224	70
219	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	125	75
220	AB018114	Arabidopsis thaliana	RING finger protein-like	111	38
221	D38112	Homo sapiens	ATPase subunit 6	475	84
222	V00662	Homo sapiens	cytochrome B	466	77
223	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	175	85
224	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	125	38
225	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	86	65
226	X77816	Rattus norvegicus	PR-Vbeta1	130	54
227	U09500	Homo sapiens	cytochrome b	274	62
228	AF081104	Mus musculus domesticus	ORF2	111	36
229	AF090942	Homo sapiens	PRO0657	88	57
230	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	76	57
231	G03472	Homo sapiens	Human secreted protein, SEQ ID NO: 7553.	101	66
232	B12310	Homo sapiens	Human secreted protein encoded by gene 10 clone HDPGP94.	116	54
233	AF010400	Homo sapiens	transaldolase-related protein	253	77
234	AF197913	Helicoverpa armigera nuclear polyhedrosis virus	basic DNA-binding protein BDBP	137	50

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
235	AF090931	Homo sapiens	PRO0483	123	75
236	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	185	86
237	M19503	Homo sapiens	ORF1; putative	99	40
238	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	93	58
239	AF014883	Homo sapiens	NADH dehydrogenase subunit 2	305	65
240	G03102	Homo sapiens	Human secreted protein, SEQ ID NO: 7183.	60	44
241	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	79	50
242	U15647	Mus musculus	reverse transcriptase	117	47
243	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	104	56
244	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	94	45
245	AK023542	Homo sapiens	unnamed protein product	82	38
246	X55702	Drosophila melanogaster	polycomb protein	84	31
247	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	129	65
248	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	154	70
249	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	142	63
250	Y17832	Human endogenous retrovirus K	env protein	297	71
251	U93568	Homo sapiens	p40	103	46
252	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	201	47
253	AF090895	Homo sapiens	PRO0117	139	60
254	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	185	72
255	L27428	Homo sapiens	reverse transcriptase	156	40
256	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	157	59
257	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	118	70
258	AF194537	Homo sapiens	NAG13	141	38
259	B01372	Homo sapiens	Neuron-associated protein.	115	71
260	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	113	53
261	M22332	Homo sapiens	unknown protein	78	45
262	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	70	78
263	X61296	Rattus norvegicus	open reading frame 2	108	36
264	AF016099	Mus musculus	endonuclease/reverse transcriptase	178	45
265	G03303	Homo sapiens	Human secreted protein, SEQ ID NO: 7384.	81	63
266	Y01154	Homo sapiens	Protein sequence Seq Id 54 from WO9901020.	116	84
267	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	118	52
268	AF119855	Homo sapiens	PRO1847	74	70
269	AF109907	Homo sapiens	S164	85	61
270	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	137	63
271	X92485	Plasmodium vivax	pval	107	72
272	AF194537	Homo sapiens	NAG13	167	51

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
273	U93564	Homo sapiens	p40	104	40
274	L27428	Homo sapiens	reverse transcriptase	142	56
275	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	150	60
276	X61296	Rattus norvegicus	open reading frame 2	96	48
277	AF090931	Homo sapiens	PRO0483	140	65
278	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	231	66
279	AF130089	Homo sapiens	PRO2550	164	60
280	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	98	58
281	L22548	Homo sapiens	collagen type XVIII alpha 1	92	38
282	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	68
283	AF116715	Homo sapiens	PRO2829	160	75
284	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	111	53
285	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	94	53
286	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	120	53
287	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	147	66
288	U93572	Homo sapiens	putative p150	125	32
289	AL050399	Arabidopsis thaliana	putative proline-rich protein	142	44
290	X92485	Plasmodium vivax	pva1	147	43
291	AB047600	Macaca fascicularis	hypothetical protein	172	66
292	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	108	55
293	D38115	Pongo pygmaeus	NADH dehydrogenase subunit 5	342	71
294	AF090942	Homo sapiens	PRO0657	99	66
295	M61185	Bos taurus	glutamic acid-rich protein	114	44
296	M13100	Rattus norvegicus	unknown protein	107	43
297	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	114	50
298	X92485	Plasmodium vivax	pva1	93	78
299	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	127	75
300	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	115	42
301	L24521	Homo sapiens	transformation-related protein	117	60
302	X83413	Human herpesvirus 6	U88	219	49
303	U93567	Homo sapiens	putative p150	130	48
304	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:75.	72	61
305	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	153	68
306	D38112	Homo sapiens	cytochrome c oxidase subunit 3	532	79
307	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	84	53
308	L27428	Homo sapiens	reverse transcriptase	151	72
309	M69297	Homo sapiens	ORF 3	145	43
310	X92485	Plasmodium vivax	pva1	81	60
311	L27428	Homo sapiens	reverse transcriptase	103	41

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
312	AF130079	Homo sapiens	PRO2852	135	49
313	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	110	58
314	AF090928	Homo sapiens	PRO0470	88	48
315	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	175	64
316	U93568	Homo sapiens	putative p150	148	46
317	AF119855	Homo sapiens	PRO1847	108	84
318	P60839	Homo sapiens	Sequence of human serum albumin (HSA) on plasmid pXL53.	175	50
319	W46424	Homo sapiens	Human macrophage stimulating protein (MSP).	257	69
320	AL049547	Homo sapiens	dJ34F7.2 (CREB-RP (G13))	247	64
321	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	110	66
322	AF016099	Mus musculus	endonuclease/reverse transcriptase	102	48
323	AF090930	Homo sapiens	PRO0478	141	72
324	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	126	44
325	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	146	59
326	R59842	Homo sapiens	ApoE4L1 protease.	95	60
327	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	84	61
328	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	123	66
329	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	125	65
330	AF119855	Homo sapiens	PRO1847	121	80
331	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	364	71
332	AK000496	Homo sapiens	unnamed protein product	145	41
333	D00570	Mus musculus	open reading frame (196 AA)	153	53
334	AF119855	Homo sapiens	PRO1847	116	74
335	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	50
336	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	129	56
337	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	107	59
338	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	115	72
339	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	117	50
340	AK022217	Homo sapiens	unnamed protein product	127	70
341	U43360	Peromyscus maniculatus	reverse transcriptase	115	75
342	AF118086	Homo sapiens	PRO1992	141	73
343	X92485	Plasmodium vivax	pval	96	59
344	AF106677	Drosophila melanogaster	dissatisfaction	90	48
345	U12693	Homo sapiens	cytochrome oxidase subunit II	239	91
346	L27428	Homo sapiens	reverse transcriptase	95	56
347	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	133	69
348	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	81	51
349	X51616	Volvox carteri	SULFATED SURFACE GLYCOPROTEIN 185	110	41

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
350	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	158	55
351	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	183	60
352	AL390114	Leishmania major	extremely cysteine/valine rich protein	151	51
353	R95913	Homo sapiens	Neural thread protein.	95	56
354	AF061340	Artibeus jamaicensis	cytochrome c oxidase subunit III	346	70
355	AF090895	Homo sapiens	PRO0117	126	60
356	AF016099	Mus musculus	endonuclease/reverse transcriptase	121	48
357	AF118086	Homo sapiens	PRO1992	159	73
358	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	85	89
359	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	98	50
360	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	110	57
361	M13100	Rattus norvegicus	unknown protein	122	34
362	Y36203	Homo sapiens	Human secreted protein #75.	108	63
363	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	83	75
364	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	212	65
365	AF130051	Homo sapiens	PRO0898	136	71
366	AF068294	Homo sapiens	HDCMB45P	188	65
367	M10546	Homo sapiens	cytochrome oxidase I	225	70
368	S80119	Rattus sp.	reverse transcriptase homolog	188	45
369	U70935	Peromyscus maniculatus	reverse transcriptase	75	48
370	AF118082	Homo sapiens	PRO1902	98	79
371	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	106	40
372	AF014903	Pan troglodytes	NADH dehydrogenase subunit 2	169	41
373	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	93	48
374	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	94	66
375	G03107	Homo sapiens	Human secreted protein, SEQ ID NO: 7188.	90	80
376	U93568	Homo sapiens	putative p150	140	56
377	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	140	50
378	AF090942	Homo sapiens	PRO0657	154	66
379	U93568	Homo sapiens	putative p150	149	36
380	U93570	Homo sapiens	p40	184	57
381	L27428	Homo sapiens	reverse transcriptase	128	60
382	AF194537	Homo sapiens	NAG13	114	35
383	AF116712	Homo sapiens	PRO2738	109	56
384	D38112	Homo sapiens	cytochrome c oxidase subunit 3	405	81
385	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	116	63
386	M22334	Homo sapiens	unknown protein	124	39
387	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	97	52
388	D38112	Homo sapiens	NADH dehydrogenase subunit 5	327	94
389	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	157	70
390	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	129	62
391	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	259	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
392	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	137	63
393	U43360	Peromyscus maniculatus	reverse transcriptase	129	54
394	AK023582	Homo sapiens	unnamed protein product	148	46
395	M22332	Homo sapiens	unknown protein	128	41
396	AF118086	Homo sapiens	PRO1992	160	71
397	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	101	52
398	D38112	Homo sapiens	cytochrome c oxidase subunit 3	199	66
399	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	234	78
400	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	107	40
401	AF000996	Homo sapiens	ubiquitous TPR motif, Y isoform	116	61
402	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	145	37
403	AF118082	Homo sapiens	PRO1902	97	55
404	AF202635	Homo sapiens	PP1200	126	55
405	V00662	Homo sapiens	cytochrome oxidase I	352	68
406	AF229067	Homo sapiens	PADI-H protein	129	71
407	AL390114	Leishmania major	extremely cysteine/valine rich protein	197	38
408	L26251	Trypanosoma brucei	CR5	95	46
409	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	310	62
410	X92485	Plasmodium vivax	pva1	96	68
411	M64793	Rattus norvegicus	salivary proline-rich protein	128	40
412	Y19192	Talpa europaea	cytochrome oxidase subunit I	431	83
413	M10546	Homo sapiens	cytochrome oxidase I	299	86
414	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	220	81
415	AF205385	Pan troglodytes	NADH dehydrogenase subunit 5	296	89
416	X58438	Mus musculus	proline rich protein	112	50
417	U70932	Peromyscus leucopus	reverse transcriptase	89	51
418	V00662	Homo sapiens	cytochrome oxidase III	200	84
419	AF017789	Homo sapiens	putative transcription factor CA150	120	41
420	M10546	Homo sapiens	cytochrome oxidase I	183	69
421	AL359782	Trypanosoma brucei	possible (hfv-6) u1102, variant a dna, complete virion genome.	166	44
422	AF130051	Homo sapiens	PRO0898	158	59
423	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	86	52
424	D38116	Pan paniscus	cytochrome c oxidase subunit 3	342	82
425	U93570	Homo sapiens	putative p150	133	41
426	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	67
427	D13951	Nicotiana tabacum	extensin precursor	140	42
428	L27428	Homo sapiens	reverse transcriptase	104	34
429	R95913	Homo sapiens	Neural thread protein.	118	49
430	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	206	97
431	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	88	55
432	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	98	54
433	J05042	Oryctolagus	alpha-1 (VIII) collagen precursor	91	48

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		cuniculus			
434	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	105	56
435	U93572	Homo sapiens	putative p150	118	38
436	U93569	Homo sapiens	putative p150	100	30
437	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	126	81
438	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	166	71
439	U52077	Homo sapiens	mariner transposase	187	52
440	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	80	45
441	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	104	71
442	AE003727	Drosophila melanogaster	CG16718 gene product	301	48
443	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	221	74
444	U35730	Mus musculus	jerky	159	26
445	X53581	Rattus norvegicus	ORF3	192	46
446	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	142	52
447	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	156	38
448	AF194537	Homo sapiens	NAG13	315	70
449	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	93	66
450	X92099	Brugia pahangi	collagen	126	44
451	AF090930	Homo sapiens	PRO0478	88	60
452	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	93	40
453	AF081114	Mus musculus domesticus	ORF2	108	32
454	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	173	65
455	S80119	Rattus sp.	reverse transcriptase homolog	197	54
456	G02535	Homo sapiens	Human secreted protein, SEQ ID NO: 6616.	89	68
457	R95913	Homo sapiens	Neural thread protein.	114	48
458	U09116	Homo sapiens	ORF1, encodes a 40 kDa product	160	39
459	X92485	Plasmodium vivax	pval	99	52
460	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	100	52
461	S80119	Rattus sp.	reverse transcriptase homolog	138	48
462	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	211	67
463	X97707	Pongo pygmaeus abelii	stopcodon created by posttranscriptional polyadenylation	229	76
464	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	119	67
465	L27428	Homo sapiens	reverse transcriptase	154	40
466	AK000496	Homo sapiens	unnamed protein product	140	69
467	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	114	61
468	G00589	Homo sapiens	Human secreted protein, SEQ ID NO: 4670.	146	69
469	D38112	Homo sapiens	cytochrome c oxidase subunit 3	286	79
470	D38112	Homo sapiens	NADH dehydrogenase subunit 4	448	86
471	M10546	Homo sapiens	cytochrome oxidase I	296	79

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
472	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	102	48
473	AL080253	Arabidopsis thaliana	putative snRNP protein	103	42
474	X99452	Lycopersicon esculentum	extensin-like protein Dif54	108	25
475	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	68	34
476	AB012223	Canis familiaris	ORF2	78	66
477	AF130089	Homo sapiens	PRO2550	113	71
478	G03652	Homo sapiens	Human secreted protein, SEQ ID NO: 7733.	390	97
479	AF210651	Homo sapiens	NAG18	146	80
480	AB029309	Homo sapiens	Npw38-binding protein NpwBP	103	40
481	AF194537	Homo sapiens	NAG13	118	31
482	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	115	45
483	L27428	Homo sapiens	reverse transcriptase	184	47
484	U93570	Homo sapiens	putative p150	101	50
485	AF194537	Homo sapiens	NAG13	213	52
486	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	82
487	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	204	86
488	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	140	53
489	U93574	Homo sapiens	putative p150	86	54
490	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	83	56
491	AJ271872	Nicotiana glauca	extensin	220	47
492	U11288	Drosophila melanogaster	diaphanous protein	113	33
493	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	184	70
494	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	68
495	AF119900	Homo sapiens	PRO2822	148	65
496	AB026542	Homo sapiens	WASP-family protein	96	38
497	D86853	Catharanthus roseus	extensin	104	34
498	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	109	47
499	G00492	Homo sapiens	Human secreted protein, SEQ ID NO: 4573.	109	67
500	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	112	62
501	AF119901	Homo sapiens	PRO2831	116	82
502	AF238235	Entamoeba histolytica	diaphanous protein	120	41
503	M22332	Homo sapiens	unknown protein	123	49
504	AF119851	Homo sapiens	PRO1722	204	52
505	X61296	Rattus norvegicus	open reading frame 2	107	45
506	AF118082	Homo sapiens	PRO1902	145	52
507	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	103	68
508	X55685	Lycopersicon esculentum	extensin (class I)	175	39
509	X92485	Plasmodium	pva1	117	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
510	AF090942	Homo sapiens	PRO0657	95	77
511	U93569	Homo sapiens	putative p150	120	54
512	U93574	Homo sapiens	putative p150	140	49
513	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	196	63
514	L27428	Homo sapiens	reverse transcriptase	132	37
515	U93565	Homo sapiens	putative p150	101	45
516	U93574	Homo sapiens	putative p150	178	35
517	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	81	27
518	AF053538	Alvinella pompejana	fibrillar collagen chain FAp1 alpha	112	36
519	X52235	Homo sapiens	ORFII	148	35
520	AF130051	Homo sapiens	PRO0898	98	61
521	L02106	Drosophila melanogaster	ribonucleoprotein	143	40
522	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	202	70
523	U93570	Homo sapiens	putative p150	159	43
524	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	210	100
525	L27428	Homo sapiens	reverse transcriptase	128	38
526	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	96	65
527	X53581	Rattus norvegicus	ORF4	130	42
528	U93570	Homo sapiens	putative p150	195	35
529	AF130089	Homo sapiens	PRO2550	132	43
530	AK024455	Homo sapiens	FLJ00047 protein	126	54
531	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	123	61
532	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	210	44
533	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	109	42
534	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	120	62
535	M64793	Rattus norvegicus	salivary proline-rich protein	124	37
536	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	122	50
537	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	118	43
538	A23786	Beta vulgaris	chitinase 1	91	33
539	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	116	39
540	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	102	67
541	S80119	Rattus sp.	reverse transcriptase homolog	191	50
542	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	155	77
543	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	125	91
544	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	146	62
545	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	74	45
546	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	94	75
547	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	510	86
548	AP000616	Oryza sativa	similar to RING-H2 finger protein	146	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			RHA1a (AF078683)		
549	Y08061	Homo sapiens	Human c-myb protein fragment.	128	82
550	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	153	77
551	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	121	56
552	X92485	Plasmodium vivax	pval	103	50
553	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	129	46
554	L27428	Homo sapiens	reverse transcriptase	149	44
555	AF194537	Homo sapiens	NAG13	157	45
556	Y13247	Homo sapiens	FB19 protein	106	42
557	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	100	54
558	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	176	68
559	S80119	Rattus sp.	reverse transcriptase homolog	113	43
560	AY008270	Homo sapiens	cholesteryl ester transfer protein	107	95
561	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	140	63
562	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	347	68
563	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	93	40
564	D38114	Gorilla gorilla	cytochrome c oxidase subunit 3 (COIII)	329	74
565	Y36156	Homo sapiens	Human secreted protein #28.	153	56
566	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	131	48
567	D38112	Homo sapiens	cytochrome c oxidase subunit 3	406	94
568	AF130079	Homo sapiens	PRO2852	101	55
569	AF081114	Mus musculus domesticus	ORF2	123	40
570	L22030	Glycine max	hydroxyproline-rich glycoprotein	65	45
571	D86853	Catharanthus roseus	extensin	168	39
572	AF104415	Mus musculus	gene trap locus-13	179	66
573	AF130089	Homo sapiens	PRO2550	114	56
574	X67863	Mus musculus	T2	115	42
575	S80119	Rattus sp.	reverse transcriptase homolog	101	28
576	S80119	Rattus sp.	reverse transcriptase homolog	150	57
577	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	142	74
578	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	106	57
579	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	46
580	L24521	Homo sapiens	transformation-related protein	110	38
581	D38112	Homo sapiens	cytochrome c oxidase subunit 3	537	84
582	AF090895	Homo sapiens	PRO0117	127	80
583	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	145	70
584	X55681	Lycopersicon esculentum	extensin (class I)	112	38
585	D38112	Homo sapiens	cytochrome c oxidase subunit 3	473	60
586	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	144	68
587	U47855	Araneus diadematus	fibroin-3	124	30
588	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	150	75
589	U93567	Homo sapiens	putative p150	225	47

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
590	X71602	Nicotiana tabacum	extensin	147	33
591	X57527	Homo sapiens	alpha 1(VIII) collagen	103	42
592	G03112	Homo sapiens	Human secreted protein, SEQ ID NO: 7193.	75	47
593	R28916	Homo sapiens	Type III procollagen (prior art).	116	48
594	R95913	Homo sapiens	Neural thread protein.	116	37
595	U11880	Petromyzon marinus	cytochrome oxidase subunit I	127	52
596	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	84	62
597	L27428	Homo sapiens	reverse transcriptase	158	40
598	M55251	Canis familiaris	glycoprotein 80	559	86
599	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	100
600	M18094	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	143	33
601	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	154	54
602	X73481	Drosophila hydei	mst101(2)	107	42
603	M81321	Macaca fascicularis	proline-rich protein	114	39
604	X05561	Homo sapiens	alpha-1 chain precursor (AA -27 to 917) (2953 is 2nd base in codon)	109	42
605	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	82	62
606	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	83	64
607	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	107	44
608	L27428	Homo sapiens	reverse transcriptase	147	43
609	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	113	61
610	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	151	82
611	U93568	Homo sapiens	putative p150	144	32
612	AB022223	Arabidopsis thaliana	extensin protein-like	186	58
613	Z70684	Caenorhabditis elegans	F28D1.8	108	49
614	M11901	Rattus norvegicus	proline-rich salivary protein	133	36
615	X92485	Plasmodium vivax	pva1	120	42
616	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	175	89
617	U83280	Leishmania donovani	39 kDa antigen	111	51
618	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	137	67
619	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	120	53
620	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	92	45
621	AF130089	Homo sapiens	PRO2550	123	34
622	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	133	59
623	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	127	45
624	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	205	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
625	X07882	Homo sapiens	Po protein	119	39
626	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	70	100
627	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	141	51
628	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	141	54
629	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	115	46
630	X63368	Homo sapiens	HSJ1b	151	52
631	AF130089	Homo sapiens	PRO2550	155	47
632	X92485	Plasmodium vivax	pval	102	61
633	K03205	Homo sapiens	salivary proline-rich protein precursor	102	39
634	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	171	74
635	X92485	Plasmodium vivax	pval	95	73
636	S80119	Rattus sp.	reverse transcriptase homolog	114	58
637	U15647	Mus musculus	reverse transcriptase	170	42
638	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	130	76
639	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	83	36
640	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	96	34
641	X61296	Rattus norvegicus	open reading frame 2	166	35
642	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	127	35
643	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP:CS24_HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	115	35
644	AF081111	Mus musculus domesticus	ORF2	168	33
645	AK027208	Homo sapiens	unnamed protein product	90	51
646	AF016099	Mus musculus	endonuclease/reverse transcriptase	101	59
647	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	149	76
648	AF273441	Pongo pygmaeus	NADH dehydrogenase subunit 3	121	58
649	L27428	Homo sapiens	reverse transcriptase	173	58
650	AF119851	Homo sapiens	PRO1722	176	53
651	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:125.	168	68
652	AF130089	Homo sapiens	PRO2550	130	36
653	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	126	41
654	AK000385	Homo sapiens	unnamed protein product	195	63
655	AB041881	Rattus norvegicus	cytoplasmic dynein heavy chain	158	100
656	X61047	Hydra sp.	mini-collagen	60	38
657	M22332	Homo sapiens	unknown protein	100	50
658	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	143	62
659	AF194537	Homo sapiens	NAG13	95	48
660	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	120	50
661	U83303	Homo sapiens	line-1 reverse transcriptase	86	32
662	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	169	53
663	W48351	Homo sapiens	Human breast cancer related protein	120	72

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCRB2.		
664	U15647	Mus musculus	reverse transcriptase	148	50
665	R95913	Homo sapiens	Neural thread protein.	161	59
666	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	134	80
667	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	117	44
668	AB018705	Mus musculus	ORF2	115	32
669	D38112	Homo sapiens	NADH dehydrogenase subunit 4	280	75
670	X53581	Rattus norvegicus	ORF4	71	39
671	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	201	66
672	R95913	Homo sapiens	Neural thread protein.	144	78
673	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	164	46
674	AF118082	Homo sapiens	PRO1902	137	49
675	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	91	43
676	D00570	Mus musculus	open reading frame (251 AA)	112	72
677	AF194537	Homo sapiens	NAG13	238	56
678	M13100	Rattus norvegicus	unknown protein	146	51
679	U15647	Mus musculus	reverse transcriptase	123	54
680	R95913	Homo sapiens	Neural thread protein.	145	55
681	R59842	Homo sapiens	ApoE4L1 protease.	107	63
682	AF130089	Homo sapiens	PRO2550	94	51
683	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	129	69
684	AF093748	Homo sapiens	KH type splicing regulatory protein; KSRP	93	50
685	U93569	Homo sapiens	putative p150	133	58
686	G03095	Homo sapiens	Human secreted protein, SEQ ID NO: 7176.	117	64
687	Y36243	Homo sapiens	Human secreted protein encoded by gene 20.	69	73
688	AF116712	Homo sapiens	PRO2738	133	56
689	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	134	53
690	U93563	Homo sapiens	putative p150	132	49
691	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	349	70
692	AF090895	Homo sapiens	PRO0117	115	63
693	AF130089	Homo sapiens	PRO2550	132	80
694	S80119	Rattus sp.	reverse transcriptase homolog	101	43
695	U15647	Mus musculus	reverse transcriptase	120	64
696	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	132	59
697	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	128	72
698	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	182	47
699	D38112	Homo sapiens	cytochrome c oxidase subunit 1	459	83
700	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	148	73
701	AF003535	Homo sapiens	ORF2-like protein	125	49
702	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	89	41
703	L27428	Homo sapiens	reverse transcriptase	255	50
704	AF130089	Homo sapiens	PRO2550	87	55
705	G03052	Homo sapiens	Human secreted protein, SEQ ID NO:	113	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7133.		
706	Y79140	Homo sapiens	Human haemopoietic stem cell regulatory protein SCM3.	211	88
707	U15647	Mus musculus	reverse transcriptase	94	47
708	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	153	66
709	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	107	50
710	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	163	64
711	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	146	65
712	U93565	Homo sapiens	putative p150	108	33
713	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	108	37
714	M24732	Homo sapiens	lamin-like protein	92	35
715	D38112	Homo sapiens	cytochrome c oxidase subunit 3	306	79
716	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	462	85
717	AF004715	Homo sapiens	jerky gene product homolog	100	42
718	X92485	Plasmodium vivax	pval	84	48
719	AF130089	Homo sapiens	PRO2550	132	74
720	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	125	43
721	AK024455	Homo sapiens	FLJ00047 protein	108	68
722	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	146	46
723	X83413	Human herpesvirus 6	U88	269	41
724	X92485	Plasmodium vivax	pval	117	43
725	X92485	Plasmodium vivax	pval	97	41
726	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	102	73
727	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	118	43
728	A23786	Beta vulgaris	chitinase 1	91	33
729	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	107	49
730	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	131	59
731	W49717	Homo sapiens	Protein polymer adhesive substrate PPAS1-C.	148	29
732	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	95	45
733	X96731	Ostertagia circumcincta	cuticular collagen	104	37
734	AF130089	Homo sapiens	PRO2550	118	40
735	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	166	100
736	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	494	86
737	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	188	69
738	D38112	Homo sapiens	cytochrome c oxidase subunit 3	593	91
739	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	102	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
740	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	111	54
741	A23786	Beta vulgaris	chitinase I	106	36
742	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	71	72
743	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	184	61
744	AE003629	Drosophila melanogaster	CG17108 gene product	76	36
745	U93563	Homo sapiens	putative p150.	145	50
746	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	68	66
747	AF217973	Homo sapiens	unknown	113	79
748	AC006161	Arabidopsis thaliana	putative CENP-B/ARS-binding protein-like protein	112	31
749	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	106	47
750	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	115	54
751	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	99	72
752	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	85	48
753	X92485	Plasmodium vivax	pva1	89	73
754	U93563	Homo sapiens	putative p150	186	68
755	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	116	50
756	AF194537	Homo sapiens	NAG13	138	40
757	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	112	79
758	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	119	61
759	AF130079	Homo sapiens	PRO2852	138	40
760	X92485	Plasmodium vivax	pva1	88	77
761	U93050	Mus musculus	poly(A) binding protein II	95	35
762	V01555	Human herpesvirus 4	BYRF1, encodes EBNA-2 (Dambaugh et al, 1984; Dillner et al, 1984)	80	41
763	V00662	Homo sapiens	ATPase 6	337	83
764	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	117	41
765	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	423	81
766	R95913	Homo sapiens	Neural thread protein.	114	66
767	V00662	Homo sapiens	cytochrome oxidase I	223	83
768	D38112	Homo sapiens	NADH dehydrogenase subunit 4	268	83
769	V00662	Homo sapiens	cytochrome oxidase I	357	81
770	D38112	Homo sapiens	NADH dehydrogenase subunit 4	296	71
771	AF026211	Caenorhabditis elegans	Similar to cuticular collagen	95	39
772	AK024455	Homo sapiens	FLJ00047 protein	108	53
773	X92485	Plasmodium vivax	pva1	95	39
774	AF130051	Homo sapiens	PRO0898	123	38
775	AB012223	Canis familiaris	ORF2	174	51
776	AB028664	Paralichthys olivaceus	cytochrome oxidase subunit-3	268	57
777	V00662	Homo sapiens	cytochrome oxidase I	436	85
778	X52235	Homo sapiens	ORFII	125	47
779	U93569	Homo sapiens	putative p150	235	49

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
780	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	262	76
781	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	239	70
782	AF090942	Homo sapiens	PRO0657	146	69
783	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	85	66
784	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	209	62
785	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	184	60
786	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	158	60
787	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	293	86
788	AF130089	Homo sapiens	PRO2550	153	64
789	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	131	57
790	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	100	51
791	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	116	80
792	Y36203	Homo sapiens	Human secreted protein #75.	104	77
793	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	117	58
794	AF090930	Homo sapiens	PRO0478	130	68
795	AK024455	Homo sapiens	FLJ00047 protein	114	61
796	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	141	70
797	AF130089	Homo sapiens	PRO2550	273	85
798	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	134	66
799	AF130051	Homo sapiens	PRO0898	162	80
800	G03560	Homo sapiens	Human secreted protein, SEQ ID NO: 7641.	179	70
801	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	75	51
802	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	103	34
803	D38484	Hylobates syndactylus	Cytochrome C oxidase subunit I (COXI)	263	70
804	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	112	41
805	X92485	Plasmodium vivax	pval	103	38
806	AF194537	Homo sapiens	NAG13	285	51
807	AF121360	Drosophila melanogaster	DNZDHC/NEW1 zinc finger protein 11	179	47
808	X92485	Plasmodium vivax	pval	131	46
809	D13951	Nicotiana tabacum	extensin precursor	88	41
810	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	174	73
811	U93565	Homo sapiens	putative p150	118	38
812	AF118082	Homo sapiens	PRO1902	88	54
813	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	132	42
814	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	114	50
815	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	113	43
816	K02576	Homo sapiens	salivary proline-rich protein 1	148	40

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
817	AF217449	Schistosoma mekongi	NADH dehydrogenase subunit 6	102	37
818	AB012223	Canis familiaris	ORF2	101	54
819	X71602	Nicotiana tabacum	extensin	162	45
820	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	154	36
821	R95913	Homo sapiens	Neural thread protein.	153	61
822	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	125	61
823	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	364	57
824	U43360	Peromyscus maniculatus	reverse transcriptase	121	48
825	AF194537	Homo sapiens	NAG13	224	58
826	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	437	72
827	AF051782	Homo sapiens	diaphanous 1	108	38
828	AF194537	Homo sapiens	NAG13	92	45
829	D38112	Homo sapiens	cytochrome c oxidase subunit 3	492	75
830	M64791	Rattus norvegicus	salivary proline-rich protein	110	46
831	X55685	Lycopersicon esculentum	extensin (class I)	108	31
832	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	117	34
833	U93564	Homo sapiens	putative p150	84	40
834	U93563	Homo sapiens	putative p150	262	54
835	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	214	80
836	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	107	48
837	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	158	76
838	AF194537	Homo sapiens	NAG13	153	60
839	U52077	Homo sapiens	mariner transposase	344	67
840	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	104	46
841	W90847	Homo sapiens	Human lymphocyte targeted peptide #15.	130	92
842	M64791	Rattus norvegicus	salivary proline-rich protein	114	36
843	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	196	43
844	X92485	Plasmodium vivax	pva1	102	73
845	X61048	Hydra sp.	mini-collagen	106	41
846	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	92	48
847	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	112	54
848	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	128	68
849	AF194537	Homo sapiens	NAG13	141	46
850	U43360	Peromyscus maniculatus	reverse transcriptase	121	45
851	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	153	58
852	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	220	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
853	X92485	Plasmodium vivax	pva1	127	45
854	AF134305	Homo sapiens	Scar3	99	38
855	D38112	Homo sapiens	NADH dehydrogenase subunit 2	343	68
856	S80119	Rattus sp.	reverse transcriptase homolog	159	56
857	AF130089	Homo sapiens	PRO2550	112	40
858	AK024372	Homo sapiens	unnamed protein product	129	50
859	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	103	76
860	D38112	Homo sapiens	cytochrome c oxidase subunit 3	279	80
861	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	96	44
862	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	83	40
863	AF210651	Homo sapiens	NAG18	122	63
864	AF016099	Mus musculus	endonuclease/reverse transcriptase	109	51
865	X55685	Lycopersicon esculentum	extensin (class I)	115	34
866	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	107	80
867	X92485	Plasmodium vivax	pva1	105	41
868	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	127	62
869	X92485	Plasmodium vivax	pva1	105	38
870	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	90	56
871	Y27571	Homo sapiens	Human secreted protein encoded by gene No. 5.	128	72
872	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	123	36
873	AF130089	Homo sapiens	PRO2550	160	82
874	AF118082	Homo sapiens	PRO1902	143	65
875	U93564	Homo sapiens	putative p150	180	44
876	M10546	Homo sapiens	cytochrome oxidase I	248	75
877	U83303	Homo sapiens	linc-1 reverse transcriptase	127	52
878	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	106	35
879	U11288	Drosophila melanogaster	diaphanous protein	93	46
880	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	71	47
881	B08942	Homo sapiens	Human secreted protein sequence encoded by gene 18 SEQ ID NO:99.	95	40
882	AF130089	Homo sapiens	PRO2550	137	44
883	AF090942	Homo sapiens	PRO0657	142	73
884	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	97	60
885	X61296	Rattus norvegicus	open reading frame 2	106	43
886	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	91	57
887	X14963	Homo sapiens	collagen-like protein (447 AA)	130	51
888	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	117	55
889	L25616	Homo sapiens	CGI protein	150	62
890	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	171	66
891	Y86472	Homo sapiens	Human gene 52-encoded protein	107	40

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			fragment, SEQ ID NO:387.		
892	X52318	Bos taurus	histone H2A.Z (AA 1-127)	356	79
893	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	102	46
894	D38112	Homo sapiens	cytochrome c oxidase subunit 1	173	75
895	X92485	Plasmodium vivax	pva1	109	47
896	L76159	Homo sapiens	FRG1 gene product	100	35
897	D50926	Homo sapiens	The KIAA0136 gene product is novel.	280	89
898	X04011	Homo sapiens	precursor polypeptide	114	95
899	M90656	Homo sapiens	gamma-glutamylcysteine synthetase	101	90
900	R95913	Homo sapiens	Neural thread protein.	95	75
901	L27428	Homo sapiens	reverse transcriptase	81	47
902	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	104	53
903	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	105	76
904	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	126	37
905	AF130089	Homo sapiens	PRO2550	88	82
906	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	230	50
907	L27428	Homo sapiens	reverse transcriptase	114	64
908	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	142	71
909	U93570	Homo sapiens	putative p150	130	41
910	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	91	63
911	L27428	Homo sapiens	reverse transcriptase	168	46
912	X92485	Plasmodium vivax	pva1	91	60
913	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	103	64
914	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	96	64
915	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	121	51
916	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	87	77
917	M12099	Mus musculus	proline-rich protein	129	44
918	M15530	Homo sapiens	B-cell growth factor	88	51
919	AF130079	Homo sapiens	PRO2852	158	88
920	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	103	77
921	X53581	Rattus norvegicus	ORF4	124	32
922	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	110	50
923	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	99	36
924	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	80	47
925	AC006127	Homo sapiens	BRG-1-HUMAN ; nuclear protein GRB1; homeotic gene regulator; SNF2-BETA; MITOTIC GROWTH AND TRANSCRIPTION ACTIVATOR; POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L4	442	92
926	L17318	Rattus norvegicus	proline-rich proteoglycan	126	39
927	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	321	76

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
928	AC006161	<i>Arabidopsis thaliana</i>	putative CENP-B/ARS-binding protein-like protein	97	35
929	X02873	<i>Daucus carota</i>	put. precursor	112	38
930	U93563	<i>Homo sapiens</i>	putative p150	125	70
931	AB012223	<i>Canis familiaris</i>	ORF2	202	50
932	AF053538	<i>Alvinella pompejana</i>	fibrillar collagen chain FAp1 alpha	114	37
933	G03790	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7871.	107	57
934	U49973	<i>Homo sapiens</i>	ORF1; MER37; putative transposase similar to pogo element	283	54
935	U41017	<i>Caenorhabditis elegans</i>	repetitive region; weakly similar to E. gracilis major membrane skeletal protein (PIR:A43417)	107	33
936	U47855	<i>Araneus diadematus</i>	fibroin-3	109	33
937	G03133	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7214.	95	43
938	W48351	<i>Homo sapiens</i>	Human breast cancer related protein BCRB2.	108	50
939	M13101	<i>Rattus norvegicus</i>	unknown protein	121	40
940	G00689	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 4770.	117	46
941	AF010144	<i>Homo sapiens</i>	neuronal thread protein AD7c-NTP	88	62
942	L27428	<i>Homo sapiens</i>	reverse transcriptase	86	45
943	U93564	<i>Homo sapiens</i>	putative p150	279	40
944	Y64890	<i>Homo sapiens</i>	Human 5' EST related polypeptide SEQ ID NO:1051.	110	48
945	L27428	<i>Homo sapiens</i>	reverse transcriptase	238	66
946	AF194537	<i>Homo sapiens</i>	NAG13	146	47
947	G02538	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 6619.	81	55
948	AC006161	<i>Arabidopsis thaliana</i>	putative CENP-B/ARS-binding protein-like protein	113	37
949	AF194537	<i>Homo sapiens</i>	NAG13	106	66
950	Y14437	<i>Homo sapiens</i>	Human secreted protein encoded by gene 27 clone HSAWA27.	74	75
951	G04067	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 8148.	78	66
952	Y19767	<i>Homo sapiens</i>	SEQ ID NO 485 from WO9922243.	85	72
953	U44838	<i>Glycine max</i>	extensin	145	39
954	R13556	<i>Homo sapiens</i>	Protein encoded downstream of hhc_M oncoprotein.	131	39
955	G03801	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7882.	128	53
956	G00354	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 4435.	103	74
957	AF130089	<i>Homo sapiens</i>	PRO2550	120	37
958	G03043	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7124.	115	71
959	AF090942	<i>Homo sapiens</i>	PRO0657	83	63
960	L27428	<i>Homo sapiens</i>	reverse transcriptase	121	30
961	G03714	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7795.	157	68
962	AF090942	<i>Homo sapiens</i>	PRO0657	138	61
963	U83280	<i>Leishmania donovani</i>	39 kDa antigen	101	53
964	U93566	<i>Homo sapiens</i>	p40	102	31

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
965	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	104	63
966	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	136	40
967	AF090930	Homo sapiens	PRO0478	158	80
968	AB012223	Canis familiaris	ORF2.	94	36
969	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	127	54
970	X53581	Rattus norvegicus	ORF4	163	43
971	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	109	56
972	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	82	47
973	Y69166	Homo sapiens	A mature human N-acetylglucosaminyl transferase protein.	95	80
974	G03095	Homo sapiens	Human secreted protein, SEQ ID NO: 7176.	74	51
975	U93574	Homo sapiens	putative p150	140	43
976	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	79	65
977	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	116	55
978	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	148	63
979	AF130114	Homo sapiens	PRO2459	121	61
980	K03202	Homo sapiens	salivary proline-rich protein precursor	99	40
981	AF116909	Homo sapiens	unknown	115	42
982	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	106	75
983	Y14674	Plasmodium falciparum	glutamate-cysteine ligase	106	66
984	AF229067	Homo sapiens	PADI-H protein	152	60
985	AF119900	Homo sapiens	PRO2822	142	48
986	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	119	70
987	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	106	60
988	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	81	51
990	U35730	Mus musculus	jerky	133	29
991	AF113685	Homo sapiens	PRO0974	136	63
992	U52077	Homo sapiens	mariner transposase	497	77
993	Z97211	Schizosaccharomyces pombe	kinesin-like protein	197	47
994	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	124	68
995	U93563	Homo sapiens	putative p150	157	50
996	AB015802	Acetobacter xylinus	similar to cellulose complementing protein of A. xylinum ATCC23869	140	54
997	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	144	60
998	D38116	Pan paniscus	cytochrome c oxidase subunit 1	352	75
999	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	524	78
1000	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	377	70
1001	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	109	50
1002	AL390114	Leishmania major	extremely cysteine/valine rich protein	249	61
1003	M14702	Murine leukemia	pol polyprotein	206	48

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		virus			
1004	Z21507	Homo sapiens	human elongation factor-1-delta	511	85
1005	L27428	Homo sapiens	reverse transcriptase	176	63
1006	D38112	Homo sapiens	NADH dehydrogenase subunit 5	332	77
1007	AF090895	Homo sapiens	PRO0117	162	66
1008	G03102	Homo sapiens	Human secreted protein, SEQ ID NO: 7183.	140	65
1009	U44838	Glycine max	extensin	166	33
1010	AF251290	Plasmodium falciparum	glutamic acid-rich protein	114	52
1011	L27428	Homo sapiens	reverse transcriptase	114	52
1012	AF130089	Homo sapiens	PRO2550	114	77
1013	G04092	Homo sapiens	Human secreted protein, SEQ ID NO: 8173.	81	44
1014	AF090895	Homo sapiens	PRO0117	97	65
1015	AF130089	Homo sapiens	PRO2550	168	83
1016	AF079367	Mesocricetus auratus	cytochrome c oxidase subunit III	276	52
1017	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	94	44
1018	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	114	46
1019	AF090944	Homo sapiens	PRO0663	137	50
1020	Y21166	Homo sapiens	Human bcl2 proto-oncogene mutant protein fragment 14.	84	36
1021	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	140	37
1022	AL049608	Arabidopsis thaliana	extensin-like protein	105	34
1023	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	152	52
1024	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	125	66
1025	M12140	Homo sapiens	envelope protein	143	62
1026	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	200	58
1027	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	266	67
1028	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	97	31
1029	G02950	Homo sapiens	Human secreted protein, SEQ ID NO: 7031.	102	56
1030	G02482	Homo sapiens	Human secreted protein, SEQ ID NO: 6563.	76	63
1031	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	74	56
1032	X90568	Homo sapiens	Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE	389	100
1033	G02654	Homo sapiens	Human secreted protein, SEQ ID NO: 6735.	96	40
1034	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	316	60
1035	AF194537	Homo sapiens	NAG13	208	52
1036	L27428	Homo sapiens	reverse transcriptase	166	51
1037	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	107	44
1038	AF116638	Homo sapiens	PRO1546	56	61
1039	U93570	Homo sapiens	putative p150	138	40
1040	AF130089	Homo sapiens	PRO2550	150	91
1041	AK024455	Homo sapiens	FLJ00047 protein	151	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1042	Y36156	Homo sapiens	Human secreted protein #28.	97	41
1043	U93568	Homo sapiens	putative p150	124	34
1044	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	208	71
1045	U93563	Homo sapiens	putative p150	246	54
1046	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	131	64
1047	U93563	Homo sapiens	putative p150	127	30
1048	AF130114	Homo sapiens	PRO2459	117	67
1049	U12919	Mus musculus	adenyl cyclase type VII	170	68
1050	AC008054	Leishmania major	L8453.1	129	30
1051	X99467	Medicago truncatula	ENOD20	110	38
1052	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	150	76
1053	AF116712	Homo sapiens	PRO2738	109	44
1054	M96256	Homo sapiens	rapamycin binding protein	168	56
1055	U15647	Mus musculus	reverse transcriptase	86	37
1056	AL024498	Homo sapiens	dJ417M14.2 (novel serine/threonine-protein kinase (ortholog of mouse and rat MAK (male germ cell-associated kinase)))	190	72
1057	AF090942	Homo sapiens	PRO0657	103	63
1058	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	156	68
1059	AF081114	Mus musculus domesticus	ORF2	134	47
1060	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	180	83
1061	U70935	Peromyscus maniculatus	reverse transcriptase	126	45
1062	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	84	55
1063	U15647	Mus musculus	reverse transcriptase	95	38
1064	U93567	Homo sapiens	putative p150	128	58
1065	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	130	66
1066	X92485	Plasmodium vivax	pval	119	62
1067	U93567	Homo sapiens	p40	161	48
1068	D38112	Homo sapiens	cytochrome c oxidase subunit 3	540	84
1069	U93570	Homo sapiens	putative p150	107	59
1070	AF321051	Chalino lobus tuberculatus	cytochrome c oxidase subunit III	333	71
1071	U93567	Homo sapiens	p40	99	28
1072	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	105	66
1073	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	136	59
1074	U93572	Homo sapiens	putative p150	140	53
1075	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	66	43
1076	AL049608	Arabidopsis thaliana	extensin-like protein	105	37
1077	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	94	66
1078	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	81	57
1079	G04091	Homo sapiens	Human secreted protein, SEQ ID NO:	83	35

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			8172.		
1080	AF162149	Mycoplasma bovis	variable surface lipoprotein	103	41
1081	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	148	75
1082	U43360	Peromyscus maniculatus	reverse transcriptase	121	42
1083	U93564	Homo sapiens	p40	97	42
1084	AF229067	Homo sapiens	PADI-H protein	145	61
1085	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	221	60
1086	U88573	Homo sapiens	NBR2	165	67
1087	Y36156	Homo sapiens	Human secreted protein #28.	93	72
1088	AF194537	Homo sapiens	NAG13	142	62
1089	B08976	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:133.	93	62
1090	AF194537	Homo sapiens	NAG13	155	40
1091	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	103	35
1092	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	195	40
1093	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	91	46
1094	X53581	Rattus norvegicus	ORF4	106	62
1095	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	129	51
1096	Y86473	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:388.	72	33
1097	U40342	Mus musculus	ninein	152	44
1098	M24732	Homo sapiens	lamin-like protein	92	37
1099	X92485	Plasmodium vivax	pval	111	67
1100	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	156	86
1101	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	116	90
1102	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	158	71
1103	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	97	36
1104	U93572	Homo sapiens	putative p150	168	56
1105	U93570	Homo sapiens	putative p150	96	40
1106	L27428	Homo sapiens	reverse transcriptase	188	43
1107	X53581	Rattus norvegicus	ORF4	141	43
1108	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	344	77
1109	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	126	68
1110	U93569	Homo sapiens	putative p150	156	38
1111	AF118086	Homo sapiens	PRO1992	135	54
1112	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	71	63
1113	AF016099	Mus musculus	endonuclease/reverse transcriptase	124	62
1114	L27428	Homo sapiens	reverse transcriptase	200	40
1115	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	101	50
1116	L27428	Homo sapiens	reverse transcriptase	122	70
1117	G00637	Homo sapiens	Human secreted protein, SEQ ID NO:	148	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4718.		
1118	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	116	65
1119	D38484	Hylobates syndactylus	Cytochrome C oxidase subunit 1 (COXI)	315	89
1120	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	115	76
1121	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	136	68
1122	AF013990	Homo sapiens	ubiquitin C-terminal hydrolase	163	50
1123	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	94	55
1124	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	154	65
1125	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	106	53
1126	AF130089	Homo sapiens	PRO2550	76	72
1127	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	92	59
1128	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	80	59
1129	AF119855	Homo sapiens	PRO1847	146	70
1130	AF194537	Homo sapiens	NAG13	182	66
1131	L27428	Homo sapiens	reverse transcriptase	173	38
1132	U93570	Homo sapiens	putative p150	119	34
1133	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	157	68
1134	AJ004810	Zea mays	cytochrome P450 monooxygenase	79	87
1135	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	138	70
1136	G01502	Homo sapiens	Human secreted protein, SEQ ID NO: 5583.	81	73
1137	AB018705	Mus musculus	ORF2	138	36
1138	L20321	Homo sapiens	protein serine/threonine kinase	150	63
1139	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	92	60
1140	AF194537	Homo sapiens	NAG13	115	33
1141	U93564	Homo sapiens	putative p150	135	51
1142	D86853	Catharanthus roseus	extensin	142	37
1143	D00570	Mus musculus	open reading frame (251 AA)	213	50
1144	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	62	38
1145	Z70684	Caenorhabditis elegans	F28D1.8	105	32
1146	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	79	54
1147	Y36156	Homo sapiens	Human secreted protein #28.	151	62
1148	A23786	Beta vulgaris	chitinase 1	98	37
1149	AF129756	Homo sapiens	BAT2	177	52
1150	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	147	73
1151	L27428	Homo sapiens	reverse transcriptase	77	31
1152	U34044	Homo sapiens	selenium donor protein	238	48
1153	AK024455	Homo sapiens	FLJ00047 protein	78	78
1154	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	197	67
1155	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	120	64
1156	U25281	Rattus norvegicus	SH3 domain binding protein	98	34
1157	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	138	54

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1158	AF194537	Homo sapiens	NAG13	106	48
1159	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	357	69
1160	U93572	Homo sapiens	p40	89	47
1161	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	184	68
1162	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	123	57
1163	AF116712	Homo sapiens	PRO2738	129	69
1164	V00662	Homo sapiens	cytochrome oxidase I	465	69
1165	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	118	57
1166	L26163	Mus musculus	histone H1e	104	37
1167	X70343	Nicotiana glauca	extensin	95	33
1168	AF130051	Homo sapiens	PRO0898	117	43
1169	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	104	48
1170	L27428	Homo sapiens	reverse transcriptase	149	33
1171	G00497	Homo sapiens	Human secreted protein, SEQ ID NO: 4578.	108	62
1172	AF030277	Tragalaphus speki	cytochrome oxidase subunit III	266	54
1173	L22030	Glycine max	hydroxyproline-rich glycoprotein	87	38
1174	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	168	45
1175	U43627	Arabidopsis thaliana	extensin	111	42
1176	U43627	Arabidopsis thaliana	extensin	98	29
1177	U93565	Homo sapiens	putative p150	89	58
1178	J01047	Caenorhabditis elegans	collagen	108	39
1179	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	170	68
1180	AF016099	Mus musculus	endonuclease/reverse transcriptase	113	36
1181	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	134	65
1182	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	107	62
1183	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	124	45
1184	D38112	Homo sapiens	NADH dehydrogenase subunit 2	418	86
1185	U87607	Rattus norvegicus	putative RNA binding protein 1	106	41
1186	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	381	75
1187	D38112	Homo sapiens	cytochrome c oxidase subunit I	434	79
1188	U83303	Homo sapiens	line-1 reverse transcriptase	75	35
1189	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	159	68
1190	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	146	68
1191	AF118086	Homo sapiens	PRO1992	146	81
1192	W12842	Homo sapiens	Truncated pro-alpha 1(III) chain.	106	35
1193	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	67	34
1194	G03556	Homo sapiens	Human secreted protein, SEQ ID NO: 7637.	116	74
1195	Y30681	Homo sapiens	Splice variant ZAP-1B protein of the human tumor suppressor gene ZAP-1.	132	82

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1196	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	75	48
1197	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	254	73
1198	U93570	Homo sapiens	p40	103	30
1199	AL390114	Leishmania major	extremely cysteine/valine rich protein	145	39
1200	AK024455	Homo sapiens	FLJ00047 protein	115	56
1201	AF090942	Homo sapiens	PRO0657	88	64
1202	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	124	70
1203	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	113	46
1204	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	81	41
1205	U35730	Mus musculus	jerky.	107	27
1206	U15647	Mus musculus	reverse transcriptase	191	45
1207	U15647	Mus musculus	reverse transcriptase	124	50
1208	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	140	58
1209	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	91	54
1210	AF119900	Homo sapiens	PRO2822	160	81
1211	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	68
1212	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	142	45
1213	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	125	61
1214	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	102	61
1215	G03560	Homo sapiens	Human secreted protein, SEQ ID NO: 7641.	101	46
1216	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	270	58
1217	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	105	46
1218	AC002483	Homo sapiens	putative product from mRNA sequence CG003 from BRCA2 region; match to U50534 (NID:g1685103)	378	97
1219	AF090895	Homo sapiens	PRO0117	130	58
1220	AF113685	Homo sapiens	PRO0974	117	60
1221	X61295	Rattus norvegicus	L1 retroposon, a portion of its ORF2 sequence	126	50
1222	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	148	70
1223	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	99	56
1224	U93574	Homo sapiens	putative p150	93	44
1225	AF130051	Homo sapiens	PRO0898	133	69
1226	U93563	Homo sapiens	putative p150	125	47
1227	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	220	47
1228	U93564	Homo sapiens	putative p150	116	47
1229	W21733	Homo sapiens	NIP-1 encoded by clone 59.	138	63
1230	U15647	Mus musculus	reverse transcriptase	105	42
1231	U93563	Homo sapiens	putative p150	299	54
1232	R95913	Homo sapiens	Neural thread protein.	138	51
1233	AF130079	Homo sapiens	PRO2852	203	70
1234	X53581	Rattus norvegicus	ORF3	106	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1235	AF118086	Homo sapiens	PRO1992	144	81
1236	X92485	Plasmodium vivax	pval	125	71
1237	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	116	75
1238	U93572	Homo sapiens	putative p150	133	40
1239	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	69	56
1240	AF130089	Homo sapiens	PRO2550	136	41
1241	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	109	53
1242	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	161	75
1243	G02752	Homo sapiens	Human secreted protein, SEQ ID NO: 6833.	87	45
1244	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	128	58
1245	U93570	Homo sapiens	putative p150	161	50
1246	Z70684	Caenorhabditis elegans	F28D1.8	121	45
1247	AF257305	Homo sapiens	ASH1	576	89
1248	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	98	68
1249	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	107	43
1250	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	91
1251	U63542	Homo sapiens	FAP protein	116	61
1252	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	109	53
1253	AF068294	Homo sapiens	HDCMB45P	251	63
1254	AF090895	Homo sapiens	PRO0117	111	60
1255	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	201	75
1256	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	116	51
1257	AB033032	Homo sapiens	KIAA1206 protein	115	80
1258	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	122	60
1259	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	137	68
1260	AB032906	Hylobates pileatus	dopamine receptor D4	96	35
1261	AF022985	Caenorhabditis elegans	Similar to collagen; coded for by C. elegans cDNA yk55f3.3; coded for by C. elegans cDNA yk66d5.3; coded for by C. elegans cDNA yk71e4.3; coded for by C. elegans cDNA yk55f3.5; coded for by C. elegans cDNA yk66d5.5; coded for by C. elegans cDNA yk71e4.5	106	38
1262	U93566	Homo sapiens	p40	182	39
1263	L20096	Manduca sexta	ribosomal protein s7	227	59
1264	AF119901	Homo sapiens	PRO2831	103	71
1265	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	219	97
1266	D90279	Homo sapiens	collagen alpha 1(V) chain precursor	120	42
1267	L27428	Homo sapiens	reverse transcriptase	111	41
1268	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	126	68
1269	AF016099	Mus musculus	endonuclease/reverse transcriptase	102	34

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1270	AF130089	Homo sapiens	PRO2550	96	69
1271	U12707	Homo sapiens	Wiskott-Aldrich syndrome protein	121	45
1272	AF165310	Homo sapiens	ATP cassette binding transporter 1	243	100
1273	R95913	Homo sapiens	Neural thread protein.	110	70
1274	X92485	Plasmodium vivax	pval	106	65
1275	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	104	56
1276	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	53	36
1277	X03725	Mus musculus	ORF 2 (466 aa)	103	41
1278	U93570	Homo sapiens	putative p150	98	43
1279	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	159	83
1280	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	167	71
1281	AJ271871	Nicotiana sylvestris	putative extensin	105	36
1282	K03205	Homo sapiens	salivary proline-rich protein precursor	119	32
1283	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	124	66
1284	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	135	50
1285	A31039	Nicotiana glauca	PRP3	112	36
1286	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	116	72
1287	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	289	67
1288	S80119	Rattus sp.	reverse transcriptase homolog	112	33
1289	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	203	76
1290	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	151	53
1291	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	128	82
1292	AF130089	Homo sapiens	PRO2550	127	62
1293	AF003535	Homo sapiens	ORF2-like protein	101	48
1294	Y19610	Homo sapiens	SEQ ID NO 328 from WO9922243.	100	42
1295	L27428	Homo sapiens	reverse transcriptase	126	36
1296	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	140	71
1297	L24433	Oncorhynchus mykiss	complement component C3	359	31
1298	AC004381	Homo sapiens	SA gene	443	55
1299	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	180	64
1300	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	135	66
1301	D84391	Mus musculus	reverse transcriptase	106	48
1302	D13951	Nicotiana glauca	extensin precursor	134	42
1303	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	73
1304	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	93	38
1305	Y13620	Homo sapiens	BCL9	102	39
1306	U93567	Homo sapiens	putative p150	245	63
1307	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	130	70
1308	AL355774	Streptomyces coelicolor A3(2)	putative integral membrane protein	136	40
1309	W54966	Homo sapiens	Synthetic human type III collagen	124	41

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			SYN-C3.		
1310	M20670	Plasmodium vivax	circumsporozoite protein	107	34
1311	AF151366	Arabidopsis thaliana	arginine/serine-rich protein	114	36
1312	G03099	Homo sapiens	Human secreted protein, SEQ ID NO: 7180.	76	43
1313	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	109	85
1314	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	111	37
1315	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	123	62
1316	R95913	Homo sapiens	Neural thread protein.	98	58
1317	AF113685	Homo sapiens	PRO0974	170	47
1318	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	122	61
1319	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	99	68
1320	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	270	56
1321	U93569	Homo sapiens	putative p150	124	37
1322	AF090931	Homo sapiens	PRO0483	111	85
1323	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	85	44
1324	M18094	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	131	43
1325	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	144	54
1326	AF194537	Homo sapiens	NAG13	125	49
1327	L27428	Homo sapiens	reverse transcriptase	111	45
1328	U93568	Homo sapiens	putative p150	112	30
1329	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	110	51
1330	L27428	Homo sapiens	reverse transcriptase	142	53
1331	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	98	88
1332	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	113	55
1333	X71602	Nicotiana tabacum	extensin	113	35
1334	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	129	41
1335	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	112	50
1336	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	102	68
1337	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	95	51
1338	U43360	Peromyscus maniculatus	reverse transcriptase	114	60
1339	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	142	55
1340	X55685	Lycopersicon esculentum	extensin (class I)	123	31
1341	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	118	70
1342	X71629	Mus musculus	msg1	106	57
1343	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	105	79

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1344	G03435	Homo sapiens	Human secreted protein, SEQ ID NO: 7516.	116	85
1345	AF161356	Homo sapiens	HSPC093	88	88
1346	J01435	Rattus norvegicus	ATPase	348	66
1347	U93563	Homo sapiens	putative p150	142	36
1348	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	87	66
1349	AF090942	Homo sapiens	PRO0657	152	54
1350	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	143	63
1351	U93572	Homo sapiens	putative p150	113	84
1352	X92485	Plasmodium vivax	pval	130	70
1353	X61047	Hydra sp.	mini-collagen	105	36
1354	AF115549	Homo sapiens	Wiskott-Aldrich Syndrome protein	128	46
1355	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	91	39
1356	AF194537	Homo sapiens	NAG13	148	63
1357	AF130079	Homo sapiens	PRO2852	139	73
1358	X53581	Rattus norvegicus	ORF4	208	43
1359	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	195	50
1360	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	328	69
1361	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	126	65
1362	G02451	Homo sapiens	Human secreted protein, SEQ ID NO: 6532.	97	47
1363	X53581	Rattus norvegicus	ORF4	110	35
1364	U93569	Homo sapiens	putative p150	123	41
1365	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	114	63
1366	X61294	Rattus norvegicus	L1 retroposon, a portion of its ORF2 sequence	153	43
1367	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	69	80
1368	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	80	46
1369	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	113	26
1370	X92485	Plasmodium vivax	pval	106	46
1371	U90946	Dictyostelium discoideum	myosin heavy chain kinase B	114	62
1372	L27428	Homo sapiens	reverse transcriptase	98	61
1373	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	124	80
1374	U49974	Homo sapiens	mariner transposase	137	57
1375	AC004891	Homo sapiens	contactin-like; similar to U87224 (PID:g1857710)	234	58
1376	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	132	60
1377	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	317	51
1378	AF118082	Homo sapiens	PRO1902	102	42
1379	AF115549	Homo sapiens	Wiskott-Aldrich Syndrome protein	186	45
1380	U93567	Homo sapiens	putative p150	116	38
1381	U49973	Homo sapiens	ORF1; MER37; putative transposase	218	47

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			similar to pogo element		
1382	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:75.	87	66
1383	AF090895	Homo sapiens	PRO0117	68	82
1384	U93570	Homo sapiens	putative p150	178	39
1385	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	132	43
1386	AF130089	Homo sapiens	PRO2550	142	35
1387	L27428	Homo sapiens	reverse transcriptase	163	49
1388	X61296	Rattus norvegicus	open reading frame 2	123	44
1389	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	138	67
1390	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	147	57
1391	U93570	Homo sapiens	putative p150	110	28
1392	R95913	Homo sapiens	Neural thread protein.	104	35
1393	L27428	Homo sapiens	reverse transcriptase	101	39
1394	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	147	47
1395	AF216972	Homo sapiens	p8 protein	118	49
1396	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	160	58
1397	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	312	62
1398	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	97	62
1399	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	125	54
1400	X92485	Plasmodium vivax	pva1	124	39
1401	U93563	Homo sapiens	putative p150	131	36
1402	X67863	Mus musculus	T2	160	48
1403	K02576	Homo sapiens	salivary proline-rich protein 1	94	39
1404	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	84	73
1405	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	71	71
1406	M18094	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	138	31
1407	AF134304	Homo sapiens	Scar2	118	40
1408	Y08061	Homo sapiens	Human c-myb protein fragment.	121	82
1409	U93574	Homo sapiens	putative p150	179	43
1410	U93563	Homo sapiens	putative p150	98	43
1411	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	124	46
1412	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	149	56
1413	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	148	48
1414	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	155	82
1415	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	92	52
1416	AF119855	Homo sapiens	PRO1847	82	70
1417	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	130	34
1418	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	99	39
1419	AF130079	Homo sapiens	PRO2852	114	69
1420	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	133	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1421	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	115	44
1422	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	111	77
1423	R95913	Homo sapiens	Neural thread protein.	128	80
1424	L26953	Homo sapiens	chromosomal protein	104	34
1425	U83280	Leishmania donovani	39 kDa antigen	105	51
1426	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	98	75
1427	U83303	Homo sapiens	line-1 reverse transcriptase	149	40
1428	AF090895	Homo sapiens	PRO0117	111	75
1429	AF119855	Homo sapiens	PRO1847	88	56
1430	AF229067	Homo sapiens	PADI-H protein	157	51
1431	D38112	Homo sapiens	cytochrome c oxidase subunit 3	509	79
1432	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	333	62
1433	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	149	57
1434	AF161356	Homo sapiens	HSPC093	180	46
1435	U93570	Homo sapiens	putative p150	116	48
1436	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	171	73
1437	U83280	Leishmania donovani	39 kDa antigen	106	80
1438	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	103	73
1439	U15647	Mus musculus	reverse transcriptase	233	44
1440	L27428	Homo sapiens	reverse transcriptase	78	40
1441	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	115	68
1442	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	77	63
1443	M22332	Homo sapiens	unknown protein	153	62
1444	M11901	Rattus norvegicus	proline-rich salivary protein	102	40
1445	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	101	66
1446	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	125	74
1447	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	90	66
1448	X76208	Drosophila melanogaster	protein 33-specific exons	123	48
1449	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	178	79
1450	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	109	45
1451	S80119	Rattus sp.	reverse transcriptase homolog	115	54
1452	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	70	63
1453	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	105	40
1454	AK024455	Homo sapiens	FLJ00047 protein	109	53
1455	AC007258	Arabidopsis thaliana	Hypothetical protein	105	37
1456	AF194537	Homo sapiens	NAG13	208	52
1457	U63542	Homo sapiens	FAP protein	111	84
1458	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	111	65
1459	AF090931	Homo sapiens	PRO0483	84	43

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1460	R95913	Homo sapiens	Neural thread protein.	106	69
1461	R95913	Homo sapiens	Neural thread protein.	109	40
1462	U93564	Homo sapiens	putative p150	237	42
1463	AB029309	Homo sapiens	Npw38-binding protein NpwBP	97	37
1464	U44838	Glycine max	extensin	97	33
1465	AL050341	Homo sapiens	dJ39G22.1 (rearranged L-myc fusion sequence (ZN-15 related zinc finger protein))	121	45
1466	L27428	Homo sapiens	reverse transcriptase	94	34
1467	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	117	58
1468	Y17221	Homo sapiens	Human secreted protein (clone fk317-3).	98	48
1469	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	123	55
1470	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	147	67
1471	AF109907	Homo sapiens	S164	133	35
1472	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	142	36
1473	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	152	90
1474	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	157	45
1475	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	398	58
1476	U49974	Homo sapiens	mariner transposase	201	59
1477	U49974	Homo sapiens	mariner transposase	206	60
1478	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	117	72
1479	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	146	82
1480	U93567	Homo sapiens	putative p150	202	42
1481	K02576	Homo sapiens	salivary proline-rich protein 1	101	46
1482	U87607	Rattus norvegicus	putative RNA binding protein 1	100	37
1483	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	124	75
1484	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	108	62
1485	U15647	Mus musculus	reverse transcriptase	115	73
1486	AF194537	Homo sapiens	NAG13	132	42
1487	M11902	Mus musculus	proline-rich salivary protein	118	40
1488	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	102	64
1489	AF009668	multiple sclerosis associated retrovirus	polyprotein	110	48
1490	AK023542	Homo sapiens	unnamed protein product	114	37
1491	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	133	50
1492	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	184	47
1493	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	222	53
1494	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	94	50
1495	AF109907	Homo sapiens	S164	259	45
1496	R95913	Homo sapiens	Neural thread protein.	110	51
1497	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	299	80

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1498	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	158	65
1499	L26953	Homo sapiens	chromosomal protein	104	67
1500	AF090895	Homo sapiens	PRO0117	145	68
1501	U93572	Homo sapiens	p40	115	42
1502	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	133	50
1503	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	143	56
1504	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	119	69
1505	W00838	Homo sapiens	Tumour necrosis factor-related gene product.	105	52
1506	AF109907	Homo sapiens	S164	184	43
1507	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	288	67
1508	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	131	69
1509	AK000241	Homo sapiens	unnamed protein product	167	72
1510	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	153	60
1511	S62928	Homo sapiens	PRB1M protein precursor	157	39
1512	AB012223	Canis familiaris	ORF2	116	40
1513	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	109	59
1514	AF220264	Homo sapiens	MOST-1	108	80
1515	X53581	Rattus norvegicus	ORF4	96	44
1516	V00662	Homo sapiens	cytochrome oxidase III	433	74
1517	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	263	70
1518	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	266	70
1519	M24732	Homo sapiens	lamin-like protein	107	44
1520	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	131	51
1521	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	81	68
1522	AF194537	Homo sapiens	NAG13	116	42
1523	X92485	Plasmodium vivax	pval	85	42
1524	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	125	50
1525	AB041228	Homo sapiens	G protein-coupled receptor TGR-1	220	100
1526	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	138	70
1527	U52077	Homo sapiens	mariner transposase	237	56
1528	L27428	Homo sapiens	reverse transcriptase	189	40
1529	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	355	78
1530	L13610	Mus musculus	IFN-response element binding factor 2	90	37
1531	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	90	64
1532	U11288	Drosophila melanogaster	diaphanous protein	138	38
1533	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	429	63
1534	L27428	Homo sapiens	reverse transcriptase	249	55
1535	U93570	Homo sapiens	putative p150	114	31
1536	AF130089	Homo sapiens	PRO2550	111	47

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1537	X55687	Lycopersicon esculentum	extensin (class II)	63	28
1538	U15647	Mus musculus	reverse transcriptase	110	42
1539	AK024455	Homo sapiens	FLJ00047 protein-	139	80
1540	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	128	48
1541	AC024788	Caenorhabditis elegans	Hypothetical protein Y46E12A.d	80	46
1542	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	132	73
1543	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	90	32
1544	G02971	Homo sapiens	Human secreted protein, SEQ ID NO: 7052.	71	63
1545	R95913	Homo sapiens	Neural thread protein.	118	55
1546	D38116	Pan paniscus	cytochrome c oxidase subunit 1	218	78
1547	D38112	Homo sapiens	cytochrome c oxidase subunit 1	370	71
1548	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	119	65
1549	AJ004810	Zea mays	cytochrome P450 monooxygenase	140	70
1550	AF113685	Homo sapiens	PRO0974	115	47
1551	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	172	75
1552	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	366	94
1553	W40113	Homo sapiens	Human alpha-2(IV) collagen protein.	117	59
1554	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	138	76
1555	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	113	40
1556	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	502	89
1557	AF130089	Homo sapiens	PRO2550	98	55
1558	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	109	43
1559	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	183	52
1560	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	180	52
1561	AF202893	Mus musculus	Kif21b	254	85
1562	M63421	Drosophila melanogaster	csp32	104	39
1563	G03652	Homo sapiens	Human secreted protein, SEQ ID NO: 7733.	129	69
1564	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	98	59
1565	AJ132106	Bos taurus	SCO-spondin	114	40
1566	AL390114	Leishmania major	extremely cysteine/valine rich protein	119	66
1567	AF161356	Homo sapiens	HSPC093	100	38
1568	AF119851	Homo sapiens	PRO1722	94	72
1569	L27428	Homo sapiens	reverse transcriptase	107	48
1570	X99451	Lycopersicon esculentum	extensin-like protein Dif10	104	32
1571	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	126	59
1572	X73481	Drosophila hydei	mst101(2)	105	41
1573	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	133	50
1574	G04063	Homo sapiens	Human secreted protein, SEQ ID NO:	154	51

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			8144.		
1575	D38112	Homo sapiens	NADH dehydrogenase subunit 4	323	83
1576	AF062008	Caenorhabditis elegans ---	unknown	111	54
1577	X92485	Plasmodium vivax	pva1	81	57
1578	U93570	Homo sapiens	p40	102	33
1579	AF090944	Homo sapiens	PRO0663	132	59
1580	AL137798	Homo sapiens	dJ1182A14.5.1 (novel gene (isoform 1))	182	53
1581	X92485	Plasmodium vivax	pva1	120	44
1582	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	160	47
1583	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	135	54
1584	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	119	52
1585	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	82	55
1586	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	152	60
1587	D28482	Homo sapiens	SCR2	390	83
1588	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	122	59
1589	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	117	50
1590	AF118078	Homo sapiens	PRO1848	118	59
1591	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	56	78
1592	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	118	80
1593	U93571	Homo sapiens	p40	170	77
1594	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	230	51
1595	L27428	Homo sapiens	reverse transcriptase	138	45
1596	X97707	Pongo pygmaeus abelii	stopcodon created by posttranscriptional polyadenylation	139	61
1597	X98710	Homo sapiens	COL1A1 and PDGFB fusion transcript	107	31
1598	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	97	58
1599	AF210651	Homo sapiens	NAG18	86	89
1600	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	148	48
1601	J03770	Mus musculus	homeobox protein	99	35
1602	AF119901	Homo sapiens	PRO2831	119	56
1603	AL031673	Homo sapiens	dJ694B14.1 (PUTATIVE novel KRAB box protein with 18 C2H2 type Zinc finger domains)	233	44
1604	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	66
1605	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	89	44
1606	D88461	Rattus rattus	N-WASP	123	43
1607	AF090942	Homo sapiens	PRO0657	107	61
1608	U35730	Mus musculus	jerky	105	34
1609	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	108	45
1610	B06334	Homo sapiens	Human subtilisin-kexin isoenzyme 1.	474	84
1611	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	101	90
1612	AK024455	Homo sapiens	FLJ00047 protein	83	55
1613	D86853	Catharanthus	extensin	123	39

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		roseus.			
1614	AF119851	Homo sapiens	PRO1722	135	59
1615	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	142	57
1616	AF194537	Homo sapiens	NAG13	154	63
1617	AF119851	Homo sapiens	PRO1722	91	62
1618	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	92	48
1619	AK024455	Homo sapiens	FLJ00047 protein	147	60
1620	AF217973	Homo sapiens	unknown	116	67
1621	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	102	41
1622	K02576	Homo sapiens	salivary proline-rich protein 1	108	40
1623	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	135	44
1624	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	322	62
1625	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	356	72
1626	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	113	65
1627	X92485	Plasmodium vivax	pval	90	45
1628	AF090895	Homo sapiens	PRO0117	156	61
1629	AF116661	Homo sapiens	PRO1438	87	54
1630	M13100	Rattus norvegicus	unknown protein	109	76
1631	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	147	60
1632	AF119851	Homo sapiens	PRO1722	107	70
1633	M64792	Rattus norvegicus	salivary proline-rich protein	109	46
1634	L27428	Homo sapiens	reverse transcriptase	109	38
1635	AF118082	Homo sapiens	PRO1902	80	40
1636	R95913	Homo sapiens	Neural thread protein.	118	88
1637	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	79	60
1638	U93570	Homo sapiens	putative p150	128	54
1639	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	127	69
1640	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	171	68
1641	AF194537	Homo sapiens	NAG13	140	66
1642	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	101	50
1643	M64793	Rattus norvegicus	salivary proline-rich protein	117	33
1644	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	123	50
1645	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	96	70
1646	L27428	Homo sapiens	reverse transcriptase	86	84
1647	X92485	Plasmodium vivax	pval	137	40
1648	U15647	Mus musculus	reverse transcriptase	93	68
1649	K02576	Homo sapiens	salivary proline-rich protein 1	131	41
1650	AF116712	Homo sapiens	PRO2738	107	57
1651	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	139	72
1652	X05472	Rattus	ORF 3	84	51

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		norvegicus			
1653	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	122	71
1654	U93566	Homo sapiens	p40	117	52
1655	AF217536	Homo sapiens	truncated mevalonate kinase	141	70
1656	AF090895	Homo sapiens	PRO0117	125	60
1657	X92485	Plasmodium vivax	pval	114	45
1658	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	192	61
1659	Y86473	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:388.	73	30
1660	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	331	74
1661	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	127	69
1662	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	312	67
1663	S80119	Rattus sp.	reverse transcriptase homolog	99	59
1664	U43360	Peromyscus maniculatus	reverse transcriptase	106	45
1665	M76729	Homo sapiens	pro-alpha-1 type V collagen	172	47
1666	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	97	54
1667	AF169388	Mus musculus	alpha 4 collagen IV	84	38
1668	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	84	66
1669	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	428	80
1670	M29622	Mus musculus	open reading frame 2	74	46
1671	W90838	Homo sapiens	Human lymphocyte targeted peptide #6.	98	100
1672	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	55	58
1673	AF090931	Homo sapiens	PRO0483	72	39
1674	AF051782	Homo sapiens	diaphanous 1	116	49
1675	U57361	Rattus norvegicus	collagen XII alpha 1	108	48
1676	AF182844	Homo sapiens	VPS28 protein	395	95
1677	L27428	Homo sapiens	reverse transcriptase	189	47
1678	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	142	53
1679	U93565	Homo sapiens	putative p150	214	40
1680	AK002129	Homo sapiens	unnamed protein product	128	57
1681	X03145	Homo sapiens	pot. ORF V	93	48
1682	X63005	Mus musculus	proline-rich protein	108	38
1683	AF118082	Homo sapiens	PRO1902	117	42
1684	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	157	58
1685	R95913	Homo sapiens	Neural thread protein.	92	66
1686	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	111	61
1687	X61296	Rattus norvegicus	open reading frame 2	104	38
1688	AB012223	Canis familiaris	ORF2	98	39
1689	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	278	72
1690	U52077	Homo sapiens	mariner transposase	175	56
1691	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	83	46

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1692	AF061128	Plasmodium falciparum	merozoite surface protein 1	85	44
1693	X77722	Homo sapiens	interferon alpha/beta receptor	89	60
1694	M13100	Rattus norvegicus	unknown protein	94	40
1695	AF202635	Homo sapiens	PP1200	114	60
1696	AK001116	Homo sapiens	unnamed protein product	127	53
1697	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	162	53
1698	AF118078	Homo sapiens	PRO1848	93	42
1699	X92485	Plasmodium vivax	pval	147	49
1700	M63819	Plasmodium falciparum	malaria antigen	101	64
1701	AF090930	Homo sapiens	PRO0478	146	76
1702	AB009993	Mus musculus	collagen al(V)	94	40
1703	AL390114	Leishmania major	extremely cysteine/valine rich protein	169	66
1704	AF130089	Homo sapiens	PRO2550	145	38
1705	X83413	Human herpesvirus 6	U88	113	58
1706	S60088	Homo sapiens	putative adhesion molecule=ADMLX	151	86
1707	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	176	52
1708	AF130079	Homo sapiens	PRO2852	174	41
1709	Y28682	Homo sapiens	Human pp392_3 secreted protein.	557	99
1710	M14423	Mus musculus	pro-alpha-1 type I collagen	112	34
1711	D13623	Rattus sp.	p34 protein	128	45
1712	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	84	41
1713	X97675	Homo sapiens	plakophilin 2b	121	60
1714	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	102	51
1715	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	171	48
1716	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	99	63
1717	S80119	Rattus sp.	reverse transcriptase homolog	140	57
1718	L27428	Homo sapiens	reverse transcriptase	103	46
1719	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	154	78
1720	AF130089	Homo sapiens	PRO2550	106	35
1721	G03652	Homo sapiens	Human secreted protein, SEQ ID NO: 7733.	147	49
1722	G03703	Homo sapiens	Human secreted protein, SEQ ID NO: 7784.	111	72
1723	AF016099	Mus musculus	endonuclease/reverse transcriptase	132	60
1724	X92485	Plasmodium vivax	pval	96	62
1725	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	249	52
1726	M81321	Macaca fascicularis	proline-rich protein	132	45
1727	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	119	69
1728	U93564	Homo sapiens	p40	129	58
1729	U93574	Homo sapiens	putative p150	113	76
1730	AF130089	Homo sapiens	PRO2550	136	61
1731	L05608	Cercopithecine	glycoprotein gl	100	46

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		herpesvirus 2			
1732	U15647	Mus musculus	reverse transcriptase	138	36
1733	U93574	Homo sapiens	putative p150	187	43
1734	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	155	64
1735	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	102	64
1736	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	118	64
1737	G00490	Homo sapiens	Human secreted protein, SEQ ID NO: 4571.	110	58
1738	AF090942	Homo sapiens	PRO0657	163	55
1739	U11288	Drosophila melanogaster	diaphanous protein	149	46
1740	L27428	Homo sapiens	reverse transcriptase	108	33
1741	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	76	54
1742	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	165	59
1743	AC003682	Homo sapiens	R28830_1	179	63
1744	X65165	Volvox carteri	extensin	173	49
1745	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	114	62
1746	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	89	41
1747	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	115	42
1748	U93565	Homo sapiens	putative p150	125	37
1749	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	121	45
1750	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	139	53
1751	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	87	80
1752	L27428	Homo sapiens	reverse transcriptase	133	42
1753	U93570	Homo sapiens	putative p150	126	57
1754	U22376	Homo sapiens	alternatively spliced product using exon 13A	134	50
1755	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	175	76
1756	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	60
1757	U54788	Mus musculus	Wiskott-Aldrich Syndrome Protein	158	44
1758	Y86579	Homo sapiens	Human gene 92-encoded protein fragment, SEQ ID NO:496.	109	88
1759	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	123	73
1760	Y86579	Homo sapiens	Human gene 92-encoded protein fragment, SEQ ID NO:496.	113	92
1761	Y86579	Homo sapiens	Human gene 92-encoded protein fragment, SEQ ID NO:496.	110	81
1762	U08020	Mus musculus	collagen pro-alpha-1 type I chain	105	34
1763	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	90	45
1764	U93569	Homo sapiens	putative p150	148	36
1765	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	116	45
1766	X02873	Daucus carota	put. precursor	112	47
1767	X92485	Plasmodium vivax	pval	100	45
1768	R95913	Homo sapiens	Neural thread protein.	96	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1769	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	114	51
1770	X97675	Homo sapiens	plakophilin 2b	115	70
1771	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	151	58
1772	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	131	85
1773	AF130089	Homo sapiens	PRO2550	158	69
1774	U23552	Ailuropoda melanoleuca	cytochrome b	206	78
1775	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	98	53
1776	AF116715	Homo sapiens	PRO2829	134	67
1777	AC008054	Leishmania major	L8453.1	114	28
1778	AF037364	Homo sapiens	paraneoplastic neuronal antigen MA1	397	73
1779	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	132	60
1780	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	168	64
1781	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	80	36
1782	AF174482	Homo sapiens	polycomb 3	133	46
1783	U93563	Homo sapiens	putative p150	196	70
1784	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	142	59
1785	AF194537	Homo sapiens	NAG13	114	38
1786	U21123	Drosophila melanogaster	ena polypeptide	120	44
1787	AF200187	cercopithecine herpesvirus 15	EBNA2-like protein	108	30
1788	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	97	56
1789	M64792	Rattus norvegicus	salivary proline-rich protein	128	40
1790	X92485	Plasmodium vivax	pva1	98	51
1791	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	114	34
1792	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	197	81
1793	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	145	71
1794	AF104923	Homo sapiens	putative transcription factor	142	59
1795	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	133	60
1796	AC003113	Arabidopsis thaliana	F24O1.6	57	62
1797	M22332	Homo sapiens	unknown protein	118	29
1798	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	100	71
1799	AL390114	Leishmania major	extremely cysteine/valine rich protein	154	37
1800	U93570	Homo sapiens	p40	103	56
1801	X99452	Lycopersicon esculentum	extensin-like protein Dif54	101	28
1802	L27428	Homo sapiens	reverse transcriptase	102	34
1803	L27428	Homo sapiens	reverse transcriptase	141	43
1804	M18933	Mus musculus	alpha-1 type-III collagen precursor	118	30
1805	X92485	Plasmodium vivax	pva1	106	67
1806	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	118	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1807	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	105	33
1808	X97675	Homo sapiens	plakophilin 2b	154	61
1809	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	130	53
1810	X92485	Plasmodium vivax	pval	133	54
1811	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	121	66
1812	Y17833	Human endogenous retrovirus K	env protein	119	81
1813	AF119851	Homo sapiens	PRO1722	130	58
1814	X53581	Rattus norvegicus	ORF4	158	50
1815	G03473	Homo sapiens	Human secreted protein, SEQ ID NO: 7554.	111	74
1816	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	153	68
1817	M19155	Plasmodium falciparum	S-antigen precursor	164	50
1818	AF118082	Homo sapiens	PRO1902	90	75
1819	W40353	Homo sapiens	Human unspecified protein from US5702907.	110	52
1820	U93563	Homo sapiens	putative p150	114	35
1821	U41538	Caenorhabditis elegans	proline rich	95	52
1822	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	154	45
1823	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	131	53
1824	AF130089	Homo sapiens	PRO2550	128	40
1825	AF090944	Homo sapiens	PRO0663	103	45
1826	AC003113	Arabidopsis thaliana	F24O1.18	107	40
1827	AF194537	Homo sapiens	NAG13	85	28
1828	AF009668	multiple sclerosis associated retrovirus	polyprotein	185	41
1829	AF016099	Mus musculus	endonuclease/reverse transcriptase	155	42
1830	X69465	Sus scrofa	ryanodine receptor 1	516	86
1831	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	108	40
1832	U88966	Homo sapiens	rapamycin associated protein FRAP2	434	89
1833	M19155	Plasmodium falciparum	S-antigen precursor	105	32
1834	AF085809	Mus musculus	synapsin Ib	98	33
1835	AK023003	Homo sapiens	unnamed protein product	393	81
1836	Y41740	Homo sapiens	Human PRO701 protein sequence.	429	78
1837	M36913	Zea mays	cell wall protein (put.); putative	72	35
1838	X63005	Mus musculus	proline-rich protein	98	40
1839	X83413	Human herpesvirus 6	U88	149	45
1840	AF134304	Homo sapiens	Scar2	87	37
1841	AC024772	Caenorhabditis elegans	contains similarity to Mus musculus alpha-NAC, muscle-specific form (GB:U48363)	131	25
1842	AB002366	Homo sapiens	KIAA0368	153	75
1843	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	140	47

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1844	AL035526	Arabidopsis thaliana	extensin-like protein	93	33
1845	D26156	Homo sapiens	hSNF2b	91	34
1846	M14228	Gallus gallus	c-beta-3 beta-tubulin	598	83
1847	AK022217	Homo sapiens	unnamed protein product	97	56
1848	AJ250042	Homo sapiens	Rab5 GDP/GTP exchange factor homologue	174	83
1849	W23949	Homo sapiens	Human phosphoinositide 3OH-kinase p101 subunit.	143	28
1850	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	101	63
1851	AB017114	Homo sapiens	AD 3	113	100
1852	D00570	Mus musculus	open reading frame (251 AA)	174	55
1853	A67510	Mus musculus	MUS MUSCULUS GENOMIC DNA CONTAINING N ALLELE OF FV1 GENE.	133	42
1854	U49974	Homo sapiens	mariner transposase	214	82
1855	U93569	Homo sapiens	p40	95	31
1856	D89729	Homo sapiens	CRM1 protein	475	90
1857	AF090895	Homo sapiens	PRO0117	89	36
1858	AF015926	Homo sapiens	ezrin-radixin-moesin binding phosphoprotein-50	117	73
1859	D13721	Gallus gallus	NF-kB p65 subunit	223	56
1860	K03204	Homo sapiens	salivary proline-rich protein precursor	111	32
1861	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	195	52
1862	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	331	69
1863	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	80	35
1864	L27428	Homo sapiens	reverse transcriptase	84	51
1865	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	106	46
1866	U53585	Mycobacterium avium	fibronectin attachment protein	86	36
1867	AF255446	Cryptosporidium parvum	Dip1-associated protein C	134	45
1868	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	81	63
1869	AP000001	Pyrococcus horikoshii	235aa long hypothetical protein	108	40
1870	M13100	Rattus norvegicus	unknown protein	121	53
1871	X67863	Mus musculus	T2	101	35
1872	S80119	Rattus sp.	reverse transcriptase homolog	151	43
1873	W73633	Homo sapiens	Human secreted protein clone.	140	44
1874	U57053	Homo sapiens	myosin-ID	203	82
1875	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	92	54
1876	M21097	Homo sapiens	CD19 differentiation antigen	432	79
1877	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	150	52
1878	U25281	Rattus norvegicus	SH3 domain binding protein	108	36
1879	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	117	48
1880	X73113	Homo sapiens	fast MyBP-C	599	77
1881	AX028128	Homo sapiens	unnamed protein product	162	43
1882	G03789	Homo sapiens	Human secreted protein, SEQ ID NO:	138	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7870.		
1883	Y00664	Homo sapiens	open reading frame 1 (AA 1 - 86)	74	34
1884	U86587	Mus musculus	phosphatidylinositol 3-kinase catalytic subunit p110 delta	204	77
1885	X67337	Homo sapiens	Human pre-mRNA cleavage factor I 68 kDa subunit	148	37
1886	Y13829	Homo sapiens	MBNL protein	117	63
1887	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	119	80
1888	R95913	Homo sapiens	Neural thread protein.	91	64
1889	L39059	Homo sapiens	transcription factor SL1	92	34
1890	M69297	Homo sapiens	ORF 3	169	48
1891	R95913	Homo sapiens	Neural thread protein.	91	62
1892	Z28201	Saccharomyces cerevisiae	ORF YKL202w	95	51
1893	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	90	51
1894	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	183	73
1895	Y10055	Homo sapiens	phosphoinositide 3-kinase	564	84
1896	AF093775	Mus musculus	alpha-actinin 3	375	85
1897	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	82	66
1898	M21904	Homo sapiens	4F2 heavy chain antigen	386	80
1899	AB028997	Homo sapiens	KIAA1074 protein	145	38
1900	U97553	murid herpesvirus 4	unknown	98	41
1901	AB011142	Homo sapiens	KIAA0570 protein	209	95
1902	AF194537	Homo sapiens	NAG13	161	55
1903	U93564	Homo sapiens	putative p150	142	33
1904	M29399	Homo sapiens	erythrocyte membrane protein band 4.2	413	90
1905	Y27400	Homo sapiens	Human P450 reductase functional fragment sequence.	294	67
1906	Y28503	Homo sapiens	HGFH3 Human Growth Factor Homologue 3.	167	100
1907	AF128625	Homo sapiens	CDC42-binding protein kinase beta	509	89
1908	AB029147	Cucumis sativus	expressed in cucumber hypocotyls	98	41
1909	X13783	Homo sapiens	alpha-1 type 2 collagen (714 AA)	87	43
1910	AF240630	Mus musculus	IQ motif containing GTPase activating protein 1	330	48
1911	AF129075	Homo sapiens	T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA)	511	90
1912	AF011450	Mus musculus	type XV collagen	87	28
1913	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	124	75
1914	AF171230	Vigna unguiculata	phosphatidic acid phosphatase beta	112	53
1915	AF016099	Mus musculus	endonuclease/reverse transcriptase	100	47
1916	M94131	Homo sapiens	mucin	97	37
1917	X13885	Nicotiana tabacum	extensin (AA 1-620)	120	34
1918	AF186605	Homo sapiens	MLL2 protein	115	29
1919	M12130	Mus musculus	RNA polymerase II	498	83
1920	AL049794	Homo sapiens	dJ777L9.1 (novel protein similar to mouse kinesin-like proteins KIF1A and KIF1B)	514	90
1921	D83703	Homo sapiens	peroxisome assembly factor-2	233	64
1922	Y11922	Homo sapiens	Human 5' EST secreted protein SEQ ID No: 522.	162	77

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1923	AC002481	Homo sapiens	similar to nitrogen permease regulator; similar to P39923 (PID:g730170), match to AA233630 (NID:g1856833) and AA399402 (NID:g2053147)	223	79
1924	D82060	Homo sapiens	membrane protein with histidine rich charge clusters	115	40
1925	U49974	Homo sapiens	mariner transposase	195	61
1926	S80119	Rattus sp.	reverse transcriptase homolog	104	40
1927	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	79	68
1928	S79639	Homo sapiens	EXT1=putative tumour suppressor/hereditary multiple exostoses candidate gene	430	88
1929	X58063	Brugia pahangi	major protein component of the microfilarial sheath	104	43
1930	AF119855	Homo sapiens	PRO1847	132	64
1931	AJ005577	Homo sapiens	6-phosphofructo-2-kinase	326	90
1932	AF020261	Santalum album	proline rich protein	93	33
1933	AJ272204	Homo sapiens	hypothetical protein	321	52
1934	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	116	39
1935	A61971	unidentified	MCSP	328	79
1936	U93564	Homo sapiens	putative p150	217	54
1937	U97553	murid herpesvirus 4	unknown	113	38
1938	AF194537	Homo sapiens	NAG13	90	37
1939	AF226044	Homo sapiens	HSNFRK	403	85
1940	X83413	Human herpesvirus 6	U88	303	50
1941	AJ007628	Rattus norvegicus	ELK channel 1	112	38
1942	AF104328	Arabidopsis thaliana	cell wall-plasma membrane linker protein homolog	135	35
1943	AF130089	Homo sapiens	PRO2550	93	63
1944	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	102	34
1945	M19419	Mus musculus	proline-rich salivary protein	121	40
1946	U57316	Homo sapiens	histone acetyltransferase	132	73
1947	AL163302	Homo sapiens	human type XVIII collagen	79	34
1948	AB020746	Arabidopsis thaliana	protein kinase-like protein	117	36
1949	AJ011738	Homo sapiens	In1b	209	85
1950	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	155	48
1951	AF119569	Homo sapiens	patched 2	166	89
1952	AB002107	Homo sapiens	hPer	118	39
1953	X98834	Homo sapiens	zinc finger protein Hsa12	430	70
1954	Y19641	Homo sapiens	SEQ ID NO 359 from WO9922243.	96	64
1955	U93569	Homo sapiens	putative p150	157	44
1956	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	85	53
1957	AB013729	Mus musculus	semaphorin Y	106	38
1958	AC005360	Homo sapiens	FAA	338	68
1959	AJ223075	Homo sapiens	TRIP protein	598	95
1960	AC004022	Homo sapiens	serum paraoxonase/arylesterase 3	147	62
1961	AF076776	Drosophila melanogaster	helicase DOMINO A	157	45
1962	AF265555	Homo sapiens	ubiquitin-conjugating BIR-domain enzyme APOLLON	587	77
1963	AF229642	Mus musculus	DXImx46e protein	127	91

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
1964	U72520	Mus musculus	mena protein	89	31
1965	W40309	Homo sapiens	Human ITAK protein.	179	32
1966	AJ388557	Canis familiaris	zinc finger protein	826	56
1967	Y92515	Homo sapiens	Human OXRE-12.	224	53
1968	Y17832	Human endogenous retrovirus K	pol protein	187	49
1969	Y41245	Homo sapiens	Human Y218 protein.	220	78
1970	AB052738	Sus scrofa	Smad3	366	85
1971	AB007644	Arabidopsis thaliana	contains similarity to phytoeyanin/early nodulin-like protein-gene_id:K19P17.3	106	32
1972	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	122	57
1973	AL357472	Homo sapiens	VPS33B	112	31
1974	AF151902	Homo sapiens	CGI-144 protein	112	95
1975	AL137260	Homo sapiens	hypothetical protein	148	92
1976	U89505	Homo sapiens	Hlark	408	89
1977	U67328	Mus musculus	NIPI-like protein	168	73
1978	AK026435	Homo sapiens	unnamed protein product	601	94
1979	Y14318	Homo sapiens	peroxisomal ABC-transporter	507	96
1980	U63630	Homo sapiens	MCM4	570	90
1981	AF118090	Homo sapiens	PRO2044	154	84
1982	AF016370	Homo sapiens	U4/U6 small nuclear ribonucleoprotein hPrp3	422	63
1983	AB011154	Homo sapiens	KIAA0582 protein	420	80
1984	AB011422	Homo sapiens	Trad	201	67
1985	AL390156	Homo sapiens	hypothetical protein	230	97
1986	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	163	44
1987	M12523	Homo sapiens	alloburnin Venezia	411	91
1988	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	145	63
1989	Y36156	Homo sapiens	Human secreted protein #28.	107	80
1990	AF161356	Homo sapiens	HSPC093	156	57
1991	G03443	Homo sapiens	Human secreted protein, SEQ ID NO: 7524.	132	72
1992	AF119851	Homo sapiens	PRO1722	126	52
1993	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	228	60
1994	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	113	40
1995	G02469	Homo sapiens	Human secreted protein, SEQ ID NO: 6550.	118	58
1996	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	137	57
1997	X75068	Bos taurus	plasmalemmal porin	85	85
1998	Y64869	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1030.	92	80
1999	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	275	79
2000	AF118078	Homo sapiens	PRO1848	111	57
2001	S80119	Rattus sp.	reverse transcriptase homolog	120	61
2002	AB011110	Homo sapiens	KIAA0538 protein	146	73
2003	M15530	Homo sapiens	B-cell growth factor	94	64
2004	AF225918	Mus musculus	intestinal cell kinase	216	77
2005	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	125	85
2006	D84391	Mus musculus	reverse transcriptase	135	38
2007	AF090930	Homo sapiens	PRO0478	101	86

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2008	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	156	66
2009	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	165	49
2010	AF113685	Homo sapiens	PRO0974	124	63
2011	AF130079	Homo sapiens	PRO2852	141	78
2012	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	94	51
2013	AF090944	Homo sapiens	PRO0663	67	53
2014	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	151	58
2015	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	223	75
2016	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	137	78
2017	L26953	Homo sapiens	chromosomal protein	120	74
2018	G03646	Homo sapiens	Human secreted protein, SEQ ID NO: 7727.	68	57
2019	G03646	Homo sapiens	Human secreted protein, SEQ ID NO: 7727.	64	42
2020	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	334	63
2021	L26953	Homo sapiens	chromosomal protein	112	64
2022	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	139	69
2023	U93569	Homo sapiens	putative p150	187	89
2024	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	80	72
2025	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	142	71
2026	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	77	66
2027	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	372	73
2028	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	159	80
2029	AF194537	Homo sapiens	NAG13	158	57
2030	L26251	Trypanosoma brucei	CR5	110	41
2031	AF197913	Helicoverpa armigera nuclear polyhedrosis virus	basic DNA-binding protein BDBP	149	55
2032	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	115	80
2033	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	157	82
2034	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	133	75
2035	G03646	Homo sapiens	Human secreted protein, SEQ ID NO: 7727.	104	67
2036	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	137	71
2037	AF130089	Homo sapiens	PRO2550	146	55
2038	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	81	73
2039	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	66
2040	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	159	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2041	B01372	Homo sapiens	Neuron-associated protein.	95	79
2042	V01555	Human herpesvirus 4	BYRF1, encodes EBNA-2 (Dambaugh et al, 1984; Dillner et al, 1984)	108	77
2043	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	125	65
2044	AF118086	Homo sapiens	PRO1992	103	64
2045	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	64
2046	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	108	51
2047	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	133	68
2048	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	155	64
2049	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	125	53
2050	AL390114	Leishmania major	extremely cysteine/valine rich protein	112	56
2051	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	70	62
2052	X61045	Hydra sp.	mini-collagen	99	46
2053	X83413	Human herpesvirus 6	U88	148	73
2054	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	75	63
2055	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	104	75
2056	X16524	Dictyostelium discoideum	coding region (AA 1 - 437)	104	51
2057	R95913	Homo sapiens	Neural thread protein.	83	77
2058	AF118080	Homo sapiens	PRO1880	126	61
2059	AJ276003	Homo sapiens	GAR1 protein	136	59
2060	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	120	70
2061	X01918	Drosophila melanogaster	salivary gland glue protein	179	40
2062	U00029	Saccharomyces cerevisiae	Yhr217cp	110	46
2063	AF130051	Homo sapiens	PRO0898	143	80
2064	AF006061	Homo sapiens	placental growth hormone isoform hGH-V3	121	85
2065	G02409	Homo sapiens	Human secreted protein, SEQ ID NO: 6490.	129	66
2066	U82303	Homo sapiens	unknown	92	68
2067	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	368	79
2068	L27428	Homo sapiens	reverse transcriptase	186	58
2069	AF130051	Homo sapiens	PRO0898	164	73
2070	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	271	73
2071	AF130051	Homo sapiens	PRO0898	110	56
2072	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	117	67
2073	AF157706	Human herpesvirus 6B	B4	104	49
2074	AL049608	Arabidopsis thaliana	extensin-like protein	120	41
2075	AP002460	Arabidopsis thaliana	gene_id:F1D9.26-unknown protein	150	27
2076	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	130	85

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2077	M11897	Mus musculus	proline-rich salivary protein	125	42
2078	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	66	75
2079	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	185	47
2080	AJ006470	Homo sapiens	cartilage-associated protein (CASP)	139	84
2081	AK024509	Homo sapiens	unnamed protein product	132	83
2082	U93564	Homo sapiens	putative p150	137	67
2083	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	99	71
2084	B01372	Homo sapiens	Neuron-associated protein.	148	81
2085	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	114	76
2086	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	255	63
2087	AF194537	Homo sapiens	NAG13	122	78
2088	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	108	74
2089	AF130079	Homo sapiens	PRO2852	149	77
2090	U93574	Homo sapiens	p40	260	96
2091	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	99	76
2092	AF194537	Homo sapiens	NAG13	125	51
2093	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	319	72
2094	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	159	56
2095	U93572	Homo sapiens	putative p150	195	57
2096	X83413	Human herpesvirus 6	U88	132	57
2097	AF010400	Homo sapiens	transaldolase-related protein	463	89
2098	U93563	Homo sapiens	putative p150	128	35
2099	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	160	43
2100	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	133	43
2101	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	97	71
2102	K02401	Homo sapiens	chorionic somatomammotropin	628	90
2103	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	141	80
2104	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	309	63
2105	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	192	37
2106	Y59772	Homo sapiens	Human normal ovarian tissue derived protein 49.	261	89
2107	AF202051	Homo sapiens	NM23-H8	680	100
2108	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	127	54
2109	L22029	Glycine max	hydroxyproline-rich glycoprotein	121	36
2110	D26135	Homo sapiens	diacylglycerol kinase gamma	172	100
2111	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	159	56
2112	X65488	Homo sapiens	hnRNP U protein	117	70
2113	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhla.	116	35
2114	AF130051	Homo sapiens	PRO0898	93	62
2115	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	260	53
2116	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	70

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2117	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	304	71
2118	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	70	66
2119	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	118	84
2120	S79410	Mus musculus	nuclear localization signal binding protein	94	94
2121	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	304	73
2122	M11901	Rattus norvegicus	proline-rich salivary protein	83	32
2123	AK025047	Homo sapiens	unnamed protein product	116	48
2124	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	95	72
2125	AF138883	Bos taurus	type II collagen cyanogen bromide fragment CB10	103	40
2126	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	186	100
2127	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	117	52
2128	AF194537	Homo sapiens	NAG13	126	66
2129	AB015802	Acetobacter xylinus	similar to cellulose complementing protein of A. xylinum ATCC23869	109	80
2130	AF187147	Mus musculus	drebrin A	110	38
2131	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	148	42
2132	L36341	Aspergillus nidulans	regulatory protein	130	49
2133	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	119	58
2134	AF116689	Homo sapiens	PRO2168	113	81
2135	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	191	38
2136	M81321	Macaca fascicularis	proline-rich protein	125	43
2137	A18812	Brassica napus	extensin	106	34
2138	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	104	41
2139	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	191	92
2140	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	196	90
2141	Y57285	Homo sapiens	Human GPCR protein (HGPRP) sequence (clone ID 2214673).	507	78
2142	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	201	47
2143	AF090944	Homo sapiens	PRO0663	164	53
2144	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	390	76
2145	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	198	70
2146	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	119	82
2147	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	194	45
2148	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	91	60
2149	AF090942	Homo sapiens	PRO0657	129	66
2150	AF130089	Homo sapiens	PRO2550	372	82
2151	AC009991	Arabidopsis	unknown protein	81	59

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		thaliana			
2152	AF090942	Homo sapiens	PRO0657	93	53
2153	R13319	Homo sapiens	Partial Human Natural Killer receptor.	215	89
2154	AC008075	Arabidopsis thaliana	F24J5.4	139	36
2155	AL390114	Leishmania major	extremely cysteine/valine rich protein	148	50
2156	S79410	Mus musculus	nuclear localization signal binding protein	112	58
2157	AK024455	Homo sapiens	FLJ00047 protein	152	66
2158	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	85	80
2159	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	165	75
2160	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	145	45
2161	AF119900	Homo sapiens	PRO2822	138	71
2162	AJ223953	Homo sapiens	hPTTG	106	62
2163	AK023542	Homo sapiens	unnamed protein product	76	52
2164	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	118	84
2165	U41038	Caenorhabditis elegans	Similar to cadherin-type repeat	137	65
2166	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	348	88
2167	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	108	84
2168	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	114	48
2169	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	125	67
2170	AF130089	Homo sapiens	PRO2550	142	65
2171	Y19609	Homo sapiens	SEQ ID NO 327 from WO9922243.	103	65
2172	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	104	39
2173	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	91	50
2174	D38435	Homo sapiens	homologue of yeast PMS1	314	96
2175	AF119851	Homo sapiens	PRO1722	230	69
2176	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	100	63
2177	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	137	44
2178	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP:CS24_HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	139	42
2179	AL049608	Arabidopsis thaliana	extensin-like protein	286	57
2180	L17318	Rattus norvegicus	proline-rich proteoglycan	148	40
2181	AK024455	Homo sapiens	FLJ00047 protein	97	63
2182	R95913	Homo sapiens	Neural thread protein.	100	69
2183	AF266479	Homo sapiens	rectachrome 1	148	81
2184	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	64	70
2185	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	107	40
2186	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	110	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2187	AF137273	Gallus gallus	alpha 1 (V) collagen	103	43
2188	K03205	Homo sapiens	salivary proline-rich protein precursor	115	36
2189	D90064	Homo sapiens	NCA-W272	271	100
2190	AF130089	Homo sapiens	PRO2550	137	68
2191	X65165	Volvox carteri	extensin	113	62
2192	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	154	59
2193	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	148	59
2194	U52077	Homo sapiens	mariner transposase	257	53
2195	B12310	Homo sapiens	Human secreted protein encoded by gene 10 clone HDPGP94.	98	79
2196	D38112	Homo sapiens	NADH dehydrogenase subunit 5	180	77
2197	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	121	65
2198	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	126	64
2199	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	101	67
2200	AJ007042	Homo sapiens	TRX5 protein	264	75
2201	AF130051	Homo sapiens	PRO0898	71	61
2202	AK024455	Homo sapiens	FLJ00047 protein	153	62
2203	U83303	Homo sapiens	line-1 reverse transcriptase	95	52
2204	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	128	82
2205	AF090895	Homo sapiens	PRO0117	163	69
2206	G03806	Homo sapiens	Human secreted protein, SEQ ID NO: 7887.	154	69
2207	R95913	Homo sapiens	Neural thread protein.	103	86
2208	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	144	78
2209	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	100	65
2210	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	111	45
2211	AF090931	Homo sapiens	PRO0483	63	90
2212	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	100	74
2213	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	98	41
2214	M76671	Lycopersicon esculentum	extensin (class II)	137	35
2215	X03717	Homo sapiens	pot. unidentified reading frame	98	54
2216	R95913	Homo sapiens	Neural thread protein.	109	48
2217	AF118086	Homo sapiens	PRO1992	138	79
2218	AF081484	Homo sapiens	alpha-tubulin isoform 1	343	95
2219	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	157	84
2220	AF141347	Homo sapiens	alpha-tubulin	571	94
2221	AF071172	Homo sapiens	HERC2	187	84
2222	M17783	Homo sapiens	glia-derived nexin precursor	529	83
2223	AF081484	Homo sapiens	alpha-tubulin isoform 1	588	85
2224	AK026072	Homo sapiens	unnamed protein product	199	57
2225	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	161	61
2226	Z70684	Caenorhabditis elegans	F28D1.8	126	41
2227	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	124	63

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2228	AF119855	Homo sapiens	PRO1847	108	74
2229	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	122	55
2230	AF090944	Homo sapiens	PRO0663	146	61
2231	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	152	74
2232	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	80	59
2233	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	129	58
2234	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	143	60
2235	AK024455	Homo sapiens	FLJ00047 protein	133	71
2236	Y87103	Homo sapiens	Human secreted protein sequence SEQ ID NO:142.	99	59
2237	U87607	Rattus norvegicus	putative RNA binding protein I	111	38
2238	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	119	63
2239	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	75	65
2240	L27428	Homo sapiens	reverse transcriptase	136	40
2241	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	122	82
2242	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	105	95
2243	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	79	48
2244	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	145	75
2245	U09116	Homo sapiens	ORF1, encodes a 40 kDa product	346	87
2246	U82303	Homo sapiens	unknown	155	79
2247	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	105	45
2248	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	105	47
2249	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	63
2250	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	124	62
2251	X81206	Drosophila hydei	histone H3.3	101	71
2252	AF155581	Danio rerio	proteasome subunit beta 7	92	52
2253	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	172	60
2254	AF084225	Homo sapiens	cytochrome P450 2E1	114	46
2255	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	136	64
2256	AL132841	Caenorhabditis elegans	Y15E3A.3	147	90
2257	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	297	59
2258	U93563	Homo sapiens	putative p150	218	66
2259	L22650	Homo sapiens	early lymphoid activation protein	82	55
2260	AF194537	Homo sapiens	NAG13	117	56
2261	U43360	Peromyscus maniculatus	reverse transcriptase	130	82
2262	G00366	Homo sapiens	Human secreted protein, SEQ ID NO: 4447.	86	66
2263	AL021918	Homo sapiens	b3418.1 (Kruppel related Zinc Finger protein 184)	372	61
2264	AL390114	Leishmania major	extremely cysteine/valine rich protein	122	71

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2265	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	123	79
2266	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	204	95
2267	L29029	Chlamydomonas reinhardtii	amino acid feature: Rod protein domain, aa 266 .. 468; amino acid feature: globular protein domain, aa 32 .. 265	141	58
2268	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	499	84
2269	A11693	Homo sapiens	start codon not included	594	87
2270	AB014554	Homo sapiens	KIAA0654 protein	141	63
2271	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	112	60
2272	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	118	54
2273	Y20852	Homo sapiens	Human neurofilament-H mutant protein fragment 11.	125	35
2274	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	92	66
2275	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	198	64
2276	U15647	Mus musculus	reverse transcriptase	100	72
2277	AJ004810	Zea mays	cytochrome P450 monooxygenase	129	43
2278	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	111	67
2279	G00589	Homo sapiens	Human secreted protein, SEQ ID NO: 4670.	112	68
2280	L27428	Homo sapiens	reverse transcriptase	150	60
2281	K03202	Homo sapiens	salivary proline-rich protein precursor	142	40
2282	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	321	54
2283	D00570	Mus musculus	open reading frame (251 AA)	169	56
2284	Y02887	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	86	54
2285	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	144	50
2286	AF119901	Homo sapiens	PRO2831	116	82
2287	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	126	73
2288	AF130089	Homo sapiens	PRO2550	102	75
2289	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	113	70
2290	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	127	64
2291	L26953	Homo sapiens	chromosomal protein	137	53
2292	AF161356	Homo sapiens	HSPC093	100	57
2293	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	138	68
2294	X03145	Homo sapiens	pot. ORF I	120	43
2295	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	83	52
2296	AK024455	Homo sapiens	FLJ00047 protein	98	66
2297	G00262	Homo sapiens	Human secreted protein, SEQ ID NO: 4343.	123	73
2298	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	349	73
2299	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	109	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2300	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	100	81
2301	AF251290	Plasmodium falciparum	glutamic acid-rich protein	112	40
2302	AF155232	Pisum sativum	extensin	89	36
2303	AF130089	Homo sapiens	PRO2550	83	50
2304	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	84	51
2305	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	86	30
2306	AP002031	Arabidopsis thaliana	gene_id:K3D20.3~	168	44
2307	AF157321	Homo sapiens	30 kDa protein	309	64
2308	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	170	57
2309	M76546	Helianthus annuus	hydroxyproline-rich protein	198	42
2310	Y27607	Homo sapiens	Human secreted protein encoded by gene No. 41.	207	100
2311	AF130089	Homo sapiens	PRO2550	106	66
2312	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	117	60
2313	R10755	Homo sapiens	Non-A non-B hepatitis specific antigenic protein encoded by phageclone lambda HC2533.	114	80
2314	AB032910	Hylobates muelleri	dopamine receptor D4	108	40
2315	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	159	59
2316	AK024455	Homo sapiens	FLJ00047 protein	134	58
2317	AF238235	Entamoeba histolytica	diaphanous protein	103	51
2318	U15647	Mus musculus	reverse transcriptase	101	37
2319	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	117	51
2320	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	163	78
2321	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	97	48
2322	D00570	Mus musculus	open reading frame (196 AA)	122	39
2323	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	122	75
2324	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	118	79
2325	U44838	Glycine max	extensin	126	36
2326	Y87103	Homo sapiens	Human secreted protein sequence SEQ ID NO:142.	99	59
2327	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	408	79
2328	AF194537	Homo sapiens	NAG13	181	66
2329	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	405	75
2330	X53581	Rattus norvegicus	ORF4	116	45
2331	L26953	Homo sapiens	chromosomal protein	108	67
2332	L27428	Homo sapiens	reverse transcriptase	117	76
2333	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	84	50
2334	AF191687	Homo sapiens	alanine-glyoxylate aminotransferase homolog	100	37
2335	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	84	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2336	AL390114	Leishmania major	extremely cysteine/valine rich protein	106	53
2337	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	168	65
2338	R95913	Homo sapiens	Neural thread protein.	164	67
2339	AF090942	Homo sapiens	PRO0657	122	81
2340	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	107	90
2341	AF090942	Homo sapiens	PRO0657	124	60
2342	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	126	83
2343	AB013454	Rattus norvegicus	NaPi-2 beta	143	77
2344	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	127	73
2345	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	146	45
2346	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	120	40
2347	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	109	55
2348	Y36203	Homo sapiens	Human secreted protein #75.	138	78
2349	L26953	Homo sapiens	chromosomal protein	131	57
2350	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	120	65
2351	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	144	58
2352	AF130051	Homo sapiens	PRO0898	155	70
2353	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	134	76
2354	L27428	Homo sapiens	reverse transcriptase	141	71
2355	L26953	Homo sapiens	chromosomal protein	128	66
2356	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	148	75
2357	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	115	62
2358	B12310	Homo sapiens	Human secreted protein encoded by gene 10 clone HDPGP94.	115	50
2359	M76546	Helianthus annuus	hydroxyproline-rich protein	103	43
2360	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	82	80
2361	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	95	72
2362	M64793	Rattus norvegicus	salivary proline-rich protein	117	41
2363	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	98	80
2364	AL451017	Neurospora crassa	related to UI SMALL NUCLEAR RIBONUCLEOPROTEIN C	152	45
2365	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	85	55
2366	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	101	77
2367	AF093097	Homo sapiens	putative RNA-binding protein Q99	248	97
2368	U52077	Homo sapiens	mariner transposase	227	74
2369	X07882	Homo sapiens	Po protein	102	38
2370	U44838	Glycine max	extensin	102	32
2371	AB012223	Canis familiaris	ORF2	158	60
2372	AF025467	Caenorhabditis	contains similarity to drosophila DNA-	104	42

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		<i>elegans</i>	binding protein K10 (NID:g8148)		
2373	G04091	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 8172.	107	40
2374	G04078	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 8159.	106	67
2375	AF118086	<i>Homo sapiens</i>	PRO1992	169	65
2376	W48351	<i>Homo sapiens</i>	Human breast cancer related protein BCRB2.	95	55
2377	G03798	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7879.	121	59
2378	Y85062	<i>Homo sapiens</i>	Interleukin 1 converting enzyme homologue (ICEL) protein sequence.	141	70
2379	R95913	<i>Homo sapiens</i>	Neural thread protein.	120	50
2380	U93572	<i>Homo sapiens</i>	putative p150	124	53
2381	G02538	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 6619.	195	66
2382	U52077	<i>Homo sapiens</i>	mariner transposase	282	67
2383	G04067	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 8148.	113	43
2384	AJ242540	<i>Volvox carteri f. nagariensis</i>	hydroxyproline-rich glycoprotein DZ-HRGP	112	37
2385	G03714	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7795.	88	75
2386	AF130089	<i>Homo sapiens</i>	PRO2550	160	62
2387	W88627	<i>Homo sapiens</i>	Secreted protein encoded by gene 94 clone HPMBQ32.	166	61
2388	AF130089	<i>Homo sapiens</i>	PRO2550	103	71
2389	AB027890	<i>Schizosaccharomyces pombe</i>	Hypothetical protein	116	100
2390	U93570	<i>Homo sapiens</i>	putative p150	151	54
2391	Y19767	<i>Homo sapiens</i>	SEQ ID NO 485 from WO9922243.	110	71
2392	G03797	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7878.	109	67
2393	AE001381	<i>Plasmodium falciparum</i>	hypothetical protein	94	34
2394	Y86248	<i>Homo sapiens</i>	Human secreted protein HCHPF68, SEQ ID NO:163.	156	62
2395	G03052	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7133.	57	56
2396	U42471	<i>Mus musculus</i>	Wiscott-Aldrich Syndrome protein homolog	107	43
2397	AF210651	<i>Homo sapiens</i>	NAG18	162	54
2398	M11901	<i>Rattus norvegicus</i>	proline-rich salivary protein	116	34
2399	S80864	<i>Homo sapiens</i>	cytochrome c-like polypeptide	115	68
2400	G00365	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 4446.	141	54
2401	M13100	<i>Rattus norvegicus</i>	unknown protein	148	46
2402	G03793	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7874.	133	70
2403	Y91577	<i>Homo sapiens</i>	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	366	94
2404	AF113685	<i>Homo sapiens</i>	PRO0974	112	56
2405	Y36495	<i>Homo sapiens</i>	Fragment of human secreted protein encoded by gene 27.	98	67
2406	R41001	<i>Homo sapiens</i>	Human myotonic dystrophy gene protein.	207	68
2407	AL390114	<i>Leishmania</i>	probable (hhv-6) u1102, variant a	127	63

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		major	DNA, complete virion genome		
2408	G03101	Homo sapiens	Human secreted protein, SEQ ID NO: 7182.	378	95
2409	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:125.	250	86
2410	U72520	Mus musculus	mena protein	115	40
2411	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	44
2412	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	109	85
2413	AF119901	Homo sapiens	PRO2831	113	66
2414	R95913	Homo sapiens	Neural thread protein.	93	57
2415	B01372	Homo sapiens	Neuron-associated protein.	104	83
2416	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	130	50
2417	J02459	bacteriophage lambda	K (tail component;199)	720	92
2418	J04694	Mus musculus	alpha-1 type IV collagen	103	43
2419	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	145	61
2420	W26496	Homo sapiens	CD2 associated intracellular protein CAIP LS02-21.	115	80
2421	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	145	38
2422	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	158	73
2423	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	156	70
2424	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	122	61
2425	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	95	59
2426	U93565	Homo sapiens	putative p150	147	75
2427	AL390114	Leishmania major	extremely cysteine/valine rich protein	246	53
2428	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	138	61
2429	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	112	75
2430	D13892	Homo sapiens	carboxyl methyltransferase	181	68
2431	X97675	Homo sapiens	plakophilin 2b	131	65
2432	G02896	Homo sapiens	Human secreted protein, SEQ ID NO: 6977.	108	70
2433	X03145	Homo sapiens	pot. ORF III	180	82
2434	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	77	86
2435	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	421	67
2436	M64793	Rattus norvegicus	salivary proline-rich protein	111	38
2437	AF210651	Homo sapiens	NAG18	128	72
2438	AF016099	Mus musculus	endonuclease/reverse transcriptase	232	46
2439	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	122	53
2440	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	136	80
2441	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	139	54
2442	AF090895	Homo sapiens	PRO0117	115	61
2443	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	125	70

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2444	G00594	Homo sapiens	Human secreted protein, SEQ ID NO: 4675.	71	80
2445	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	81	37
2446	AF090895	Homo sapiens	PRO0117	86	64
2447	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	103	86
2448	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	94	61
2449	L21936	Homo sapiens	succinate dehydrogenase flavoprotein subunit	168	91
2450	AF090942	Homo sapiens	PRO0657	134	71
2451	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	126	87
2452	K03179	Homo sapiens	pro-alpha-1 type-I collagen	120	44
2453	AF118082	Homo sapiens	PRO1902	143	46
2454	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	114	68
2455	AF130089	Homo sapiens	PRO2550	125	89
2456	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	134	71
2457	Y36243	Homo sapiens	Human secreted protein encoded by gene 20.	93	75
2458	Y09945	Rattus norvegicus	putative integral membrane transport protein	166	46
2459	AF130052	Homo sapiens	PRO0956	75	48
2460	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	162	76
2461	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	123	69
2462	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	157	48
2463	X83413	Human herpesvirus 6	U88	236	50
2464	G00517	Homo sapiens	Human secreted protein, SEQ ID NO: 4598.	181	53
2465	X83413	Human herpesvirus 6	U88	218	50
2466	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	147	57
2467	X83413	Human herpesvirus 6	U88	196	53
2468	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	61
2469	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	101	46
2470	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	221	56
2471	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	136	63
2472	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	122	94
2473	AF161361	Homo sapiens	HSPC098	120	60
2474	M76546	Helianthus annuus	hydroxyproline-rich protein	142	40
2475	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	130	58
2476	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	78	48
2477	AL160371	Leishmania	probable (hhv-6) u1102, variant a	86	46

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		major	DNA, complete virion genome		
2478	G01478	Homo sapiens	Human secreted protein, SEQ ID NO: 5559.	96	66
2479	AL033545	Arabidopsis thaliana	extensin-like protein	114	40
2480	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	142	59
2481	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	146	62
2482	AL132902	Caenorhabditis elegans	Y71A12B.4	160	37
2483	AF154502	Homo sapiens	quiescent cell proline dipeptidase	439	88
2484	AF010326	Drosophila melanogaster	short form of CHIP	56	42
2485	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	119	50
2486	W31186	Homo sapiens	Human p160 polypeptide 160.2.	115	60
2487	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	103	74
2488	L26953	Homo sapiens	chromosomal protein	129	68
2489	Y21418	Homo sapiens	Human high mobility group protein HMGI-C mutant fragment 2.	96	46
2490	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	366	94
2491	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	158	76
2492	U12707	Homo sapiens	Wiskott-Aldrich syndrome protein	144	47
2493	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	117	81
2494	X92485	Plasmodium vivax	pva1	116	64
2495	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	92	64
2497	AF161483	Homo sapiens	HSPC134	211	78
2498	X05006	Homo sapiens	S-protein	298	92
2499	AB032911	Hylobates agilis	dopamine receptor D4	89	42
2500	M98502	Mus musculus	pMLZ-4	325	90
2501	Y94920	Homo sapiens	Human secreted protein clone pm412_12 protein sequence SEQ ID NO:46.	569	85
2502	AB049054	Homo sapiens	brain link protein-1	224	90
2503	AF064604	Homo sapiens	KE03 protein	224	37
2504	Z69727	Schizosaccharomyces pombe	putative dna-directed rna polymerase iii 130 kd polypeptide (ec 2.7.7.6)	384	61
2505	M11901	Rattus norvegicus	proline-rich salivary protein	147	43
2506	AJ010604	Mus musculus	L-Sox5 protein	366	87
2507	X83413	Human herpesvirus 6	U88	203	46
2508	AJ277425	Globodera pallida	putative cuticular collagen	125	40
2509	AB017919	Homo sapiens	peptidylarginine deiminase type V	148	81
2510	AF001947	Homo sapiens	U4/U6-associated RNA splicing factor	583	97
2511	AJ238520	Homo sapiens	putative transcription factor-like nuclear regulator	722	100
2512	AL390736	Homo sapiens	bA209J19.1.1 (GW112 protein)	557	84
2513	D84223	Homo sapiens	leucyl tRNA synthetase	1113	100
2514	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	174	56

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2515	U60803	Homo sapiens	clathrin heavy chain 2	111	92
2516	AJ388557	Canis familiaris	zinc finger protein	826	56
2517	AB027251	Homo sapiens	zinc finger protein (ZFD25)	631	85
2518	AK023160	Homo sapiens	unnamed protein product	168	54
2519	D87326	Mus musculus	GSG2	575	73
2520	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	100	42
2521	X67688	Homo sapiens	transketolase	120	66
2522	AF074086	Homo sapiens	protease	390	86
2523	AF220509	Homo sapiens	transcription associated factor TAFII31L	801	99
2524	AL078463	Homo sapiens	dJ365119.1 (KIAA0456)	374	92
2525	AF038995	Mus musculus	putative RNA helicase RCK	160	93
2526	M60618	Homo sapiens	nuclear autoantigen	116	75
2527	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	101	57
2528	X68790	Homo sapiens	Bactericidal /Permeability Increasing Protein	136	90
2529	A01592	Homo sapiens	haemoglobin A beta chain	508	94
2530	U89277	Homo sapiens	polyhomeotic 1 homolog	404	79
2531	X90845	Rattus norvegicus	alpha1 spectrin	507	87
2532	AL137081	Arabidopsis thaliana	phenylalanine-tRNA synthetase-like protein	178	33
2533	Y18046	Homo sapiens	FGFR1 oncogene partner (FOP)	363	100
2534	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	113	42
2535	X61047	Hydra sp.	mini-collagen	102	38
2536	AB006330	Mus musculus	SOX5	559	94
2537	AC006283	Arabidopsis thaliana	En/Spm-like transposon protein	149	33
2538	AF196779	Homo sapiens	JM11 protein	139	57
2539	AK000741	Homo sapiens	unnamed protein product	233	47
2540	Y18046	Homo sapiens	FGFR1 oncogene partner (FOP)	315	84
2541	U54996	Homo sapiens	HZW10	371	81
2542	G02631	Homo sapiens	Human secreted protein, SEQ ID NO: 6712.	99	45
2543	M95610	Homo sapiens	alpha-2 IX collagen	93	34
2544	AF071173	Mus musculus	Herc2	349	82
2545	AB000516	Homo sapiens	DSIF p160	600	93
2546	AL355178	Homo sapiens	dJ947L8.1.6 (novel CUB and Sushi (SCR repeat) domain protein)	395	90
2547	U93574	Homo sapiens	putative p150	235	76
2548	X80035	Oryctolagus cuniculus	cysteine rich hair keratin associated protein	99	31
2549	U58088	Homo sapiens	Hs-CUL-2	592	86
2550	L26953	Homo sapiens	chromosomal protein	131	63
2551	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	99	61
2552	U39412	Homo sapiens	alpha SNAP	159	54
2553	AF248651	Homo sapiens	RNA-binding protein BRUNOL4	569	93
2554	AJ006519	Rattus norvegicus	ASIC-beta	164	73
2555	U93570	Homo sapiens	putative p150	169	52
2556	AF104328	Arabidopsis thaliana	cell wall-plasma membrane linker protein homolog	105	29
2557	AB028975	Homo sapiens	KIAA1052 protein	610	83
2558	AJ245621	Homo sapiens	CTL2 protein	286	47

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2559	AF090944	Homo sapiens	PRO0663	174	78
2560	Y17832	Human endogenous retrovirus K	pol protein	411	63
2561	AF109907	Homo sapiens	S164	279	44
2562	A09561	synthetic construct	human serum albumin	680	91
2563	U48359	Gallus gallus	kinesin light chain	575	81
2564	R63235	Homo sapiens	CNS neural thread protein HB4.	435	88
2565	D38112	Homo sapiens	NADH dehydrogenase subunit 4	623	89
2566	AF154916	Chlamydomonas reinhardtii	variable flagellar number protein	117	36
2567	AF181657	Drosophila melanogaster	BcDNA.LD34475	261	42
2568	M12530	Homo sapiens	transferrin precursor	693	87
2569	U96915	Homo sapiens	sin3 associated polypeptide p18	651	93
2570	R74205	Homo sapiens	Human death associated protein DAP-2.	285	27
2571	AL078593	Homo sapiens	dJ210B1.1 (KIAA0680)	107	37
2572	AF293405	Phaseolus coccineus	seed-micropylar-endothelium-specific protein	88	39
2573	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	110	49
2574	AB024601	Pseudomonas aeruginosa	uridylyl transferase	120	37
2575	AB050893	Anadara nodifera	cytochrome c oxidase subunit 1	111	79
2576	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	130	72
2577	M17697	Homo sapiens	glutamate dehydrogenase	369	61
2578	AF045640	Caenorhabditis elegans	C11D2.4 gene product	264	43
2579	U71382	Homo sapiens	OB binding protein-1	273	86
2580	AF116661	Homo sapiens	PRO1438	114	61
2581	AK000496	Homo sapiens	unnamed protein product	153	55
2582	A67510	Mus musculus	MUS MUSCULUS GENOMIC DNA CONTAINING N ALLELE OF FV1 GENE.	190	38
2583	Y44851	Homo sapiens	Human CD39-L66 protein.	205	97
2584	AB029151	Homo sapiens	D29	253	73
2585	AF039023	Homo sapiens	Ran-GTP binding protein; RanBP6	765	94
2586	AF054180	Homo sapiens	hematopoietic cell derived zinc finger protein	116	34
2587	AF283645	Homo sapiens	folate transporter/carrier	580	82
2588	AF090930	Homo sapiens	PRO0478	132	67
2589	AC002339	Arabidopsis thaliana	putative ABC transporter	238	34
2590	M34668	Homo sapiens	protein tyrosine phosphatase (EC 3.1.3.48)	627	86
2591	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	141	63
2592	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	142	63
2593	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	146	54
2594	AF047437	Homo sapiens	sperm acrosomal protein	526	74
2595	U28789	Mus musculus	PACT	528	71
2596	AB002366	Homo sapiens	KIAA0368	615	83
2597	AL049610	Homo sapiens	dJ1055C14.2 (KIAA0026 (transcription factor-like protein	704	93

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			MRGX))		
2598	G01279	Homo sapiens	Human secreted protein, SEQ ID NO: 5360.	385	79
2599	AF090895	Homo sapiens	PRO0117	142	61
2600	D29763	Mus musculus	seizure-related gene product 6 precursor	119	76
2601	U20158	Homo sapiens	SLP-76	108	53
2602	D38112	Homo sapiens	NADH dehydrogenase subunit 2	242	78
2603	D38112	Homo sapiens	NADH dehydrogenase subunit 2	233	73
2604	L24804	Homo sapiens	p23	259	62
2605	Y12102	Homo sapiens	Human 5' EST secreted protein SEQ ID NO: 415.	132	92
2606	U79284	Homo sapiens	SEC14L	614	81
2607	AF202635	Homo sapiens	PPI200	105	47
2608	AF277374	Homo sapiens	enhancer of polycomb	254	85
2609	X03484	Homo sapiens	raf protein (aa 1-648)	600	82
2610	U15637	Homo sapiens	CD40 binding protein	465	82
2611	U40265	Trypanosoma cruzi	ATPase subunit 6	98	31
2612	AF090942	Homo sapiens	PRO0657	125	48
2613	V00662	Homo sapiens	cytochrome oxidase I	605	82
2614	U46920	Homo sapiens	metaxin	748	94
2615	Y19757	Homo sapiens	SEQ ID NO 475 from WO9922243.	113	87
2616	AK025047	Homo sapiens	unnamed protein product	173	58
2617	D13866	Homo sapiens	alpha-catenin	569	96
2618	U20536	Homo sapiens	cysteine protease Mch2 isoform alpha	588	87
2619	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	608	86
2620	AF190168	Homo sapiens	serum albumin precursor	522	78
2621	A06977	Homo sapiens	albumin	607	93
2622	R14584	Homo sapiens	TGF beta 1 binding protein encoded by clone BPA 13.	339	81
2623	X56698	Xenopus laevis	42Sp48	117	47
2624	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	131	57
2625	X07881	Homo sapiens	proline-rich protein G1	116	32
2626	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	89	58
2627	A00279	synthetic construct	Human serum albumin	564	95
2628	AK021613	Homo sapiens	unnamed protein product	214	70
2629	M23613	Homo sapiens	nucleophosmin	486	82
2630	AF243424	Homo sapiens	SG2NA beta isoform	256	98
2631	G00506	Homo sapiens	Human secreted protein, SEQ ID NO: 4587.	81	60
2632	A06977	Homo sapiens	albumin	457	74
2633	A06977	Homo sapiens	albumin	563	93
2634	M81088	Rattus norvegicus	EF-1-alpha	165	68
2635	AL359587	Homo sapiens	hypothetical protein	496	82
2636	A03758	Homo sapiens	serum albumin	576	91
2637	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	127	39
2638	U93563	Homo sapiens	putative p150	186	38
2639	U68729	Meloidogyne incognita	cuticle preprocollagen	113	34
2640	AB033056	Homo sapiens	KIAA1230 protein	269	94
2641	AF116712	Homo sapiens	PRO2738	115	61
2642	W48353	Homo sapiens	Human breast cancer related protein	124	72

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCFLT2.		
2643	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	98	54
2644	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	127	64
2645	AK025116	Homo sapiens	unnamed protein product	104	64
2646	X92485	Plasmodium vivax	pva1	100	47
2647	AF130089	Homo sapiens	PRO2550	122	51
2648	AF194537	Homo sapiens	NAG13	279	83
2649	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	90	66
2650	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	148	63
2651	AF116661	Homo sapiens	PRO1438	112	46
2652	U63542	Homo sapiens	FAP protein	128	79
2653	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	133	46
2654	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICE1) protein sequence.	139	72
2655	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	164	72
2656	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene preduct.	145	51
2657	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	166	64
2658	B25722	Homo sapiens	Human secreted protein sequence encoded by gene 9 SEQ ID NO:111.	91	88
2659	X92485	Plasmodium vivax	pva1	141	60
2660	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	68	68
2661	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	96	59
2662	AF090931	Homo sapiens	PRO0483	114	74
2663	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	129	57
2664	AF090930	Homo sapiens	PRO0478	170	78
2665	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	460	77
2666	D38112	Homo sapiens	cytochrome c oxidase subunit 1	368	67
2667	AF090931	Homo sapiens	PRO0483	90	88
2668	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	121	66
2669	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	169	73
2670	AF194537	Homo sapiens	NAG13	170	42
2671	X86003	Rattus norvegicus	neuron-derived orphan receptor	104	50
2672	U63542	Homo sapiens	FAP protein	139	75
2673	AF090930	Homo sapiens	PRO0478	130	69
2674	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	161	75
2675	AK024455	Homo sapiens	FLJ00047 protein	105	53
2676	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	142	67
2677	AK000496	Homo sapiens	unnamed protein product	110	67
2678	AF116715	Homo sapiens	PRO2829	151	78
2679	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	160	72
2680	G02532	Homo sapiens	Human secreted protein, SEQ ID NO:	110	81

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6613.		
2681	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	131	75
2682	U76604	Homo sapiens	180 kDa bullous pemphigoid antigen 2/type XVII collagen	96	37
2683	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	85	55
2684	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	127	80
2685	AF090895	Homo sapiens	PRO0117	81	51
2686	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	119	52
2687	M64793	Rattus norvegicus	salivary proline-rich protein	122	41
2688	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	145	71
2689	AF130089	Homo sapiens	PRO2550	149	78
2690	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	102	47
2691	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	116	74
2692	G03064	Homo sapiens	Human secreted protein, SEQ ID NO: 7145.	130	60
2693	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	106	26
2694	AE001158	Borrelia burgdorferi	conserved hypothetical integral membrane protein	81	37
2695	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	162	76
2696	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	100
2697	AF194537	Homo sapiens	NAG13	126	90
2698	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	69
2699	U93563	Homo sapiens	putative p150	138	37
2700	AF090928	Homo sapiens	PRO0470	177	57
2701	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	75
2702	X92485	Plasmodium vivax	pva1	116	50
2703	AK024455	Homo sapiens	FLJ00047 protein	103	57
2704	D38114	Gorilla gorilla	NADH dehydrogenase subunit 2 (ND2)	137	81
2705	AF090895	Homo sapiens	PRO0117	105	51
2706	AF090944	Homo sapiens	PRO0663	121	45
2707	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	104	57
2708	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	157	85
2709	D38112	Homo sapiens	NADH dehydrogenase subunit 1	283	84
2710	AF130079	Homo sapiens	PRO2852	125	48
2711	M22334	Homo sapiens	unknown protein	131	50
2712	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	123	58
2713	S80119	Rattus sp.	reverse transcriptase homolog	230	57
2714	AF090931	Homo sapiens	PRO0483	98	85
2715	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	104	79
2716	L00016	Homo sapiens	urf5	295	93
2717	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	135	82
2718	M81321	Macaca fascicularis	proline-rich protein	117	38

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2719	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	124	57
2720	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	147	56
2721	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	132	67
2722	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	129	56
2723	D38112	Homo sapiens	cytochrome c oxidase subunit I	392	68
2724	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	182	79
2725	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	195	92
2726	W97293	Homo sapiens	An annexin binding protein (NABP-1).	193	40
2727	U12690	Homo sapiens	cytochrome oxidase subunit II	547	85
2728	V00662	Homo sapiens	cytochrome oxidase I	500	92
2729	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	110	56
2730	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	124	75
2731	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	113	57
2732	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	149	51
2733	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	101	44
2734	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	288	81
2735	Z74036	Caenorhabditis elegans	contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=58.9, E-value=3.5e-14, N=3	117	37
2736	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	154	62
2737	AK024455	Homo sapiens	FLJ00047 protein	136	60
2738	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	110	63
2739	AP002460	Arabidopsis thaliana	gene_id:F1D9.26~unknown protein	363	90
2740	D38113	Pan troglodytes	cytochrome c oxidase subunit I	358	69
2741	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	143	64
2742	L27428	Homo sapiens	reverse transcriptase	119	45
2743	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	76	63
2744	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	155	79
2745	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	114	51
2746	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	159	75
2747	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	162	79
2748	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	107	49
2749	AK024455	Homo sapiens	FLJ00047 protein	165	69
2750	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	167	72
2751	M22332	Homo sapiens	unknown protein	208	46

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2752	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	125	56
2753	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	150	65
2754	AF220264	Homo sapiens	MOST-1	130	52
2755	AK024455	Homo sapiens	FLJ00047 protein	128	58
2756	AF130051	Homo sapiens	PRO0898	162	73
2757	D38112	Homo sapiens	NADH dehydrogenase subunit 3	259	86
2758	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	124	58
2759	AJ243666	Homo sapiens	NICE-5 protein	118	84
2760	D38112	Homo sapiens	NADH dehydrogenase subunit 4	533	90
2761	G02482	Homo sapiens	Human secreted protein, SEQ ID NO: 6563.	110	39
2762	U12690	Homo sapiens	cytochrome oxidase subunit II	257	88
2763	Y73345	Homo sapiens	HTRM clone 438283 protein sequence.	624	67
2764	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	156	45
2765	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	132	58
2766	X92485	Plasmodium vivax	pval	149	53
2767	AF113685	Homo sapiens	PRO0974	131	63
2768	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	109	56
2769	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	154	71
2770	X97707	Pongo pygmaeus abelii	stopcodon created by posttranscriptional polyadenylation	185	87
2771	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	110	59
2772	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	145	60
2773	AF090944	Homo sapiens	PRO0663	118	62
2774	L26953	Homo sapiens	chromosomal protein	112	58
2775	AF090930	Homo sapiens	PRO0478	127	59
2776	AK024455	Homo sapiens	FLJ00047 protein	154	56
2777	R59843	Homo sapiens	ApoE4Lx2 protease.	103	42
2778	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	101	55
2779	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	131	64
2780	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	89	56
2782	D38113	Pan troglodytes	NADH dehydrogenase subunit 4	194	97
2783	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	124	68
2784	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	123	49
2785	U43360	Peromyscus maniculatus	reverse transcriptase	175	50
2786	W58700	Homo sapiens	Human ST-1 partial sequence.	219	100
2787	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	137	90
2788	D38112	Homo sapiens	cytochrome c oxidase subunit 3	519	76
2789	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	104	44
2790	AF130089	Homo sapiens	PRO2550	121	39
2791	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	135	63
2792	G03052	Homo sapiens	Human secreted protein, SEQ ID NO:	124	50

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7133.		
2793	M10546	Homo sapiens	cytochrome oxidase I	153	80
2794	D38112	Homo sapiens	cytochrome c oxidase subunit I	461	84
2795	AF090931	Homo sapiens	PRO0483	114	76
2796	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	107	53
2797	D38112	Homo sapiens	NADH dehydrogenase subunit 2	114	78
2798	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	115	71
2799	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	113	79
2800	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	117	48
2801	X92485	Plasmodium vivax	pval	97	80
2802	D38112	Homo sapiens	cytochrome c oxidase subunit 3	471	80
2803	AF130051	Homo sapiens	PRO0898	118	78
2804	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	78	73
2805	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	143	69
2806	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	102	62
2807	K02401	Homo sapiens	chorionic somatomammotropin	543	88
2808	Y18522	Corvus frugilegus	cytochrome oxidase subunit I	382	60
2809	G01194	Homo sapiens	Human secreted protein, SEQ ID NO: 5275.	555	93
2810	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	399	77
2811	AF007826	Homo sapiens	bax epsilon	94	39
2812	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	220	67
2813	U12690	Homo sapiens	cytochrome oxidase subunit II	495	81
2814	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	112	48
2815	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	102	75
2816	D38112	Homo sapiens	cytochrome c oxidase subunit 3	437	83
2817	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	143	66
2818	X55733	Homo sapiens	initiation factor 4B	458	80
2819	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	132	65
2820	D38112	Homo sapiens	cytochrome c oxidase subunit 3	347	68
2821	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	94	62
2822	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	118	54
2823	AF130079	Homo sapiens	PRO2852	143	54
2824	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	140	52
2825	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	161	67
2826	AF119851	Homo sapiens	PRO1722	104	70
2827	D49489	Homo sapiens	human P5	523	91
2828	M10546	Homo sapiens	cytochrome oxidase I	206	81
2829	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	138	42
2830	AF090931	Homo sapiens	PRO0483	97	80
2831	G03790	Homo sapiens	Human secreted protein, SEQ ID NO:	144	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7871.		
2832	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	112	35
2833	X92485	Plasmodium vivax	pval	103	43
2834	R32010	Homo sapiens	Rp15-TIA-1.	152	54
2835	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	153	59
2836	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	148	59
2837	AF090931	Homo sapiens	PRO0483	149	81
2838	AF130089	Homo sapiens	PRO2550	123	49
2839	AF090942	Homo sapiens	PRO0657	135	54
2840	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	124	54
2841	AF090895	Homo sapiens	PRO0117	146	55
2842	AF132200	Homo sapiens	PRO1751	98	74
2843	U12690	Homo sapiens	cytochrome oxidase subunit II	194	75
2844	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	61	59
2845	AL390114	Leishmania major	extremely cysteine/valine rich protein	171	37
2846	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	155	69
2847	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	141	58
2848	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	108	65
2849	U12690	Homo sapiens	cytochrome oxidase subunit II	441	77
2850	D38112	Homo sapiens	cytochrome c oxidase subunit 1	490	88
2851	K02401	Homo sapiens	chorionic somatomammotropin	488	90
2852	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	110	49
2853	U83280	Leishmania donovani	39 kDa antigen	131	47
2854	AF090944	Homo sapiens	PRO0663	173	72
2855	V00662	Homo sapiens	ATPase 6	392	71
2856	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	147	50
2857	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICEL) protein sequence.	113	76
2858	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	178	84
2859	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	192	92
2860	Z81068	Caenorhabditis elegans	contains similarity to Pfam domain: PF00102 (Protein-tyrosine phosphatase), Score=232.1, E-value=2.6e-66, N=1-cDNA EST yk299h6.3 comes from this gene-cDNA EST yk420b4.3 comes from this gene-cDNA EST yk439g6.3 comes from this gene-cDNA EST yk299h6.5 comes from this gene-cDNA EST yk420b4.5 comes from this gene-cDNA EST yk439g6.5 comes from this gene	104	36
2861	D38112	Homo sapiens	NADH dehydrogenase subunit 2	444	85
2862	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	168	61
2863	U93564	Homo sapiens	putative p150	132	34

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2864	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	152	50
2865	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	124	76
2866	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	145	46
2867	AF090930	Homo sapiens	PRO0478	161	61
2868	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	117	48
2869	U15647	Mus musculus	reverse transcriptase	197	40
2870	U09500	Homo sapiens	cytochrome b	394	68
2871	U09500	Homo sapiens	cytochrome b	614	92
2872	D38112	Homo sapiens	NADH dehydrogenase subunit 4	516	87
2873	D38112	Homo sapiens	NADH dehydrogenase subunit 4	458	84
2874	D38112	Homo sapiens	NADH dehydrogenase subunit 4	516	92
2875	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	87	55
2876	D38112	Homo sapiens	NADH dehydrogenase subunit 5	624	96
2877	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	160	58
2878	U32174	Dictyostelium discoideum	non-receptor tyrosine kinase	120	33
2879	D38112	Homo sapiens	ATPase subunit 6	141	54
2880	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	140	84
2881	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	93	79
2882	V00662	Homo sapiens	ATPase 6	130	87
2883	AL390114	Leishmania major	probable proteophosphoglycan	117	50
2884	AF119851	Homo sapiens	PRO1722	79	55
2885	X92485	Plasmodium vivax	pval	106	48
2886	V00662	Homo sapiens	ATPase 6	127	87
2887	D38112	Homo sapiens	NADH dehydrogenase subunit 4	191	83
2888	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	138	58
2889	X92485	Plasmodium vivax	pval	107	63
2890	M10546	Homo sapiens	cytochrome oxidase I	163	89
2891	AF090942	Homo sapiens	PRO0657	72	37
2892	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	136	56
2893	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	139	66
2894	AK024455	Homo sapiens	FLJ00047 protein	139	57
2895	AL359782	Trypanosoma brucei	possible (hhv-6) ul 102, variant a dna, complete virion genome.	111	44
2896	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	182	62
2897	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	143	73
2898	D38112	Homo sapiens	cytochrome c oxidase subunit 3	248	53
2899	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	366	68
2900	X07882	Homo sapiens	Po protein	146	41
2901	V00662	Homo sapiens	cytochrome B	517	91
2902	D38115	Pongo pygmaeus	cytochrome c oxidase subunit 3	378	67
2903	AF090931	Homo sapiens	PRO0483	117	67
2904	AF003540	Homo sapiens	Krueppel family zinc finger protein	99	54

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2905	AF130079	Homo sapiens	PRO2852	111	55
2906	D38112	Homo sapiens	cytochrome c oxidase subunit 1	427	79
2907	AF202635	Homo sapiens	PP1200	140	66
2908	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	116	41
2909	U63542	Homo sapiens	FAP protein	155	75
2910	D38114	Gorilla gorilla	cytochrome c oxidase subunit 1 (COI)	446	72
2911	AP002031	Arabidopsis thaliana	gene_id:K3D20.3~	118	35
2912	D38112	Homo sapiens	cytochrome c oxidase subunit 1	435	80
2913	D38116	Pan paniscus	cytochrome c oxidase subunit 1	469	83
2914	D38112	Homo sapiens	cytochrome c oxidase subunit 3	480	80
2915	D38112	Homo sapiens	cytochrome c oxidase subunit 1	488	86
2916	D38112	Homo sapiens	cytochrome c oxidase subunit 3	519	80
2917	D38112	Homo sapiens	cytochrome c oxidase subunit 3	172	80
2918	D38112	Homo sapiens	cytochrome c oxidase subunit 1	512	75
2919	D38112	Homo sapiens	cytochrome c oxidase subunit 1	458	79
2920	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	152	65
2921	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	324	87
2922	D38112	Homo sapiens	cytochrome c oxidase subunit 3	530	84
2923	AF157321	Homo sapiens	30 kDa protein	370	68
2924	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	174	71
2925	D38112	Homo sapiens	NADH dehydrogenase subunit 4	503	88
2926	U47624	Xenopus laevis	alpha(E)-catenin	243	94
2927	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	135	47
2928	D38112	Homo sapiens	cytochrome c oxidase subunit 3	476	78
2929	D38112	Homo sapiens	cytochrome c oxidase subunit 1	465	81
2930	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	151	58
2931	D16480	Homo sapiens	enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit of trifunctional protein	345	67
2932	D38112	Homo sapiens	NADH dehydrogenase subunit 4	212	95
2933	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	69
2934	X83427	Ornithorhynchus anatinus	cytochrome c oxidase subunit 1	460	82
2935	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	527	83
2936	D38112	Homo sapiens	NADH dehydrogenase subunit 4	448	92
2937	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	183	77
2938	X15081	Crithidia fasciculata	MURF2 protein (AA 1-348)	105	42
2939	AF194537	Homo sapiens	NAG13	151	52
2940	AJ271872	Nicotiana glauca	extensin	165	37
2941	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	91
2942	D38112	Homo sapiens	cytochrome c oxidase subunit 3	387	69
2943	D38112	Homo sapiens	cytochrome c oxidase subunit 3	509	79
2944	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	108	95
2945	J01415	Homo sapiens	MTND4	429	76
2946	AC010793	Arabidopsis thaliana	F20B17.16	99	41
2947	AF116712	Homo sapiens	PRO2738	132	60
2948	X89658	Homo sapiens	CAP-18 protein	136	49

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2949	V00662	Homo sapiens	cytochrome oxidase I	449	86
2950	D38112	Homo sapiens	NADH dehydrogenase subunit 4	438	82
2951	D38112	Homo sapiens	NADH dehydrogenase subunit 4	363	76
2952	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	92
2953	X56015	Crithidia oncopelti	NADH dehydrogenase subunit 5	102	32
2954	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	110	68
2955	Y76287	Homo sapiens	Fragment of human secreted protein encoded by gene 20.	345	78
2956	D38112	Homo sapiens	cytochrome c oxidase subunit 3	340	71
2957	D38112	Homo sapiens	cytochrome c oxidase subunit 1	456	83
2958	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	102	76
2959	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	96	84
2960	D38112	Homo sapiens	cytochrome c oxidase subunit 1	400	70
2961	X69978	Homo sapiens	XP-G factor	539	88
2962	AF203687	Homo sapiens	prolactin regulatory element-binding protein	453	77
2963	D38112	Homo sapiens	cytochrome c oxidase subunit 1	561	83
2964	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	187	92
2965	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	119	63
2966	U52077	Homo sapiens	mariner transposase	469	83
2967	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	130	53
2968	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhala.	103	42
2969	X92485	Plasmodium vivax	pva1	144	42
2970	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	127	63
2971	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	129	63
2972	Y17221	Homo sapiens	Human secreted protein (clone fk317-3).	91	56
2973	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	101	72
2974	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	130	68
2975	AF130089	Homo sapiens	PRO2550	167	46
2976	V00662	Homo sapiens	cytochrome oxidase I	539	79
2977	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	121	44
2978	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	126	72
2979	U93568	Homo sapiens	putative p150	122	30
2980	M12099	Mus musculus	proline-rich protein	119	39
2981	Z38128	Mus musculus	histone H1	117	36
2982	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	172	51
2983	AC002291	Arabidopsis thaliana	extensin	110	35
2984	M10546	Homo sapiens	cytochrome oxidase I	295	92
2985	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	171	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
2986	U18985	Homo sapiens	triadin	416	83
2987	AF155232	Pisum sativum	extensin	159	41
2988	X03145	Homo sapiens	pot. ORF V	133	44
2989	U12690	Homo sapiens	cytochrome oxidase subunit II	565	84
2990	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	127	53
2991	D38112	Homo sapiens	cytochrome c oxidase subunit I	538	83
2992	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	471	75
2993	D38113	Pan troglodytes	cytochrome c oxidase subunit I	511	72
2994	D38112	Homo sapiens	cytochrome c oxidase subunit I	301	79
2995	D38112	Homo sapiens	cytochrome c oxidase subunit I	526	78
2996	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	634	82
2997	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	158	76
2998	X77816	Rattus norvegicus	PR-Vbeta1	103	50
2999	V00662	Homo sapiens	cytochrome oxidase I	535	78
3000	L38908	Nicotiana tabacum	extensin	146	38
3001	D38112	Homo sapiens	NADH dehydrogenase subunit 2	494	87
3002	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	66
3003	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	117	46
3004	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	93	47
3005	U43627	Arabidopsis thaliana	extensin	118	37
3006	AF115549	Homo sapiens	Wiskott-Aldrich Syndrome protein	150	44
3007	G03556	Homo sapiens	Human secreted protein, SEQ ID NO: 7637.	114	73
3008	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	111	39
3009	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	109	84
3010	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	212	77
3011	X65718	Prunus dulcis	extensin	129	42
3012	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	71	76
3013	Z38128	Mus musculus	histone H1	104	32
3014	X56010	Sorghum bicolor	hydroxyproline-rich glycoprotein	102	34
3015	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	80
3016	Y34068	Homo sapiens	Histone H1 isoform H1.5 pANCA-reactive fragment (residues 69-226).	99	34
3017	X55685	Lycopersicon esculentum	extensin (class I)	142	32
3018	AJ133050	Panulirus argus	cytochrome c oxidase subunit I	125	71
3019	G03597	Homo sapiens	Human secreted protein, SEQ ID NO: 7678.	175	68
3020	U93564	Homo sapiens	putative p150	97	57
3021	D38116	Pan paniscus	cytochrome c oxidase subunit I	555	82
3022	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	147	76
3023	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	632	82
3024	AF155232	Pisum sativum	extensin	181	42
3025	V00662	Homo sapiens	cytochrome oxidase I	567	85

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3026	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	130	58
3027	W00838	Homo sapiens	Tumour necrosis factor-related gene product.	141	67
3028	AF130089	Homo sapiens	PRO2550	149	55
3029	AF090944	Homo sapiens	PRO0663	168	76
3030	D38112	Homo sapiens	NADH dehydrogenase subunit 2	122	92
3031	D38112	Homo sapiens	NADH dehydrogenase subunit 4	507	91
3032	D38112	Homo sapiens	NADH dehydrogenase subunit 2	351	87
3033	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	99	75
3034	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	113	85
3035	U93567	Homo sapiens	putative p150	173	41
3036	X92485	Plasmodium vivax	pval	122	41
3037	AF202635	Homo sapiens	PP1200	128	67
3038	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	151	83
3039	D38112	Homo sapiens	cytochrome c oxidase subunit 1	415	74
3040	D86853	Catharanthus roseus	extensin	198	40
3041	M76546	Helianthus annuus	hydroxyproline-rich protein	110	47
3042	D38112	Homo sapiens	cytochrome c oxidase subunit 3	377	95
3043	S80119	Rattus sp.	reverse transcriptase homolog	106	50
3044	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	137	55
3045	Y36156	Homo sapiens	Human secreted protein #28.	91	58
3046	U93574	Homo sapiens	putative p150	177	49
3047	AF063866	Melanoplus sanguinipes entomopoxvirus	ORF MSV233 hypothetical protein	98	37
3048	D38112	Homo sapiens	cytochrome c oxidase subunit 3	568	87
3049	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	144	63
3050	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	144	80
3051	AK027208	Homo sapiens	unnamed protein product	145	72
3052	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	166	75
3053	AF118082	Homo sapiens	PRO1902	84	50
3054	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	118	41
3055	X92485	Plasmodium vivax	pval	132	52
3056	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	117	74
3057	AL390114	Leishmania major	extremely cysteine/valine rich protein	99	72
3058	D38112	Homo sapiens	cytochrome c oxidase subunit 3	627	89
3059	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	98	57
3060	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	100	38
3061	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	159	80
3062	D38112	Homo sapiens	cytochrome c oxidase subunit 3	529	80
3063	AF130051	Homo sapiens	PRO0898	159	71
3064	AF195418	Mus musculus	ODZ3	386	94
3065	Y01158	Homo sapiens	Secreted protein encoded by gene 18	109	51

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			clone HCACJ81.		
3066	D38112	Homo sapiens	NADH dehydrogenase subunit 2	338	80
3067	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein thal.	120	50
3068	U15647	Mus musculus	reverse transcriptase	134	41
3069	D38112	Homo sapiens	cytochrome c oxidase subunit 3	397	92
3070	AF130089	Homo sapiens	PRO2550	149	55
3071	U93565	Homo sapiens	putative p150	143	37
3072	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	112	45
3073	AF090930	Homo sapiens	PRO0478	135	78
3074	AF130089	Homo sapiens	PRO2550	156	58
3075	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	267	65
3076	U83280	Leishmania donovani	39 kDa antigen	98	51
3077	D38112	Homo sapiens	cytochrome c oxidase subunit 3	626	86
3078	AF116712	Homo sapiens	PRO2738	114	59
3079	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	112	46
3080	D38112	Homo sapiens	cytochrome c oxidase subunit 1	492	80
3081	D38112	Homo sapiens	NADH dehydrogenase subunit 4	523	86
3082	D38112	Homo sapiens	cytochrome c oxidase subunit 3	515	79
3083	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	150	41
3084	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	191	97
3085	U12690	Homo sapiens	cytochrome oxidase subunit II	537	78
3086	D38112	Homo sapiens	ATPase subunit 6	300	58
3087	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	104	37
3088	K02247	Rattus norvegicus	proline-rich protein	108	41
3089	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	130	48
3090	V00662	Homo sapiens	cytochrome oxidase I	597	84
3091	M18094	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	221	43
3092	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	392	59
3093	D38116	Pan paniscus	cytochrome c oxidase subunit 1	593	84
3094	D38112	Homo sapiens	cytochrome c oxidase subunit 1	471	76
3095	R63235	Homo sapiens	CNS neural thread protein HB4.	369	98
3096	L26953	Homo sapiens	chromosomal protein	115	57
3097	G00591	Homo sapiens	Human secreted protein, SEQ ID NO: 4672.	124	57
3098	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	152	91
3099	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	153	96
3100	AC006233	Arabidopsis thaliana	hypothetical protein	65	44
3101	AF289098	Cladastis kentukea	ENOD2	107	35
3102	AF155232	Pisum sativum	extensin	142	43
3103	AF130089	Homo sapiens	PRO2550	122	81
3104	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	143	80
3105	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	104	59

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3106	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	76
3107	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	72
3108	D38112	Homo sapiens	NADH dehydrogenase subunit 4	334	85
3109	U43627	Arabidopsis thaliana	extensin	112	30
3110	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	118	100
3111	AF130089	Homo sapiens	PRO2550	137	37
3112	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	220	93
3113	A18812	Brassica napus	extensin	128	32
3114	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	63
3115	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	92	69
3116	X92485	Plasmodium vivax	pval	148	45
3117	D38112	Homo sapiens	cytochrome c oxidase subunit 1	574	80
3118	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP:CS24_HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	125	41
3119	U43627	Arabidopsis thaliana	extensin	129	32
3120	AF205385	Pan troglodytes	NADH dehydrogenase subunit 5	171	82
3121	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	90	59
3122	AF130051	Homo sapiens	PRO0898	134	82
3123	M81321	Macaca fascicularis	proline-rich protein	158	48
3124	U93563	Homo sapiens	putative p150	126	32
3125	D38114	Gorilla gorilla	NADH dehydrogenase subunit 1 (ND1)	337	92
3126	AF130089	Homo sapiens	PRO2550	155	77
3127	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	76
3128	AF090901	Homo sapiens	PRO0195	109	53
3129	AF003736	Murine leukemia virus	reverse transcriptase	164	40
3130	U25281	Rattus norvegicus	SH3 domain binding protein	88	39
3131	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	116	71
3132	D86853	Catharanthus roseus	extensin	110	33
3133	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	506	76
3134	V00662	Homo sapiens	cytochrome oxidase I	583	88
3135	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	103	68
3136	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	282	60
3137	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	119	54
3138	AF118082	Homo sapiens	PRO1902	118	51
3139	D38112	Homo sapiens	NADH dehydrogenase subunit 4	270	87
3140	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	103	48

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3141	D38112	Homo sapiens	NADH dehydrogenase subunit 5	353	74
3142	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	126	77
3143	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	115	72
3144	AF090930	Homo sapiens	PRO0478	138	73
3145	AF155232	Pisum sativum	extensin	110	34
3146	M69008	Homo sapiens	alpha-1 type XIII collagen	107	37
3147	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhala.	103	63
3148	D38112	Homo sapiens	cytochrome c oxidase subunit 1	505	84
3149	M77194	Rat leukemia virus	polymerase	167	35
3150	AP002543	Arabidopsis thaliana	gb AAD23015.1-gene_id:F15M7.16-similar to unknown protein	105	31
3151	AK024455	Homo sapiens	FLJ00047 protein	109	59
3152	K02576	Homo sapiens	salivary proline-rich protein 1	89	39
3153	J04794	Homo sapiens	aldehyde reductase (EC 1.1.1.2)	137	58
3154	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	115	70
3155	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	160	53
3156	X92485	Plasmodium vivax	pval	104	50
3157	AF194537	Homo sapiens	NAG13	207	60
3158	AF063693	Mus musculus	type XIII collagen	104	37
3159	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	91
3160	AF020191	Mus musculus	proline-rich protein 13	107	51
3161	AF194537	Homo sapiens	NAG13	170	76
3162	G02535	Homo sapiens	Human secreted protein, SEQ ID NO: 6616.	103	41
3163	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	161	58
3164	K03205	Homo sapiens	salivary proline-rich protein precursor	139	46
3165	U93570	Homo sapiens	putative p150	151	68
3166	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	144	71
3167	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	147	66
3168	L27428	Homo sapiens	reverse transcriptase	94	51
3169	X97675	Homo sapiens	plakophilin 2b	103	76
3170	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	115	54
3171	AK024455	Homo sapiens	FLJ00047 protein	98	61
3172	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	146	38
3173	D38116	Pan paniscus	NADH dehydrogenase subunit 4	467	81
3174	X92485	Plasmodium vivax	pval	88	69
3175	L26953	Homo sapiens	chromosomal protein	124	78
3176	AF042169	Homo sapiens	putative ATP-dependent mitochondrial RNA helicase	223	95
3177	AF130079	Homo sapiens	PRO2852	96	44
3178	AF273217	Mus musculus	cell proliferation related protein CAP	97	36
3179	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	90	69
3180	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	146	78
3181	AF118082	Homo sapiens	PRO1902	150	58
3182	U60315	Molluscum contagiosum	MC107L	101	44

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		virus subtype 1			
3183	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	148	61
3184	U93565	Homo sapiens	putative p150---	265	58
3185	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	79
3186	U87607	Rattus norvegicus	putative RNA binding protein 1	167	39
3187	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	160	63
3188	S80119	Rattus sp.	reverse transcriptase homolog	152	49
3189	X05300	Rattus norvegicus	ribophorin I	122	46
3190	B01372	Homo sapiens	Neuron-associated protein.	106	80
3191	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	130	83
3192	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	135	80
3193	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	98	34
3194	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	140	87
3195	AF022985	Caenorhabditis elegans	Similar to collagen	97	40
3196	D38112	Homo sapiens	cytochrome c oxidase subunit 1	452	81
3197	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	110	58
3198	X99452	Lycopersicon esculentum	extensin-like protein Dif54	100	36
3199	D86853	Catharanthus roseus	extensin	119	36
3200	AF025424	Rattus norvegicus	RNA polymerase I 127 kDa subunit	215	74
3201	U93563	Homo sapiens	putative p150	359	77
3202	K03202	Homo sapiens	salivary proline-rich protein precursor	112	37
3203	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	153	84
3204	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	128	39
3205	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	154	76
3206	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	127	64
3207	X97675	Homo sapiens	plakophilin 2b	142	51
3208	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	91	58
3209	AB026512	Ecnomiosa sp. Ecn1	cytochrome c oxidase subunit I	254	62
3210	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	163	59
3211	D38112	Homo sapiens	ATPase subunit 6	447	78
3212	V00662	Homo sapiens	ATPase 6	482	83
3213	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	151	66
3214	D38112	Homo sapiens	ATPase subunit 6	400	72
3215	D38112	Homo sapiens	cytochrome c oxidase subunit 3	569	88
3216	D38112	Homo sapiens	NADH dehydrogenase subunit 5	472	82
3217	AF090930	Homo sapiens	PRO0478	96	64
3218	G03172	Homo sapiens	Human secreted protein, SEQ ID NO:	137	46

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7253.		
3219	AF006061	Homo sapiens	placental growth hormone isoform hGH-V3	290	68
3220	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	115	63
3221	D38112	Homo sapiens	cytochrome c oxidase subunit 1	441	71
3222	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	111	59
3223	D38112	Homo sapiens	cytochrome c oxidase subunit 3	497	81
3224	L26953	Homo sapiens	chromosomal protein	95	59
3225	U83280	Leishmania donovani	39 kDa antigen	117	90
3226	AF239615	Manihot esculenta	CRANTZ hydroxyproline-rich glycoprotein	124	43
3227	D38112	Homo sapiens	NADH dehydrogenase subunit 4	442	74
3228	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	172	67
3229	X92591	Mus musculus	transcription factor	109	43
3230	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	81	54
3231	D38115	Pongo pygmaeus	cytochrome c oxidase subunit 1	476	72
3232	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	100	54
3233	U96416	Dennysus distinctus timjonesi	cytochrome b	95	40
3234	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	86
3235	M76546	Helianthus annuus	hydroxyproline-rich protein	101	40
3236	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	149	75
3237	D38112	Homo sapiens	NADH dehydrogenase subunit 5	532	76
3238	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	576	89
3239	U93567	Homo sapiens	p40	155	32
3240	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	79
3241	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	145	65
3242	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	76	62
3243	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	138	69
3244	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	115	39
3245	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	138	54
3246	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	153	69
3247	U58736	Caenorhabditis elegans	Similar to cuticular collagen	107	37
3248	U87607	Rattus norvegicus	putative RNA binding protein 1	148	45
3249	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	113	85
3250	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	166	61
3251	U15183	Mycobacterium leprae	proline-rich antigen	109	40
3252	AF130089	Homo sapiens	PRO2550	151	73

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3253	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	131	58
3254	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	80
3255	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhla.	108	57
3256	J01415	Homo sapiens	cytochrome oxidase subunit 3	156	88
3257	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	206	93
3258	Y36203	Homo sapiens	Human secreted protein #75.	111	77
3259	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	98	57
3260	D38112	Homo sapiens	cytochrome c oxidase subunit 1	345	67
3261	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	97	56
3262	L38908	Nicotiana tabacum	extensin	155	40
3263	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	95	70
3264	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	198	87
3265	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	115	69
3266	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	158	59
3267	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	105	56
3268	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	159	72
3269	D38112	Homo sapiens	NADH dehydrogenase subunit 1	200	95
3270	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	138	73
3271	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	151	90
3272	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	193	95
3273	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	111	52
3274	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	87
3275	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	86
3276	S62928	Homo sapiens	PRB1M protein precursor	104	34
3277	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	154	55
3278	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	166	100
3279	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	212	91
3280	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	118	50
3281	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	130	46
3282	M10546	Homo sapiens	cytochrome oxidase I	303	95
3283	D38112	Homo sapiens	cytochrome c oxidase subunit 1	455	81
3284	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	502	83
3285	AF118086	Homo sapiens	PRO1992	99	88
3286	D38112	Homo sapiens	cytochrome c oxidase subunit 1	489	83

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3287	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	485	88
3288	G00262	Homo sapiens	Human secreted protein, SEQ ID NO: 4343.	124	73
3289	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	158	60
3290	X92485	Plasmodium vivax	pva1	99	58
3291	AF116712	Homo sapiens	PRO2738	102	51
3292	AF119851	Homo sapiens	PRO1722	99	86
3293	AF090930	Homo sapiens	PRO0478	141	72
3294	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	151	66
3295	M64793	Rattus norvegicus	salivary proline-rich protein	107	41
3296	AK024455	Homo sapiens	FLJ00047 protein	97	53
3297	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	156	60
3298	AC007654	Arabidopsis thaliana	T19E23.7	97	49
3299	Y17221	Homo sapiens	Human secreted protein (clone fk317-3).	96	44
3300	AJ243905	Caenorhabditis elegans	SF1 protein	104	42
3301	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	96	41
3302	X89453	Rattus norvegicus	DRPLA	83	65
3303	U10099	Homo sapiens	POM-ZP3	227	52
3304	D38112	Homo sapiens	cytochrome c oxidase subunit 3	553	89
3305	L27428	Homo sapiens	reverse transcriptase	144	43
3306	D38112	Homo sapiens	cytochrome c oxidase subunit 3	388	71
3307	AF217374	Acanthaster planci	cytochrome oxidase subunit I	439	78
3308	D38112	Homo sapiens	cytochrome c oxidase subunit 1	439	82
3309	D38112	Homo sapiens	cytochrome c oxidase subunit 1	492	88
3310	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	81	65
3311	X53581	Rattus norvegicus	ORF4	140	48
3312	V00662	Homo sapiens	cytochrome B	487	88
3313	D38112	Homo sapiens	NADH dehydrogenase subunit 1	451	80
3314	V00662	Homo sapiens	cytochrome oxidase I	524	88
3315	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	518	87
3316	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	115	50
3317	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	356	69
3318	U12693	Homo sapiens	cytochrome oxidase subunit II	477	78
3319	Z67990	Caenorhabditis elegans	contains similarity to Pfam domain: PF01484 (Nematode cuticle collagen N-terminal domain), Score=27.5, E-value=0.0001, N=1	75	40
3320	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	126	75
3321	AF090930	Homo sapiens	PRO0478	166	65
3322	X92485	Plasmodium vivax	pva1	104	44
3323	D38112	Homo sapiens	cytochrome c oxidase subunit 3	513	80
3324	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	483	79

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3325	AF130089	Homo sapiens	PRO2550	121	88
3326	AC026234	Unknown	Contains weak similarity to an unknown protein T23E18.5	191	66
3327	V00662	Homo sapiens	cytochrome B	439	72
3328	U12690	Homo sapiens	cytochrome oxidase subunit II	316	75
3329	AF091711	Homo sapiens	splice variant AKAP350	106	52
3330	U93565	Homo sapiens	putative p150	125	45
3331	AF119851	Homo sapiens	PRO1722	88	72
3332	D38112	Homo sapiens	cytochrome c oxidase subunit 3	489	81
3333	V00662	Homo sapiens	cytochrome oxidase I	544	90
3334	D38112	Homo sapiens	cytochrome c oxidase subunit 1	475	80
3335	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	168	66
3336	AF146688	Takifugu rubripes	serine-threonine kinase 9	101	43
3337	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	101	50
3338	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	110	50
3339	V00662	Homo sapiens	cytochrome oxidase I	458	80
3340	K02401	Homo sapiens	chorionic somatomammotropin	209	97
3341	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	112	52
3342	X65165	Volvox carteri	extensin	146	41
3343	AL390114	Leishmania major	extremely cysteine/valine rich protein	119	51
3344	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	559	84
3345	U12690	Homo sapiens	cytochrome oxidase subunit II	508	89
3346	M11897	Mus musculus	proline-rich salivary protein	96	41
3347	U92455	Mus musculus	WW domain binding protein 7; WBP7	113	38
3348	U83280	Leishmania donovani	39 kDa antigen	105	40
3349	K03205	Homo sapiens	salivary proline-rich protein precursor	113	38
3350	D38112	Homo sapiens	cytochrome c oxidase subunit 1	542	79
3351	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	664	88
3352	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	117	85
3353	A18812	Brassica napus	extensin	103	31
3354	M10546	Homo sapiens	cytochrome oxidase I	125	78
3355	M81321	Macaca fascicularis	proline-rich protein	107	44
3356	M10546	Homo sapiens	cytochrome oxidase I	284	90
3357	D38112	Homo sapiens	cytochrome c oxidase subunit 1	513	80
3358	D38112	Homo sapiens	cytochrome c oxidase subunit 1	541	79
3359	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	543	87
3360	D38112	Homo sapiens	cytochrome c oxidase subunit 1	563	86
3361	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	179	57
3362	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	125	62
3363	AF016099	Mus musculus	endonuclease/reverse transcriptase	151	46
3364	D38112	Homo sapiens	cytochrome c oxidase subunit 3	569	82
3365	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	102	40
3366	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	143	76
3367	G02409	Homo sapiens	Human secreted protein, SEQ ID NO: 6490.	145	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3368	D38112	Homo sapiens	cytochrome c oxidase subunit 1	587	87
3369	D38112	Homo sapiens	cytochrome c oxidase subunit 1	549	82
3370	AL035526	Arabidopsis thaliana	extensin-like protein	130	39
3371	J04543	Homo sapiens	synexin	101	40
3372	Z29573	Didelphis virginiana	cytochrome c oxidase subunit 3	154	71
3373	U93568	Homo sapiens	putative p150	176	59
3374	L28748	Bos taurus	putative	146	67
3375	D38112	Homo sapiens	cytochrome c oxidase subunit 1	512	75
3376	D38112	Homo sapiens	cytochrome c oxidase subunit 1	509	78
3377	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	135	51
3378	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	557	82
3379	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	120	35
3380	X92485	Plasmodium vivax	pval	124	38
3381	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	110	78
3382	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	108	67
3383	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	115	86
3384	X98296	Homo sapiens	ubiquitin hydrolase	238	83
3385	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	494	75
3386	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	155	66
3387	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	116	65
3388	W73624	Homo sapiens	Human secreted protein clone aw92 1.	327	62
3389	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	141	76
3390	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	73	61
3391	U35730	Mus musculus	jerky	152	30
3392	U54788	Mus musculus	Wiskott-Aldrich Syndrome Protein	100	41
3393	U97674	Mesocricetus auratus	cytochrome c oxidase chain I	483	77
3394	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	539	81
3395	D38112	Homo sapiens	cytochrome c oxidase subunit 1	608	87
3396	X71602	Nicotiana tabacum	extensin	104	35
3397	L26953	Homo sapiens	chromosomal protein	100	60
3398	AF197832	Cyanocitta cristata	cytochrome oxidase I	488	76
3399	X53581	Rattus norvegicus	ORF4	140	42
3400	D38112	Homo sapiens	cytochrome c oxidase subunit 1	597	85
3401	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	656	89
3402	L26953	Homo sapiens	chromosomal protein	117	63
3403	AF052298	Drosophila silvestris	Y box protein	114	30
3404	U43360	Peromyscus maniculatus	reverse transcriptase	133	53
3405	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	151	65
3406	D38112	Homo sapiens	cytochrome c oxidase subunit 1	277	82
3407	U01849	Trypanosoma	ORF2	94	30

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		brucei			
3408	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	115	65
3409	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	86
3410	U93570	Homo sapiens	putative p150	233	52
3411	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	104	44
3412	AF090944	Homo sapiens	PRO0663	97	56
3413	X61048	Hydra sp.	mini-collagen	128	44
3414	AF118086	Homo sapiens	PRO1992	128	81
3415	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	145	61
3416	AF116695	Homo sapiens	PRO2221	169	69
3417	U31778	Human papillomavirus type 20	putative	107	50
3418	X92485	Plasmodium vivax	pval	97	54
3419	U12690	Homo sapiens	cytochrome oxidase subunit II	195	94
3420	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	144	69
3421	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	139	71
3422	G02409	Homo sapiens	Human secreted protein, SEQ ID NO: 6490.	111	63
3423	X15917	Paramecium aurelia	ORF4 protein (AA 1-156)	93	41
3424	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	99	69
3425	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	115	60
3426	Y14486	Homo sapiens	cytosolic serine hydroxymethyltransferase	196	61
3427	U93569	Homo sapiens	putative p150	110	44
3428	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	120	67
3429	AB012223	Canis familiaris	ORF2	169	44
3430	X97675	Homo sapiens	plakophilin 2b	118	60
3431	AF220264	Homo sapiens	MOST-1	153	72
3432	X64173	Zea diploperennis	hydroxyproline-rich glycoprotein	104	41
3433	AF113685	Homo sapiens	PRO0974	104	72
3434	AB002306	Homo sapiens	KIAA0308	282	83
3435	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	113	83
3436	AB012223	Canis familiaris	ORF2	108	43
3437	AK024455	Homo sapiens	FLJ00047 protein	100	65
3438	U52077	Homo sapiens	mariner transposase	381	64
3439	D38112	Homo sapiens	cytochrome c oxidase subunit I	425	84
3440	AK024455	Homo sapiens	FLJ00047 protein	123	63
3441	G02624	Homo sapiens	Human secreted protein, SEQ ID NO: 6705.	90	78
3442	Y36156	Homo sapiens	Human secreted protein #28.	126	71
3443	AF191032	Myxine glutinosa	RING3	84	63
3444	W48927	Homo sapiens	Schwannomin-binding protein C-terminal fragment.	141	57
3445	Y08061	Homo sapiens	Human c-myc protein fragment.	88	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3446	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	157	67
3447	U12690	Homo sapiens	cytochrome oxidase subunit II	281	86
3448	AF112481	Homo sapiens	RAD54B protein	392	87
3449	G00497	Homo sapiens	Human secreted protein, SEQ ID NO: 4578.	98	55
3450	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	133	90
3451	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	418	82
3452	AF130079	Homo sapiens	PRO2852	110	80
3453	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	143	73
3454	AB032254	Homo sapiens	bromodomain adjacent to zinc finger domain 2A	447	85
3455	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	134	62
3456	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	79	68
3457	D38112	Homo sapiens	cytochrome c oxidase subunit 3	545	84
3458	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	134	83
3459	D38112	Homo sapiens	NADH dehydrogenase subunit 2	277	80
3460	AK000867	Homo sapiens	unnamed protein product	474	98
3461	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	123	52
3462	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	89	30
3463	U93568	Homo sapiens	putative p150	100	46
3464	AL390114	Leishmania major	extremely cysteine/valine rich protein	156	43
3465	D38112	Homo sapiens	NADH dehydrogenase subunit 3	340	88
3466	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	119	100
3467	B01372	Homo sapiens	Neuron-associated protein.	142	75
3468	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	103	40
3469	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	139	80
3470	W54282	Homo sapiens	Protein sequence of the di-alpha haemoglobin gene contained in pSS1.	207	89
3471	AF116661	Homo sapiens	PRO1438	119	47
3472	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	129	59
3473	AF130089	Homo sapiens	PRO2550	108	86
3474	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	113	80
3475	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	590	79
3476	AF118086	Homo sapiens	PRO1992	126	69
3477	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	147	47
3478	J01415	Homo sapiens	MTND4	482	78
3479	X03404	Bos taurus	alpha subunit (aa 1-394)	583	89
3480	D38112	Homo sapiens	cytochrome c oxidase subunit 1	514	84
3481	G03628	Homo sapiens	Human secreted protein, SEQ ID NO: 7709.	242	80
3482	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	121	61
3483	X83427	Ornithorhynchus anatinus	cytochrome c oxidase subunit 1	508	78
3484	Y07754	Homo sapiens	Human secreted protein fragment	549	93

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			encoded from gene 11.		
3485	X97567	Homo sapiens	por1	388	69
3486	X97567	Homo sapiens	por1	608	84
3487	K02401	Homo sapiens	chorionic somatomammotropin	641	93
3488	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	135	71
3489	S62941	Homo sapiens	Ps 2=basic proline-rich protein(PRB1L precursor protein=basic proline-rich proteins (Ps, PmF, PmS, and Pe) precursor) {C-terminal}	116	36
3490	S74728	Homo sapiens	antiquitin=26g turgor protein homolog	549	84
3491	L13329	Homo sapiens	iduronate-2-sulfatase	564	85
3492	X79535	Homo sapiens	beta tubulin	620	88
3493	AF081484	Homo sapiens	alpha-tubulin isoform 1	578	87
3494	U09823	Oryctolagus cuniculus	elongation factor 1 alpha	631	89
3495	AF081484	Homo sapiens	alpha-tubulin isoform 1	616	90
3496	M12140	Homo sapiens	envelope protein	430	53
3497	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	123	70
3498	W48352	Homo sapiens	Human breast cancer related protein BCFL1.	104	51
3499	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	134	54
3500	Y36156	Homo sapiens	Human secreted protein #28.	143	75
3501	AF113685	Homo sapiens	PRO0974	77	81
3502	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	157	62
3503	AF090944	Homo sapiens	PRO0663	164	81
3504	AF090931	Homo sapiens	PRO0483	103	70
3505	U93570	Homo sapiens	p40	258	47
3506	AB016601	Drosophila alpina	cytochrome c oxidase subunit I	108	82
3507	AB016601	Drosophila alpina	cytochrome c oxidase subunit I	108	82
3508	AF194537	Homo sapiens	NAG13	449	78
3509	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	153	60
3510	Z70684	Caenorhabditis elegans	F28D1.8	102	37
3511	AC008113	Arabidopsis thaliana	F12A21.10	90	48
3512	M64791	Rattus norvegicus	salivary proline-rich protein	104	33
3513	AF090944	Homo sapiens	PRO0663	115	52
3514	AF240630	Mus musculus	IQ motif containing GTPase activating protein 1	152	67
3515	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	123	48
3516	AF090942	Homo sapiens	PRO0657	128	47
3517	M10546	Homo sapiens	cytochrome oxidase I	286	56
3518	AF255661	Cryptocodinium cohnii	Dinap1-interacting protein 5; Dip5	108	36
3519	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	209	93
3520	M11901	Rattus norvegicus	proline-rich salivary protein	102	38
3521	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	131	64
3522	AL359782	Trypanosoma	possible (hhv-6) u1102, variant a dna,	105	42

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		brucei	complete virion genome.		
3523	R95913	Homo sapiens	Neural thread protein.	118	72
3524	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	115	59
3525	L27428	Homo sapiens	reverse transcriptase	162	50
3526	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	118	58
3527	AF090930	Homo sapiens	PRO0478	146	66
3528	G00528	Homo sapiens	Human secreted protein, SEQ ID NO: 4609.	169	50
3529	AF194537	Homo sapiens	NAG13	119	88
3530	U93564	Homo sapiens	putative p150	234	84
3531	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	208	63
3532	U12690	Homo sapiens	cytochrome oxidase subunit II	275	92
3533	AF090931	Homo sapiens	PRO0483	126	66
3534	W05278	Homo sapiens	Tumour necrosis factor-related gene product CL6.5.40.	117	85
3535	G03076	Homo sapiens	Human secreted protein, SEQ ID NO: 7157.	173	77
3536	U21123	Drosophila melanogaster	ena polypeptide	117	45
3537	AF209061	Eubbranchipus sp.	cytochrome c oxidase I	127	80
3538	D38112	Homo sapiens	NADH dehydrogenase subunit 3	174	85
3539	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	118	45
3540	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	88	50
3541	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	128	71
3542	U74612	Homo sapiens	hepatocyte nuclear factor-3/fork head homolog 11A	111	77
3543	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	149	69
3544	D38112	Homo sapiens	cytochrome c oxidase subunit 1	470	80
3545	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	120	54
3546	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	106	42
3547	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	584	83
3548	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	635	95
3549	D38112	Homo sapiens	cytochrome c oxidase subunit 3	661	91
3550	D38112	Homo sapiens	cytochrome c oxidase subunit 1	607	86
3551	AK024455	Homo sapiens	FLJ00047 protein	88	51
3552	W88957	Homo sapiens	Polypeptide fragment encoded by gene 128.	500	86
3553	D38113	Pan troglodytes	NADH dehydrogenase subunit 4	228	95
3554	AF130092	Homo sapiens	PRO2620	165	93
3555	AL121845	Homo sapiens	dJ583P15.5.1 (novel protein (isoform 1))	659	91
3556	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	170	72
3557	D38112	Homo sapiens	cytochrome c oxidase subunit 3	599	88
3558	D38112	Homo sapiens	cytochrome c oxidase subunit 3	578	84
3559	AK000385	Homo sapiens	unnamed protein product	138	47
3560	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	112	61
3561	X97675	Homo sapiens	plakophilin 2b	123	65
3562	G02514	Homo sapiens	Human secreted protein, SEQ ID NO:	94	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6595.		
3563	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	198	90
3564	X86029	Vigna unguiculata	extensin-like protein	141	36
3565	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	77	60
3566	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	94
3567	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	203	93
3568	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	72
3569	S62928	Homo sapiens	PRB1M protein precursor	102	44
3570	D86853	Catharanthus roseus	extensin	123	40
3571	U93574	Homo sapiens	putative p150	279	56
3572	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	94	82
3573	U45964	Herpesvirus papio	LMP1	127	35
3574	Y08319	Homo sapiens	kinesin-2	254	55
3575	X97675	Homo sapiens	plakophilin 2b	134	54
3576	AF003151	Caenorhabditis elegans	contains similarity to an RNA recognition motif	137	43
3577	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	126	66
3578	U80447	Caenorhabditis elegans	coded for by C. elegans cDNA yk187f6.5; coded for by C. elegans cDNA yk187f6.3; coded for by C. elegans cDNA yk146f11.5	117	50
3579	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP:CS24_HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	126	31
3580	AJ249395	Globodera pallida	NADH-ubiquinone oxidoreductase subunit 4	85	33
3581	U09116	Homo sapiens	ORF1, encodes a 40 kDa product	139	55
3582	X97675	Homo sapiens	plakophilin 2b	125	73
3583	L26953	Homo sapiens	chromosomal protein	101	55
3584	S80343	Homo sapiens	arginyl-tRNA synthetase, ArgRS	110	67
3585	X97675	Homo sapiens	plakophilin 2b	116	84
3586	X92485	Plasmodium vivax	pval	124	50
3587	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	126	56
3588	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	136	56
3589	U63542	Homo sapiens	FAP protein	128	75
3590	D38112	Homo sapiens	cytochrome c oxidase subunit 3	642	88
3591	D38112	Homo sapiens	NADH dehydrogenase subunit 1	612	87
3592	K02401	Homo sapiens	chorionic somatomammotropin	576	86
3593	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	108	40
3594	V00662	Homo sapiens	cytochrome oxidase I	459	76
3595	AC008262	Arabidopsis thaliana	F4N2.10	136	31
3596	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	126	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3597	AF116645	Homo sapiens	PRO1708	623	91
3598	M23028	Human herpesvirus 4	nuclear antigen precursor	121	35
3599	W88816	Homo sapiens	Polypeptide fragment encoded by gene 58.	100	33
3600	X92485	Plasmodium vivax	pva1	156	36
3601	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	122	78
3602	AK000496	Homo sapiens	unnamed protein product	150	68
3603	AF083929	Mus musculus	ES18	98	40
3604	D38112	Homo sapiens	cytochrome c oxidase subunit I	537	83
3605	U12690	Homo sapiens	cytochrome oxidase subunit II	548	85
3606	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	158	57
3607	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	429	75
3608	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	122	65
3609	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	184	88
3610	D38112	Homo sapiens	NADH dehydrogenase subunit 5	224	80
3611	D38113	Pan troglodytes	cytochrome c oxidase subunit I	481	70
3612	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	166	92
3613	D38112	Homo sapiens	cytochrome c oxidase subunit I	582	83
3614	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	167	91
3615	U12690	Homo sapiens	cytochrome oxidase subunit II	582	77
3616	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP:CS24_HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	101	40
3617	D38112	Homo sapiens	cytochrome c oxidase subunit I	591	85
3618	AB037275	Cynomolgus Epstein-Barr Virus TsB-B6	EBNA-1	119	42
3619	AF061944	Homo sapiens	kinase deficient protein KDP	581	91
3620	Y34068	Homo sapiens	Histone H1 isoform H1.5 pANCA-reactive fragment (residues 69-226).	100	33
3621	AL049608	Arabidopsis thaliana	extensin-like protein	105	27
3622	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	127	69
3623	S71569	Neocallimastix patriciarum, Peptide, 860 aa	Xylanase B, XYL B {EC 3.2.1.8}	108	43
3624	U23172	Caenorhabditis elegans	similar to myoblast cell surface antigen (SP:CS24_HUMAN, P23246) and D. melanogaster No-on-transient A protein (PIR:JH0162)	101	37
3625	D38112	Homo sapiens	NADH dehydrogenase subunit 5	390	83
3626	D38112	Homo sapiens	cytochrome c oxidase subunit I	582	84
3627	D38112	Homo sapiens	cytochrome c oxidase subunit 3	637	90
3628	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	169	39
3629	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	142	77
3630	U93564	Homo sapiens	putative p150	330	90
3631	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	148	42

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3632	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	100	80
3633	G02360	Homo sapiens	Human secreted protein, SEQ ID NO: 6441.	139	65
3634	U74071	Phascolosoma sp. 'California'	cytochrome c oxidase subunit I	248	72
3635	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	121	87
3636	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	128	65
3637	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	124	63
3638	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	159	51
3639	X65582	Mus musculus	alpha-2 collagen	102	53
3640	AF090942	Homo sapiens	PRO0657	97	76
3641	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	146	69
3642	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	118	55
3643	X14576	Murine leukemia virus	gag p15 protein	134	44
3644	AF130051	Homo sapiens	PRO0898	177	48
3646	G03064	Homo sapiens	Human secreted protein, SEQ ID NO: 7145.	120	59
3647	AK000385	Homo sapiens	unnamed protein product	105	40
3648	V00662	Homo sapiens	cytochrome oxidase I	533	83
3649	AF090944	Homo sapiens	PRO0663	129	73
3650	AF090944	Homo sapiens	PRO0663	129	73
3651	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	88	60
3652	AF090930	Homo sapiens	PRO0478	92	57
3653	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	148	73
3654	AB018440	Echinococcus multilocularis	NADH dehydrogenase subunit 2	100	32
3655	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	165	68
3656	AF161356	Homo sapiens	HSPC093	106	48
3657	AF090930	Homo sapiens	PRO0478	158	85
3658	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	128	82
3659	U93574	Homo sapiens	putative p150	117	44
3660	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	149	51
3661	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	67	70
3662	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	99	62
3663	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	154	45
3664	Y27571	Homo sapiens	Human secreted protein encoded by gene No. 5.	136	77
3665	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	128	59
3666	U47855	Araneus diadematus	fibroin-3	109	39
3667	D38113	Pan troglodytes	cytochrome c oxidase subunit I	604	88
3668	K02401	Homo sapiens	chorionic somatomammotropin	636	93

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3669	AF083929	Mus musculus	ES18	133	46
3670	J01415	Homo sapiens	MTND4	620	87
3671	AK025047	Homo sapiens	unnamed protein product	160	60
3672	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	106	31
3673	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	766	94
3674	U74612	Homo sapiens	hepatocyte nuclear factor-3/fork head homolog 11A	113	69
3675	U80447	Caenorhabditis elegans	coded for by C. elegans cDNA yk187f6.5; coded for by C. elegans cDNA yk187f6.3; coded for by C. elegans cDNA yk146f11.5	113	39
3676	R63235	Homo sapiens	CNS neural thread protein HB4.	197	68
3677	U52077	Homo sapiens	mariner transposase	500	74
3678	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	174	97
3679	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	191	86
3680	AC003113	Arabidopsis thaliana	F24O1.6	102	83
3681	AF005370	Alcelaphine herpesvirus 1	putative immediate early protein	153	42
3682	G01502	Homo sapiens	Human secreted protein, SEQ ID NO: 5583.	111	62
3683	AP002543	Arabidopsis thaliana	gb AAD23015.1-gene_id:F15M7.16-similar to unknown protein	131	40
3684	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	146	64
3685	U93572	Homo sapiens	putative p150	158	43
3686	Y34068	Homo sapiens	Histone H1 isoform H1.5 pANCA-reactive fragment (residues 69-226).	98	43
3687	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	106	54
3688	L26953	Homo sapiens	chromosomal protein	128	76
3689	D38112	Homo sapiens	cytochrome c oxidase subunit 1	563	87
3690	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	109	67
3691	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	122	75
3692	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	165	85
3693	M20789	Homo sapiens	alpha-1 type I collagen	141	43
3694	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	50
3695	AF210651	Homo sapiens	NAG18	124	67
3696	AF130079	Homo sapiens	PRO2852	94	53
3697	Y19192	Talpa europaea	cytochrome oxidase subunit 1	618	85
3698	D38112	Homo sapiens	NADH dehydrogenase subunit 2	414	86
3699	D38112	Homo sapiens	cytochrome c oxidase subunit 1	487	76
3700	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	109	42
3701	AF217374	Acanthaster planci	cytochrome oxidase subunit I	563	85
3702	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	106	48
3703	D38112	Homo sapiens	cytochrome c oxidase subunit 1	522	79
3704	D67066	Bos taurus	N-WASP	219	42
3705	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	100	51
3706	G03798	Homo sapiens	Human secreted protein, SEQ ID NO:	115	44

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7879.		
3707	Z70684	Caenorhabditis elegans	F28D1.8	105	37
3708	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	125	74
3709	D38112	Homo sapiens	cytochrome c oxidase subunit 1	558	88
3710	AF217374	Acanthaster planci	cytochrome oxidase subunit 1	512	85
3711	D38112	Homo sapiens	NADH dehydrogenase subunit 2	186	80
3712	AF197854	Melithreptus lunatus	cytochrome oxidase I	189	83
3713	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	95
3714	AB029027	Homo sapiens	KIAA1104 protein	141	81
3715	L26251	Trypanosoma brucei	CR5	73	31
3716	R95913	Homo sapiens	Neural thread protein.	117	44
3717	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	95	67
3718	Y36112	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 497.	108	81
3719	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene preduct.	132	55
3720	M64923	Bos taurus	C10 protein	194	94
3721	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	115	75
3722	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	118	95
3723	AF302773	Homo sapiens	ninein-Lm isoform	157	57
3724	AK024455	Homo sapiens	FLJ00047 protein	134	59
3725	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	161	80
3726	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	121	52
3727	AF220264	Homo sapiens	MOST-1	86	88
3728	L27428	Homo sapiens	reverse transcriptase	316	62
3729	U83303	Homo sapiens	line-1 reverse transcriptase	112	46
3730	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	145	68
3731	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	118	56
3732	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	131	65
3733	AF090930	Homo sapiens	PRO0478	148	71
3734	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	140	72
3735	U93569	Homo sapiens	putative p150	270	59
3736	U93568	Homo sapiens	putative p150	151	38
3737	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	124	82
3738	X92485	Plasmodium vivax	pva1	101	44
3739	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	146	51
3740	AF090944	Homo sapiens	PRO0663	124	56
3741	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	94	47
3742	AF118086	Homo sapiens	PRO1992	124	61
3743	AF083929	Mus musculus	ES18	108	35
3744	L34685	Arabidopsis	cell wall protein	120	34

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		thaliana			
3745	AF090931	Homo sapiens	PRO0483	117	54
3746	AF090930	Homo sapiens	PRO0478	136	75
3747	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	154	59
3748	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	92	44
3749	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	98	42
3750	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	165	73
3751	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	87
3752	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	96	58
3753	U93574	Homo sapiens	putative p150	157	60
3754	X56015	Crithidia oncopelti	NADH dehydrogenase subunit 5	103	30
3755	M80613	Homo sapiens	putative	114	26
3756	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	119	54
3757	D38112	Homo sapiens	NADH dehydrogenase subunit 2	210	89
3758	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	91	58
3759	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	110	46
3760	M13100	Rattus norvegicus	unknown protein	119	46
3761	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	135	52
3762	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	84
3763	M11900	Mus musculus	15-kDa proline-rich salivary protein	125	40
3764	U63542	Homo sapiens	FAP protein	131	72
3765	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	143	76
3766	X92485	Plasmodium vivax	pval	119	54
3767	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	81	56
3768	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	98	65
3769	AB005216	Homo sapiens	Nck, Ash and phospholipase C gamma-binding protein NAP4	487	90
3770	AF026211	Caenorhabditis elegans	Similar to cuticular collagen	102	37
3771	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	91	55
3772	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	128	76
3773	AK024455	Homo sapiens	FLJ00047 protein	138	66
3774	AF090895	Homo sapiens	PRO0117	152	60
3775	AF130051	Homo sapiens	PRO0898	122	78
3776	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	100	63
3777	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	187	75
3778	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	130	56

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3779	X55685	Lycopersicon esculentum	extensin (class I)	132	38
3780	L27428	Homo sapiens	reverse transcriptase	116	53
3781	Y71066	Homo sapiens	Human membrane transport protein, MTRP-11.	188	86
3782	AL390114	Leishmania major	extremely cysteine/valine rich protein	122	67
3783	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	462	75
3784	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	127	67
3785	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	129	36
3786	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	152	78
3787	S80119	Rattus sp.	reverse transcriptase homolog.	143	40
3788	AF090942	Homo sapiens	PRO0657	134	67
3789	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	63
3790	AF116661	Homo sapiens	PRO1438	128	45
3791	K03205	Homo sapiens	salivary proline-rich protein precursor	130	38
3792	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	127	74
3793	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	101	48
3794	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	175	46
3795	K03205	Homo sapiens	salivary proline-rich protein precursor	117	40
3796	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	185	88
3797	D38112	Homo sapiens	cytochrome c oxidase subunit 3	610	84
3798	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	156	56
3799	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rh1a.	71	52
3800	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	127	77
3801	AF130079	Homo sapiens	PRO2852	164	54
3802	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rh1a.	118	45
3803	U42580	Paramecium bursaria Chlorella virus 1	Pro-rich, PAPK (20X); similar to Arabidopsis anter-specific Pro-rich protein, corresponds to Swiss-Prot Accession Number P40602	101	36
3804	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	173	87
3805	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	126	72
3806	D38112	Homo sapiens	NADH dehydrogenase subunit 4	225	85
3807	U88587	Nicotiana glauca	120 kDa style glycoprotein	118	38
3808	D38112	Homo sapiens	cytochrome c oxidase subunit 1	129	82
3809	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	122	67
3810	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	213	97
3811	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	106	63
3812	AF169974	Homo sapiens	serine racemase	153	56
3813	L27428	Homo sapiens	reverse transcriptase	175	43
3814	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	109	43

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3815	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	176	78
3816	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	112	65
3817	AF119901	Homo sapiens	PRO2831	113	55
3818	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	99	89
3819	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	91	66
3820	X92485	Plasmodium vivax	pva1	108	46
3821	AK024455	Homo sapiens	FLJ00047 protein	79	59
3822	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	178	87
3823	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	99	50
3824	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	86	94
3825	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	138	53
3826	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	88
3827	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	77	61
3828	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	139	51
3829	K03208	Homo sapiens	salivary proline-rich protein precursor	161	41
3830	U44838	Glycine max	extensin	108	47
3831	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	136	71
3832	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	205	84
3833	AL163912	Arabidopsis thaliana	glycine-rich protein atGRP-7	117	37
3834	AF130089	Homo sapiens	PRO2550	138	45
3835	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	92	76
3836	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	70
3837	X56010	Sorghum bicolor	hydroxyproline-rich glycoprotein	98	37
3838	X68249	Xenopus laevis	Proline rich protein	92	66
3839	U12690	Homo sapiens	cytochrome oxidase subunit II	262	92
3840	R63235	Homo sapiens	CNS neural thread protein HB4.	186	100
3841	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	103	64
3842	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	116	62
3843	AF164614	Homo sapiens	envelope protein	508	77
3844	AF130051	Homo sapiens	PRO0898	130	73
3845	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	144	74
3846	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	119	68
3847	M13100	Rattus norvegicus	unknown protein	129	46
3848	X97675	Homo sapiens	plakophilin 2b	145	67
3849	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	141	65
3850	K03206	Homo sapiens	salivary proline-rich protein precursor	114	42

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3851	U93574	Homo sapiens	putative p150	165	82
3852	AF090931	Homo sapiens	PRO0483	97	78
3853	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	279	80
3854	U93570	Homo sapiens	putative p150	135	38
3855	M13100	Rattus norvegicus	unknown protein	100	57
3856	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	166	63
3857	Y48576	Homo sapiens	Human breast tumour-associated protein 37.	117	49
3858	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	147	45
3859	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	150	71
3860	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	165	69
3861	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	131	83
3862	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	171	81
3863	AK000241	Homo sapiens	unnamed protein product	100	48
3864	Y36112	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 497.	121	80
3865	AK024455	Homo sapiens	FLJ00047 protein	124	69
3866	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	87	64
3867	AF116712	Homo sapiens	PRO2738	92	48
3868	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	165	62
3869	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	128	62
3870	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	94	75
3871	AK024455	Homo sapiens	FLJ00047 protein	83	72
3872	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	147	44
3873	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	113	51
3874	AF090930	Homo sapiens	PRO0478	120	63
3875	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	145	70
3876	D88674	Homo sapiens	antizyme inhibitor	147	75
3877	AF263744	Homo sapiens	erbB2-interacting protein ERBIN	212	37
3878	Y36112	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 497.	140	82
3879	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	82	35
3880	Y01181	Homo sapiens	Polypeptide fragment encoded by gene 12.	144	60
3881	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	122	60
3882	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	134	75
3883	M81321	Macaca fascicularis	proline-rich protein	101	41
3884	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	109	56
3885	AF013214	Bos taurus	acidic ribosomal phosphoprotein PO	177	94
3886	G00403	Homo sapiens	Human secreted protein, SEQ ID NO:	162	77

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4484.		
3887	Y59860	Homo sapiens	Human normal uterus tissue derived protein 23.	137	72
3888	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	147	72
3889	M64792	Rattus norvegicus	salivary proline-rich protein	104	40
3890	AF156228	Drosophila melanogaster	salivary gland secretion protein	104	35
3891	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	90	47
3892	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	138	38
3893	D38112	Homo sapiens	NADH dehydrogenase subunit 5	146	65
3894	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	34
3895	X02873	Daucus carota	put. precursor	104	48
3896	AF090942	Homo sapiens	PRO0657	135	50
3897	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	195	77
3898	X92485	Plasmodium vivax	pval	111	62
3899	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	107	70
3900	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	94	93
3901	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	163	83
3902	AF090942	Homo sapiens	PRO0657	134	65
3903	AF220264	Homo sapiens	MOST-1	74	59
3904	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	131	53
3905	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	129	85
3906	AK025047	Homo sapiens	unnamed protein product	127	73
3907	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	135	86
3908	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	134	72
3909	X77816	Rattus norvegicus	PR-Vbeta1	104	62
3910	G02654	Homo sapiens	Human secreted protein, SEQ ID NO: 6735.	114	70
3911	AK024455	Homo sapiens	FLJ00047 protein	135	61
3912	U93567	Homo sapiens	putative p150	233	63
3913	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	96	40
3914	X94976	Brassica napus	cell wall-plasma membrane linker protein	104	36
3915	P92219	Homo sapiens (human)	CR1 protein.	125	73
3916	X92485	Plasmodium vivax	pval	94	64
3917	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	105	52
3918	AF118086	Homo sapiens	PRO1992	130	87
3919	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	125	80
3920	G00412	Homo sapiens	Human secreted protein, SEQ ID NO:	162	79

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4493.		
3921	AF090930	Homo sapiens	PRO0478	128	64
3922	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	114	75
3923	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	130	65
3924	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	134	71
3925	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	102	58
3926	D63487	Homo sapiens	The KIAA0153 gene product is related to a putative C.elegans gene encoded in cosmid F42A8.	141	100
3927	U21123	Drosophila melanogaster	ena polypeptide	117	37
3928	X58438	Mus musculus	proline rich protein	136	36
3929	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	152	71
3930	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	132	73
3931	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	86	48
3932	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	110	65
3933	X92485	Plasmodium vivax	pval	116	36
3934	X97675	Homo sapiens	plakophilin 2b	129	82
3935	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	84	58
3937	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	107	56
3938	AF090895	Homo sapiens	PRO0117	166	68
3939	K02550	Oncorhynchus mykiss	70-kilodalton heat shock protein	104	38
3940	AK024455	Homo sapiens	FLJ00047 protein	112	74
3941	L26953	Homo sapiens	chromosomal protein	92	67
3942	U63542	Homo sapiens	FAP protein	135	75
3943	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	139	80
3944	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	141	67
3945	AK024455	Homo sapiens	FLJ00047 protein	123	76
3946	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	92	52
3947	W48927	Homo sapiens	Schwannomin-binding protein C-terminal fragment.	103	56
3948	AF252293	Homo sapiens	PAR3	161	44
3949	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	125	47
3950	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	59
3951	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	174	87
3952	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	152	75
3953	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	168	64
3954	R95913	Homo sapiens	Neural thread protein.	110	54
3955	AF130089	Homo sapiens	PRO2550	122	63
3956	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	119	48

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3957	Y36203	Homo sapiens	Human secreted protein #75.	121	75
3958	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	177	61
3959	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	131	69
3960	U93563	Homo sapiens	putative p150	227	62
3961	D86853	Catharanthus roseus	extensin	100	40
3962	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	101	41
3963	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	107	80
3964	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	121	42
3965	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	66
3966	M11901	Rattus norvegicus	proline-rich salivary protein	101	34
3967	AF229126	Homo sapiens	acetylcholinesterase collagen-like tail subunit isoform VII	108	36
3968	AJ006770	Cicer arietinum	extensin	86	29
3969	AF130089	Homo sapiens	PRO2550	128	82
3970	U93563	Homo sapiens	putative p150	99	48
3971	AK000496	Homo sapiens	unnamed protein product	134	71
3972	Z70684	Caenorhabditis elegans	F28D1.8	108	42
3973	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	137	72
3974	AK024455	Homo sapiens	FLJ00047 protein	132	65
3975	AK024455	Homo sapiens	FLJ00047 protein	128	85
3976	X01918	Drosophila melanogaster	salivary gland glue protein	99	40
3977	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	136	46
3978	AF229067	Homo sapiens	PADI-H protein	107	87
3979	M64793	Rattus norvegicus	salivary proline-rich protein	189	48
3980	S80119	Rattus sp.	reverse transcriptase homolog	134	49
3981	AF090901	Homo sapiens	PRO0195	106	94
3982	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	111	42
3983	X92485	Plasmodium vivax	pval	102	39
3984	G02640	Homo sapiens	Human secreted protein, SEQ ID NO: 6721.	127	64
3985	AB012162	Homo sapiens	APCL protein	190	42
3986	AF016099	Mus musculus	endonuclease/reverse transcriptase	139	65
3987	U93570	Homo sapiens	putative p150	170	71
3988	D38112	Homo sapiens	NADH dehydrogenase subunit 5	202	73
3989	D38112	Homo sapiens	NADH dehydrogenase subunit 5	244	85
3990	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	420	92
3991	D38112	Homo sapiens	NADH dehydrogenase subunit 4	272	85
3992	L38908	Nicotiana tabacum	extensin	114	40
3993	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	116	64
3994	AF090944	Homo sapiens	PRO0663	99	39
3995	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	150	75
3996	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	574	87
3997	D38112	Homo sapiens	NADH dehydrogenase subunit 4	488	76

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
3998	U52077	Homo sapiens	mariner transposase	475	70
3999	U93570	Homo sapiens	p40	111	34
4000	U15647	Mus musculus	reverse transcriptase	137	43
4001	AF116712	Homo sapiens	PRO2738	105	52
4002	AF113685	Homo sapiens	PRO0974	125	53
4003	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	92	78
4004	AF116715	Homo sapiens	PRO2829	115	73
4005	D38112	Homo sapiens	NADH dehydrogenase subunit 2	288	80
4006	D38112	Homo sapiens	cytochrome c oxidase subunit 1	614	86
4007	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	106	45
4008	U90268	Homo sapiens	Krit1	152	52
4009	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	472	96
4010	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	304	100
4011	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	472	98
4012	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	102	50
4013	G00262	Homo sapiens	Human secreted protein, SEQ ID NO: 4343.	124	73
4014	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	118	47
4015	U12690	Homo sapiens	cytochrome oxidase subunit II	522	81
4016	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	147	52
4017	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	106	57
4018	AB003476	Homo sapiens	gravin	549	91
4019	D38112	Homo sapiens	NADH dehydrogenase subunit 4	391	93
4020	U44949	Xenopus laevis	zona pellucida A glycoprotein homolog	143	32
4021	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	571	88
4022	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	554	87
4023	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	165	88
4024	AL390114	Leishmania major	extremely cysteine/valine rich protein	131	38
4025	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	583	86
4026	AF090895	Homo sapiens	PRO0117	104	49
4027	AF130056	Homo sapiens	PRO1367	80	60
4028	X97675	Homo sapiens	plakophilin 2b	157	83
4029	X67337	Homo sapiens	Human pre-mRNA cleavage factor I 68 kDa subunit	114	35
4030	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	110	74
4031	D38112	Homo sapiens	ATPase subunit 6	395	80
4032	S70718	Hemicentrotus pulcherrimus=sea urchins, tests, Peptide, 632 aa	fibrillar collagen alpha 120 and 140 chains	104	33
4033	Y12713	Mus musculus	Pro-Pol-dUTPase polyprotein	355	66
4034	AC004497	Homo sapiens	MX2	464	58
4035	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	151	61
4036	AF117888	Homo sapiens	myosin-IXa	113	34
4038	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	100	48
4039	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	153	73

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4040	D38112	Homo sapiens	NADH dehydrogenase subunit 4	338	86
4041	AF116661	Homo sapiens	PRO1438	136	53
4042	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	120	84
4043	D38112	Homo sapiens	cytochrome c oxidase subunit 3	493	85
4044	M90516	Homo sapiens	glutamine:fructose-6-phosphate amidotransferase	261	72
4045	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	102	64
4046	AF130089	Homo sapiens	PRO2550	143	78
4047	AF090942	Homo sapiens	PRO0657	119	41
4048	R95913	Homo sapiens	Neural thread protein.	138	47
4049	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	111	59
4050	X77962	Tetrahymena thermophila	fibrillarin	105	49
4051	G00338	Homo sapiens	Human secreted protein, SEQ ID NO: 4419.	144	71
4052	X02794	Friend murine leukemia virus	Pr65	107	37
4053	Y00994	Homo sapiens	Human CSR3 protein sequence.	109	38
4054	AL121585	Homo sapiens	ba504H3.1 (SNX5 (sorting nexin 5))	299	74
4055	V00662	Homo sapiens	URF 1 (NADH dehydrogenase subunit)	314	80
4056	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	65	54
4057	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	187	67
4058	AF205385	Pan troglodytes	NADH dehydrogenase subunit 5	202	89
4059	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	187	100
4060	U63542	Homo sapiens	FAP protein	142	73
4061	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	158	50
4062	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	123	44
4063	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	76	65
4064	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	165	46
4065	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	147	93
4066	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	109	76
4067	AB035523	Gallus gallus	avenaIII	101	48
4068	AC079829	Arabidopsis thaliana	Pto kinase interactor, putative	105	43
4069	AF210651	Homo sapiens	NAG18	97	77
4070	M64793	Rattus norvegicus	salivary proline-rich protein	111	43
4071	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	158	65
4072	K02576	Homo sapiens	salivary proline-rich protein 1	131	43
4073	AF038007	Homo sapiens	FIC1	153	96
4074	M33228	Trypanosoma brucei	ATPase 6	103	37
4075	U54788	Mus musculus	Wiskott-Aldrich Syndrome Protein	119	46
4076	M81321	Macaca fascicularis	proline-rich protein	104	36
4077	X52235	Homo sapiens	ORFII	192	39
4078	G00328	Homo sapiens	Human secreted protein, SEQ ID NO:	126	83

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4409.		
4079	AB026542	Homo sapiens	WASP-family protein	98	41
4080	L17318	Rattus norvegicus	proline-rich proteoglycan	105	42
4081	AF130051	Homo sapiens	PRO0898	117	42
4082	AF130089	Homo sapiens	PRO2550	85	79
4083	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	117	48
4084	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	89	40
4085	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	163	80
4086	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	144	74
4087	AF085691	Homo sapiens	multidrug resistance-associated protein 3A	197	49
4088	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	109	62
4089	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	139	51
4090	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	103	65
4091	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	159	68
4092	X92485	Plasmodium vivax	pval	95	38
4093	U93569	Homo sapiens	p40	205	40
4094	L16864	African swine fever virus	cd2 homologue	98	45
4095	X71413	Homo sapiens	ELE1	675	98
4096	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	149	60
4097	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	116	70
4098	AF090930	Homo sapiens	PRO0478	149	78
4099	AF090942	Homo sapiens	PRO0657	124	56
4100	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	139	62
4101	L26953	Homo sapiens	chromosomal protein	104	54
4102	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	128	70
4103	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	94	58
4104	U73199	Mus musculus	Rho-guanine nucleotide exchange factor	370	56
4105	AF090931	Homo sapiens	PRO0483	104	90
4106	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	133	72
4107	AF118082	Homo sapiens	PRO1902	145	49
4108	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	116	50
4109	U93564	Homo sapiens	p40	539	91
4110	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	144	54
4111	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	138	65
4112	AF217536	Homo sapiens	truncated mevalonate kinase	91	73
4113	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	120	36
4114	M17522	Paracoccus	cytochrome c1 precursor (EC 1.10.2.2)	101	41

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		denitrificans			
4115	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	121	59
4116	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	148	73
4117	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	80	85
4118	X04758	Homo sapiens	pro- alpha (V)collagen (AA 1099)	106	39
4119	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	122	47
4120	AF130089	Homo sapiens	PRO2550	132	68
4121	AF090942	Homo sapiens	PRO0657	136	48
4122	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	115	66
4123	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	72	48
4124	X92485	Plasmodium vivax	pva1	104	54
4125	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	59
4126	AK024455	Homo sapiens	FLJ00047 protein	86	61
4127	AF119855	Homo sapiens	PRO1847	99	68
4128	S80119	Rattus sp.	reverse transcriptase homolog	129	39
4129	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	156	62
4130	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	135	72
4131	R86406	Homo sapiens	Human matrix metalloprotease MMPm1a.	108	83
4132	L16461	Chlamydomonas reinhardtii	structural wall protein	87	37
4133	Y30713	Homo sapiens	Amino acid sequence of a human secreted protein.	232	95
4134	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	121	69
4135	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	135	70
4136	K02576	Homo sapiens	salivary proline-rich protein 1	134	42
4137	Y15173	Human papillomavirus type 75	E4 protein	101	38
4138	AF130089	Homo sapiens	PRO2550	130	35
4139	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	38
4140	Y36203	Homo sapiens	Human secreted protein #75.	120	48
4141	AF130089	Homo sapiens	PRO2550	139	36
4142	S80119	Rattus sp.	reverse transcriptase homolog	170	47
4143	U54636	Staphylococcus aureus	protein A	135	35
4144	AL390114	Leishmania major	extremely cysteine/valine rich protein	157	55
4145	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	112	54
4146	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	117	37
4147	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene preduct.	98	61
4148	AF130051	Homo sapiens	PRO0898	124	88
4149	G00673	Homo sapiens	Human secreted protein, SEQ ID NO:	133	67

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4754.		
4150	Z29481	Homo sapiens	3-hydroxyanthranilic acid dioxygenase	244	62
4151	M81321	Macaca fascicularis	proline-rich protein	172	50
4152	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	129	66
4153	AF119851	Homo sapiens	PRO1722	128	62
4154	AB037826	Homo sapiens	KIAA1405 protein	194	60
4155	M12099	Mus musculus	proline-rich protein	124	37
4156	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	46
4157	M11901	Rattus norvegicus	proline-rich salivary protein	124	41
4158	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	134	83
4159	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	141	74
4160	M76546	Helianthus annuus	hydroxyproline-rich protein	135	39
4161	U35730	Mus musculus	jerky	116	31
4162	Z81525	Caenorhabditis elegans	contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=35.5, E-value=4e-07, N=2	130	50
4163	AF113685	Homo sapiens	PRO0974	129	45
4164	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	168	71
4165	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	137	70
4166	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	175	72
4167	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	86	45
4168	AB000505	Daucus carota	unnamed protein product	101	43
4169	U87607	Rattus norvegicus	putative RNA binding protein 1	113	30
4170	AF119900	Homo sapiens	PRO2822	154	59
4171	AE001381	Plasmodium falciparum	hypothetical protein	106	33
4172	AE000034	Mycoplasma pneumoniae	bifunctional threonine dehydrogenase; galactosyltransferase	100	28
4173	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	100	47
4174	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	142	68
4175	AK024455	Homo sapiens	FLJ00047 protein	116	60
4176	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	94	44
4177	AK024455	Homo sapiens	FLJ00047 protein	102	59
4178	AY007557	Mycobacterium avium subsp. paratuberculosis	fibronectin-attachment protein FAP-P	98	42
4179	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	115	69
4180	M12100	Mus musculus	proline-rich protein MP-3	132	44
4181	AF090930	Homo sapiens	PRO0478	138	63
4182	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	152	75
4183	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	184	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4184	K03205	Homo sapiens	salivary proline-rich protein precursor	150	43
4185	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	128	51
4186	AF090944	Homo sapiens	PRO0663	124	49
4187	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	93	62
4188	D38112	Homo sapiens	ATPase subunit 6	439	78
4189	AF130051	Homo sapiens	PRO0898	89	57
4190	AF090930	Homo sapiens	PRO0478	137	83
4191	K03205	Homo sapiens	salivary proline-rich protein precursor	100	35
4192	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	212	91
4193	Y13247	Homo sapiens	FB19 protein	142	46
4194	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	268	93
4195	AF124729	Mus musculus	acinusS'	140	42
4196	AJ277425	Globodera pallida	putative cuticular collagen	156	43
4197	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	77
4198	Z70684	Caenorhabditis elegans	F28D1.8	97	45
4199	M64793	Rattus norvegicus	salivary proline-rich protein	119	36
4200	X62379	Mus musculus	formin, isoform IV	115	48
4201	D38113	Pan troglodytes	NADH dehydrogenase subunit 4	224	93
4202	M14820	Trypanosoma brucei	ORF2 bases 1807-2850; first start codon at 2032; putative	103	29
4203	U93572	Homo sapiens	p40	182	34
4204	D82026	Silene latifolia	glycine-rich protein	98	49
4205	AF003151	Caenorhabditis elegans	contains similarity to an RNA recognition motif	107	40
4206	L07545	Leishmania tarentolae	A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression	101	35
4207	K03205	Homo sapiens	salivary proline-rich protein precursor	104	38
4208	AF229126	Homo sapiens	acetylcholinesterase collagen-like tail subunit isoform VII	96	75
4209	AF090895	Homo sapiens	PRO0117	142	68
4210	X92485	Plasmodium vivax	pval	104	35
4211	G02828	Homo sapiens	Human secreted protein, SEQ ID NO: 6909.	173	73
4212	G02828	Homo sapiens	Human secreted protein, SEQ ID NO: 6909.	151	69
4213	AF115549	Homo sapiens	Wiskott-Aldrich Syndrome protein	122	43
4214	AF090944	Homo sapiens	PRO0663	97	39
4215	X12544	Homo sapiens	3 HLA-DR B protein precursor (AA - 29 to 267)	111	60
4216	M69065	human herpesvirus 2	ORF1	89	38
4217	AF090895	Homo sapiens	PRO0117	133	78
4218	B01372	Homo sapiens	Neuron-associated protein.	135	46
4219	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	71	47
4220	U93567	Homo sapiens	p40	170	35
4221	D00570	Mus musculus	open reading frame (251 AA)	108	28
4222	X97675	Homo sapiens	plakophilin 2b	122	47
4223	AF270937	Plutella xylostella	PxORF73 peptide	99	54

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		granulovirus			
4224	AF130089	Homo sapiens	PRO2550	144	69
4225	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	125	82
4226	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	99	62
4227	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene preduct.	172	59
4228	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	161	74
4229	AL049537	Homo sapiens	dJ1164I10.1 (brefeldin A-inhibited guanine nucleotide-exchange protein 2)	212	90
4230	AF118086	Homo sapiens	PRO1992	150	69
4231	M81321	Macaca fascicularis	proline-rich protein	130	41
4232	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	138	68
4233	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	132	56
4234	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	110	52
4235	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	124	32
4236	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	119	42
4237	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	368	56
4238	R95913	Homo sapiens	Neural thread protein.	139	55
4239	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	146	63
4240	X97675	Homo sapiens	plakophilin 2b	108	78
4241	Y36156	Homo sapiens	Human secreted protein #28.	137	65
4242	AK000385	Homo sapiens	unnamed protein product	131	33
4243	AJ252253	human herpesvirus 2	glycoprotein G-2	107	36
4244	Y99447	Homo sapiens	Human PRO1556 (UNQ764) amino acid sequence SEQ ID NO:372.	597	100
4245	Y05398	Homo sapiens	Human TIE ligand NL8 protein sequence.	424	84
4246	L00016	Homo sapiens	urf4	222	90
4247	AF134579	Zea mays	arabinogalactan protein	134	39
4248	Z34465	Zea mays	extensin-like protein	123	33
4249	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	128	62
4250	J02695	Plasmodium yoelii	circumsporozoite protein	110	33
4251	AK024455	Homo sapiens	FLJ00047 protein	136	65
4252	U02570	Homo sapiens	CDC42 GTPase-activating protein	566	93
4253	D38112	Homo sapiens	cytochrome c oxidase subunit 1	449	85
4254	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	111	63
4255	M61143	Bovine herpesvirus 1	latency-related open reading frame 2; putative	101	42
4256	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	113	43
4257	Y06294	Homo sapiens	Human transcription regulator MOP6 partial sequence.	410	79
4258	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	112	61
4259	D90252	Human papillomavirus type 5b	E4 protein	110	32

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4260	X90569	Homo sapiens	elastic titin	660	95
4261	AF090930	Homo sapiens	PRO0478	114	71
4262	AF132209	Homo sapiens	prepro-major basic protein homolog	422	72
4263	AF043102	Pneumocystis carinii	surface glycoprotein A	121	29
4264	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	132	55
4265	AF090895	Homo sapiens	PRO0117	159	62
4266	AF090930	Homo sapiens	PRO0478	143	50
4267	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	119	34
4268	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	106	61
4269	D23660	Homo sapiens	ribosomal protein	493	73
4270	AF130089	Homo sapiens	PRO2550	119	39
4271	U93564	Homo sapiens	putative p150	121	37
4272	AB033615	Mus musculus	phospholipase C-L2	485	79
4273	AF006082	Homo sapiens	Arp2	488	85
4274	Y12293	Mus musculus	lun	104	33
4275	X54289	Bos taurus	cGMP-dependent protein kinase (isoform I beta)	561	81
4276	AF119855	Homo sapiens	PRO1847	155	71
4277	J01415	Homo sapiens	MTND4	372	63
4278	AB021078	Plasmid ColIb-P9	ybbA	101	30
4279	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	110	73
4280	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	110	73
4281	AF119851	Homo sapiens	PRO1722	110	60
4282	D38116	Pan paniscus	NADH dehydrogenase subunit 1	346	92
4283	Y15908	Homo sapiens	DIA-12C protein	109	52
4284	Y30681	Homo sapiens	Splice variant ZAP-1B protein of the human tumor suppressor gene ZAP-1.	122	76
4285	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	121	42
4286	AK024455	Homo sapiens	FLJ00047 protein	135	57
4287	Y11525	Homo sapiens	CCAAT/enhancer binding protein alpha	100	32
4288	AF033122	Homo sapiens	non-p53 regulated PA26-T1 nuclear protein	128	81
4289	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	111	39
4290	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	140	58
4291	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	132	34
4292	X60432	Zea mays	prolin rich protein	118	42
4293	U09367	Homo sapiens	zinc finger protein ZNF136	461	60
4294	AF038960	Homo sapiens	SKD1 homolog	146	82
4295	AL390114	Leishmania major	extremely cysteine/valine rich protein	128	54
4296	U66561	Homo sapiens	kruppel-related zinc finger protein	512	89
4297	AF043706	Caenorhabditis elegans	contains similarity to granulins	104	55
4298	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	138	65
4299	AF152510	Homo sapiens	protocadherin gamma A3 short form protein	520	87

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4300	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	142	72
4301	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	109	50
4302	AL035440	Arabidopsis thaliana	putative protein	103	31
4303	L05500	Homo sapiens	adenylyl cyclase	655	96
4304	AF116712	Homo sapiens	PRO2738	140	54
4305	D13757	Homo sapiens	amidophosphoribosyltransferase	182	92
4306	L20450	Mus musculus	DNA-binding protein	470	64
4307	AF213386	Mus musculus	ATP-binding cassette protein	175	97
4308	X76850	Mus musculus	MAP kinase-activated protein kinase 2	154	69
4309	S80119	Rattus sp.	reverse transcriptase homolog	123	55
4310	X67337	Homo sapiens	Human pre-mRNA cleavage factor I 68 kDa subunit	110	32
4311	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	96	58
4312	Z46236	Ovis aries	keratinocyte growth factor	210	75
4313	AB020700	Homo sapiens	KIAA0893 protein	569	87
4314	AF124727	Homo sapiens	acinusS	498	88
4315	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	88	32
4316	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	122	53
4317	AF119900	Homo sapiens	PRO2822	135	58
4318	U74612	Homo sapiens	hepatocyte nuclear factor-3/fork head homolog 11A	104	70
4319	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	117	51
4320	AB026054	Homo sapiens	brain finger protein	412	90
4321	AF090944	Homo sapiens	PRO0663	133	71
4322	AF165513	Homo sapiens	vacuolar protein sorting 45 isoform	712	97
4323	Y99418	Homo sapiens	Human PRO1317 (UNQ783) amino acid sequence SEQ ID NO:277.	532	97
4324	AF163772	Leishmania major	7138.7	142	37
4325	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	128	59
4326	W40054	Homo sapiens	P300/CBP-associated transcriptional cofactor P/CAF C-terminus.	175	94
4327	AF217411	Homo sapiens	neuroligin 3 isoform HNL3	549	84
4328	U94836	Homo sapiens	ERPROT 213-21	175	87
4329	Y20763	Homo sapiens	Human neurofilament-M mutant protein fragment 45.	501	87
4330	AB037745	Homo sapiens	KIAA1324 protein	1014	99
4331	M91563	Rattus norvegicus	NMDA receptor subtype 2C	116	39
4332	G03704	Homo sapiens	Human secreted protein, SEQ ID NO: 7785.	286	76
4333	AC006841	Arabidopsis thaliana	Mutator-like transposase	130	70
4334	AP000373	Arabidopsis thaliana	jasmonate inducible protein; myrosinase binding protein-like	130	53
4335	U22961	Homo sapiens	similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	377	90
4336	AJ277426	Globodera pallida	putative cuticular collagen	112	37

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4337	U16802	Rattus norvegicus	Ca ²⁺ -dependent activator protein; calcium-dependent actin-binding protein	560	79
4338	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	118	56
4339	AB024520	Homo sapiens	notch4	93	33
4340	AF128406	Homo sapiens	nuclear prelamin A recognition factor	241	100
4341	W19771	Homo sapiens	Beta-1 integrin modulator B171.	169	100
4342	AL096828	Homo sapiens	dJ963E22.1 (Novel protein similar to NY-REN-2 Antigen)	666	88
4343	D50312	Homo sapiens	uKATP-1	542	80
4344	U84487	Homo sapiens	CX3C chemokine precursor	371	78
4345	U93569	Homo sapiens	putative p150	111	47
4346	AL161755	Streptomyces coelicolor A3(2)	putative serine/threonine protein kinase	102	30
4347	AK026162	Homo sapiens	unnamed protein product	377	98
4348	AF221759	Homo sapiens	Mam1	314	47
4349	AF165926	Homo sapiens	NUP155	147	84
4351	U50185	Rattus norvegicus	PP-1M	144	52
4352	D50455	Rattus norvegicus	phospholipase C delta4	196	70
4353	X54131	Homo sapiens	protein-tyrosine phosphatase	261	87
4354	AF151850	Homo sapiens	CGI-92 protein	255	92
4355	G03996	Homo sapiens	Human secreted protein, SEQ ID NO: 8077.	105	95
4356	U93564	Homo sapiens	putative p150	171	72
4357	AP001507	Bacillus halodurans	unknown conserved protein	159	34
4358	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	153	60
4359	AF072697	Mus musculus	SHYC	177	97
4360	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	129	69
4361	M98776	Homo sapiens	keratin 1	449	77
4362	AK024436	Homo sapiens	FLJ00026 protein	671	91
4363	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	155	49
4364	D13896	Rattus norvegicus	cytoplasmic dynein heavy chain	327	92
4365	X79389	Homo sapiens	glutathione transferase T1	164	96
4366	AB006458	Mus musculus	alpha-D-mannosidase	177	56
4367	X01060	Homo sapiens	put. transferrin receptor (aa 1-760)	160	96
4368	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	103	54
4369	AL353715	Homo sapiens	bK3184A7.3.1 (helicase-like protein NHL)	485	100
4370	AF001631	Oryctolagus cuniculus	glucose-regulated protein GRP94	118	92
4371	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	113	80
4372	AL121741	Schizosaccharomyces pombe	putative negative regulator of vesicle formation	200	41
4373	M96982	Homo sapiens	U2 snRNP auxiliary factor small subunit	279	70
4374	U47741	Homo sapiens	CREB-binding protein	123	96
4375	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	127	75
4376	Y12781	Homo sapiens	transducin (beta) like 1 protein	1056	90

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4377	W69424	Homo sapiens	Human secreted protein bg140_1.	183	97
4378	AL096700	Homo sapiens	dI499B10.2 (phosphorylase kinase, alpha 2 (liver) (PYK))	639	86
4379	AF177390	Manduca sexta	antennal specific membrane protein AMP	378	51
4380	X97675	Homo sapiens	plakophilin 2b	156	75
4381	R33713	Homo sapiens	Pg1101.	104	100
4382	AB015473	Arabidopsis thaliana	gene_id:MCM23.1~unknown protein	113	61
4383	AF116715	Homo sapiens	PRO2829	133	50
4384	AL357472	Homo sapiens	VPS33B	676	99
4385	AF090931	Homo sapiens	PRO0483	155	58
4386	U92645	Gecarcinus lateralis	alpha-1-tubulin	511	75
4387	Y36095	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 480.	202	90
4388	M64923	Bos taurus	C10 protein	218	95
4389	X98264	Homo sapiens	M-phase phosphoprotein 4	197	100
4390	AK000264	Homo sapiens	unnamed protein product	239	73
4391	M12937	Homo sapiens	ferritin heavy subunit	662	84
4392	P92219	Homo sapiens (human)	CR1 protein.	116	80
4393	X16135	Homo sapiens	L protein (AA 1-558)	759	99
4394	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	148	58
4395	AC005591	Homo sapiens	PkB-like	170	97
4396	AF161426	Homo sapiens	HSPC308	313	77
4397	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	146	61
4398	AF104921	Homo sapiens	succinyl-CoA synthetase alpha subunit	679	88
4399	AF257330	Homo sapiens	COBW-like protein	586	90
4400	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	116	65
4401	AF119851	Homo sapiens	PRO1722	101	79
4402	M55542	Homo sapiens	guanylate binding protein isoform I	230	76
4403	Y07752	Volvox carteri	pherophorin-S	459	88
4404	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	113	44
4405	U07786	Sus scrofa	beta actin	519	90
4406	A06977	Homo sapiens	albumin	586	88
4407	L20755	Cuscuta reflexa	hybrid proline-rich protein;cytokinin-induced;haustoria	112	41
4408	AB002299	Homo sapiens	KIAA0301	612	98
4409	AB001424	Mus musculus	KIF17	104	47
4410	M88108	Homo sapiens	p62	574	92
4411	AL121673	Homo sapiens	bA305P22.2 (novel protein)	415	71
4412	AF064553	Mus musculus	NSD1 protein	224	64
4413	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	107	36
4414	A06977	Homo sapiens	albumin	505	82
4415	A06977	Homo sapiens	albumin	596	90
4416	Y87116	Homo sapiens	Human secreted protein sequence SEQ ID NO:155.	123	50
4417	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	103	85
4418	G03053	Homo sapiens	Human secreted protein, SEQ ID NO: 7134.	100	54
4419	AF049606	Mus musculus	transcription factor NF-ATc isoform b	114	90

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4420	Z11190_cd1	Homo sapiens	11-DEC-1998 Interleukin-3 coding sequence from b2HFLS20W cDNA library.	354	97
4421	W64469	Homo sapiens	Human secreted protein from clone CW795_2.	203	100
4422	M12523	Homo sapiens	albumin Venezia	350	94
4423	AF130077	Homo sapiens	PRO2619	561	89
4424	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	161	64
4425	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	393	91
4426	A09561	synthetic construct	human serum albumin	651	96
4427	AL133215	Homo sapiens	bA108L7.5 (novel protein similar to Plasmodium POM1 and C. elegans F46G11.1 (Tr:Q20485))	392	100
4428	W33663	Homo sapiens	Human puromycin-sensitive aminopeptidase (PSA)-68.	172	96
4429	AB021654	Homo sapiens	DD2/bile acid-binding protein/AKR1C2/3alpha-hydroxysteroid dehydrogenase type 3	184	81
4430	W63683	Homo sapiens	Human secreted protein 3.	114	42
4431	AY008763	Homo sapiens	sentrin/SUMO-specific protease	447	96
4432	U52965	Homo sapiens	ENX-1	176	94
4433	AF180470	Mus musculus	Kiaa0575	423	77
4434	X17206	Homo sapiens	put. LLRep3 protein (AA 1-221)	581	99
4435	Y70929	Homo sapiens	Human zilla4 splice variant protein.	621	100
4436	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	135	71
4437	A06977	Homo sapiens	albumin	610	97
4438	A00279	synthetic construct	Human serum albumin	621	94
4439	L29028	Chlamydomonas eugametos	amino acid feature: N-glycosylation sites, aa 41 .. 43, 46 .. 48, 51 .. 53, 72 .. 74, 107 .. 109, 128 .. 130, 132 .. 134, 158 .. 160, 163 .. 165; amino acid feature: Rod protein domain, aa 169 .. 340; amino acid feature: globular protein domain, aa 32 .. 168	105	36
4440	AK024455	Homo sapiens	FLJ00047 protein	112	65
4441	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	133	69
4442	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	142	60
4443	AF113685	Homo sapiens	PRO0974	101	54
4444	W03627	Homo sapiens	Human follicle stimulating hormone GPR N-terminal sequence.	181	42
4445	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	132	76
4446	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	141	54
4447	L02867	Homo sapiens	paraneoplastic antigen	136	78
4448	D38435	Homo sapiens	homologue of yeast PMS1	108	66
4449	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	122	65
4450	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	142	68
4451	AF220264	Homo sapiens	MOST-1	101	40
4452	AF130079	Homo sapiens	PRO2852	97	59
4453	AF116715	Homo sapiens	PRO2829	139	69

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4454	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	144	53
4455	AF130087	Homo sapiens	PRO2411	108	73
4456	AF279891	Homo sapiens	dead box protein 15	108	58
4457	L08258	Strongylocentrotus purpuratus	kinesin light chain isoform 4	176	94
4458	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	116	78
4460	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	146	74
4461	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	156	52
4462	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	118	72
4463	AF119900	Homo sapiens	PRO2822	144	80
4464	M15530	Homo sapiens	B-cell growth factor	92	76
4465	Y17833	Human endogenous retrovirus K	env protein	107	62
4466	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	132	78
4467	AF090895	Homo sapiens	PRO0117	112	79
4468	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	146	64
4469	X97675	Homo sapiens	plakophilin 2b	119	78
4470	AF118081	Homo sapiens	PRO1900	119	74
4471	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	121	60
4472	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	63
4473	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	205	73
4474	AF130114	Homo sapiens	PRO2459	121	67
4475	AF178534	Homo sapiens	talín	213	67
4476	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	122	92
4477	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	99	66
4478	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	142	62
4479	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	153	55
4480	AF217374	Acanthaster planci	cytochrome oxidase subunit I	130	100
4481	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	110	57
4482	Y20983	Homo sapiens	Human glial fibrillary acidic protein GFAP wild type fragment 9.	110	63
4483	AF221552	Oryza sativa	proline-rich protein RiP-15	119	33
4484	L25941	Homo sapiens	integral nuclear envelope inner membrane protein	110	84
4485	AF130089	Homo sapiens	PRO2550	161	81
4486	U39742	Caenorhabditis elegans	coded for by C. elegans cDNA yk25e5.3; coded for by C. elegans cDNA yk25e5.5; similar to repeat guanylate kinase domain of D. melanogaster lethal(1) discs large-1 tumor suppressor protein (SP:DLG1_DROME, P31007) and R. norvegicus postsynaptic density protein	98	72

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			95 (PSD-95) (SP:PSD9 RAT, P31016)		
4487	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	89	81
4488	X97675	Homo sapiens	plakophilin 2b	127	88
4489	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	105	71
4490	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	160	64
4491	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	122	77
4492	U83280	Leishmania donovani	39 kDa antigen	107	76
4493	AF023142	Homo sapiens	pre-mRNA splicing SR protein rA4	141	40
4494	K02576	Homo sapiens	salivary proline-rich protein I	119	40
4495	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	98	45
4496	AF130089	Homo sapiens	PRO2550	132	75
4497	AF090930	Homo sapiens	PRO0478	160	76
4498	AF119900	Homo sapiens	PRO2822	158	55
4499	AF116661	Homo sapiens	PRO1438	126	44
4500	AF116661	Homo sapiens	PRO1438	118	42
4501	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	113	48
4502	M81321	Macaca fascicularis	proline-rich protein	154	44
4503	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	154	96
4504	D44596	Saccharomyces cerevisiae	Mdj1p heat shock protein	93	42
4505	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	163	76
4506	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	207	93
4507	U93564	Homo sapiens	p40	520	86
4508	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	135	55
4509	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	109	77
4510	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	146	66
4511	L27428	Homo sapiens	reverse transcriptase	143	87
4512	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	105	80
4513	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	97	75
4514	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	60
4515	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	73
4516	AF130051	Homo sapiens	PRO0898	141	86
4517	U12690	Homo sapiens	cytochrome oxidase subunit II	185	94
4518	G02597	Homo sapiens	Human secreted protein, SEQ ID NO: 6678.	130	100
4519	AK024455	Homo sapiens	FLJ00047 protein	152	68
4520	AF210651	Homo sapiens	NAG18	161	88
4521	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	140	68
4522	AF217374	Acanthaster planci	cytochrome oxidase subunit I	131	76

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4523	U72520	Mus musculus	mena protein	102	42
4524	J01415	Homo sapiens	cytochrome oxidase subunit 3	129	75
4525	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	108	84
4526	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	139	76
4527	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	138	89
4528	AF090931	Homo sapiens	PRO0483	91	88
4529	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	51
4530	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	130	92
4531	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	123	64
4532	L26953	Homo sapiens	chromosomal protein	102	79
4533	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	88	54
4534	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	122	40
4535	AF090944	Homo sapiens	PRO0663	113	53
4536	U15647	Mus musculus	expressed in select embryonal carcinoma cells and testicular cells; similar to Swiss-Prot Accession Number P11260	119	35
4537	L13858	Homo sapiens	guanine nucleotide exchange factor	150	81
4538	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	138	68
4539	AF090930	Homo sapiens	PRO0478	104	53
4540	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	112	64
4541	K02401	Homo sapiens	chorionic somatomammotropin	672	96
4542	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	171	67
4543	J04208	Homo sapiens	inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	455	92
4544	K02401	Homo sapiens	chorionic somatomammotropin	397	88
4545	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	155	66
4546	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	161	68
4547	R24056	Homo sapiens	hGH variant #8 - 172Arg 174Thr 176Tyr 178His.	117	62
4548	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	111	68
4549	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	124	65
4550	AF119855	Homo sapiens	PRO1847	152	68
4551	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	153	70
4552	M59217	Homo sapiens	alpha-1 type XIII collagen	98	57
4553	R83119	Homo sapiens	Human cisplatin resistance protein.	136	96
4554	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	161	72
4555	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	91	60
4556	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	70
4557	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y	101	44

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			isoform		
4558	AF130089	Homo sapiens	PRO2550	150	85
4559	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	161	56
4560	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	81	64
4561	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	115	55
4562	G03114	Homo sapiens	Human secreted protein, SEQ ID NO: 7195.	106	82
4563	AF090931	Homo sapiens	PRO0483	145	73
4564	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	358	77
4565	AF130089	Homo sapiens	PRO2550	175	85
4566	Z93244	Homo sapiens	bK116F5.2 (PUTATIVE RhoGAP (CDC42 GTPase Activating Protein) LIKE protein)	125	61
4567	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	142	56
4568	AF130089	Homo sapiens	PRO2550	125	75
4569	AF130089	Homo sapiens	PRO2550	172	82
4570	AF225961	Rattus norvegicus	RhoGEF glutamate transport modulator GTRAP48	149	78
4571	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	143	64
4572	G02640	Homo sapiens	Human secreted protein, SEQ ID NO: 6721.	157	70
4573	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	91	73
4574	X92485	Plasmodium vivax	pval	111	52
4575	U93567	Homo sapiens	p40	151	71
4576	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	90	57
4577	AC007508	Arabidopsis thaliana	F1K23.4	143	42
4578	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	145	53
4579	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	175	73
4580	G00338	Homo sapiens	Human secreted protein, SEQ ID NO: 4419.	142	76
4581	AF130079	Homo sapiens	PRO2852	117	70
4582	AF090930	Homo sapiens	PRO0478	109	57
4583	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	134	79
4584	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	149	62
4585	AF118090	Homo sapiens	PRO2044	175	97
4586	AL080243	Homo sapiens	E1A binding protein p300; match: proteins: Sw:Q09472 Sw:Q92793 Sw:P45481 Wp:CE00571 Wp:CE21117 Tr:O01368 Wp:CE08856 Wp:CE00570 Wp:CE08453 Tr:O44076	144	93
4587	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICEL) protein sequence.	140	62
4588	AJ131245	Homo sapiens	Sec24B protein	131	81
4589	W02105	Homo sapiens	Human L-asparaginase.	559	100
4590	L26953	Homo sapiens	chromosomal protein	146	71
4591	M16976	Glycine max	N-75	125	36

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4592	AF119851	Homo sapiens	PRO1722	118	61
4593	AF090931	Homo sapiens	PRO0483	99	85
4594	M20789	Homo sapiens	alpha-1 type I collagen	103	41
4595	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	97	72
4596	AF130089	Homo sapiens	PRO2550	124	71
4597	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	143	65
4598	AF118082	Homo sapiens	PRO1902	122	64
4599	AK023034	Homo sapiens	unnamed protein product	156	100
4600	AF118082	Homo sapiens	PRO1902	148	62
4601	AF119855	Homo sapiens	PRO1847	130	50
4602	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	99	77
4603	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	162	65
4604	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	135	54
4605	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	123	75
4606	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	127	74
4607	V00672	Pan troglodytes	reading frame protein 4	194	72
4608	X86791	Sus scrofa	beta-globin	156	87
4609	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	130	88
4610	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	90
4611	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	149	68
4612	AB029309	Homo sapiens	Npw38-binding protein NpwBP	120	38
4613	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	148	53
4614	AK024372	Homo sapiens	unnamed protein product	124	63
4615	AC005360	Homo sapiens	FAA	175	91
4616	D38113	Pan troglodytes	ATPase subunit 6	204	69
4617	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	122	45
4618	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	118	81
4619	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	99	90
4620	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	125	50
4621	S79410	Mus musculus	nuclear localization signal binding protein	107	45
4622	AF126163	Homo sapiens	HHLA3 protein	124	75
4623	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	109	69
4624	U38184	Trypanosoma cruzi	ATPase subunit 6	102	45
4625	U01849	Trypanosoma brucei	ORF1	97	36
4626	G03058	Homo sapiens	Human secreted protein, SEQ ID NO: 7139.	95	57
4627	M33228	Trypanosoma brucei	ATPase 6	126	37
4628	AF118086	Homo sapiens	PRO1992	113	60
4629	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	149	41

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4630	X12544	Homo sapiens	3 HLA-DR B protein precursor (AA - 29 to 267)	108	48
4631	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	46
4632	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	124	60
4633	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	151	60
4634	J01415	Homo sapiens	cytochrome oxidase subunit 3	138	100
4635	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	135	56
4636	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	100
4637	X67320	Rattus norvegicus	H1d-Histone	122	40
4638	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	181	76
4639	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	96	73
4640	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	136	54
4641	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	70
4642	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	190	56
4643	M29580	Homo sapiens	zinc finger protein 7 (ZFP7)	103	38
4645	U47741	Homo sapiens	CREB-binding protein	207	94
4646	AL035461	Homo sapiens	dJ967N21.5 (novel MCM2/3/5 family member)	213	80
4647	G03435	Homo sapiens	Human secreted protein, SEQ ID NO: 7516.	76	60
4648	AF227948	Homo sapiens	HBV pX associated protein-8; XAP-8	402	86
4649	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	143	86
4650	U93574	Homo sapiens	putative p150	121	33
4651	A02739	synthetic construct	chloramphenicol acetyltransferase	622	99
4652	AF190449	Mus musculus	putative transcription factor ALF-4	274	83
4653	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	108	76
4654	X15187	Homo sapiens	precursor polypeptide (AA -21 to 782)	763	98
4655	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	91
4656	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	169	77
4657	B01372	Homo sapiens	Neuron-associated protein.	135	83
4658	AK024455	Homo sapiens	FLJ00047 protein	151	60
4659	AC004850	Homo sapiens	vacuolar assembly protein VPS41 homolog (S53)	187	92
4660	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	181	92
4661	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	138	58
4662	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	154	78
4663	M69180	Homo sapiens	nonmuscle myosin heavy chain-A	106	84
4664	AF130089	Homo sapiens	PRO2550	117	65
4665	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	91

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4666	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	62
4667	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	111	78
4668	AF113695	Homo sapiens	PRO1365	82	71
4669	AF003540	Homo sapiens	Krueppel family zinc finger protein	111	64
4670	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	49
4671	AL109658	Homo sapiens	dJ776F14.1 (ortholog of mouse P47)	110	100
4672	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	129	62
4673	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	138	60
4674	X51591	Homo sapiens	beta-myosin heavy chain (1151 AA)	442	97
4675	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	148	76
4676	D86971	Homo sapiens	no similarities to reported gene products	133	100
4677	K02576	Homo sapiens	salivary proline-rich protein 1	142	43
4678	AF044205	Gossypium hirsutum	proline-rich protein precursor	117	39
4679	D38116	Pan paniscus	NADH dehydrogenase subunit 4	243	98
4680	AF113685	Homo sapiens	PRO0974	117	74
4681	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	193	90
4682	L26163	Mus musculus	histone H1e	111	37
4683	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	145	78
4684	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	53
4685	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	110	60
4686	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	153	72
4687	D38112	Homo sapiens	NADH dehydrogenase subunit 6	165	100
4688	W50922	Homo sapiens	Amino acid sequence of a heterogenous ribonucleotide protein.	139	100
4689	Y00281	Homo sapiens	precursor	789	100
4690	AF210651	Homo sapiens	NAG18	142	65
4691	L26953	Homo sapiens	chromosomal protein	124	72
4692	L26953	Homo sapiens	chromosomal protein	124	72
4693	U12690	Homo sapiens	cytochrome oxidase subunit II	166	80
4694	L27428	Homo sapiens	reverse transcriptase	144	87
4695	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	74
4696	W29474	Homo sapiens	Human histone H1 isoform H1S-1.	93	41
4697	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	126	56
4698	S79410	Mus musculus	nuclear localization signal binding protein	138	62
4699	G00413	Homo sapiens	Human secreted protein, SEQ ID NO: 4494.	141	54
4700	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	162	70
4701	AF003540	Homo sapiens	Krueppel family zinc finger protein	112	88
4702	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	159	59
4703	AF241242	Mus musculus	T-cell-specific T-box transcription factor T-bet	294	75
4704	Y86248	Homo sapiens	Human secreted protein HCHPF68,	152	80

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			SEQ ID NO:163.		
4705	AF038963	Homo sapiens	RNA helicase	102	70
4706	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	148	63
4707	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	145	70
4708	AF289099	Maackia amurensis	ENOD2f	113	42
4709	AF130087	Homo sapiens	PRO2411	124	57
4710	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	188	86
4711	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	138	86
4712	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	143	78
4713	AF273133	Ochotona macrotis	NADH dehydrogenase subunit 4	154	76
4714	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	104	48
4715	Z18361	Ovis aries	trichohyalin	120	33
4716	AF130089	Homo sapiens	PRO2550	152	75
4717	AF119851	Homo sapiens	PRO1722	143	60
4718	K03205	Homo sapiens	salivary proline-rich protein precursor	145	45
4719	K02401	Homo sapiens	chorionic somatomammotropin	619	96
4720	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	114	52
4721	J03756	Homo sapiens	hGH-V2	515	74
4722	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	194	93
4723	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	128	56
4724	D49490	Homo sapiens	protein disulfide isomerase-related protein (PDIR)	213	55
4725	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	138	66
4726	K02401	Homo sapiens	chorionic somatomammotropin	657	98
4727	D87459	Homo sapiens	Similar to Volvox carteri extensin (S22697)	162	80
4728	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	99	34
4729	AF090944	Homo sapiens	PRO0663	151	63
4730	M32305	Human papillomavirus type 47	E1/E4 fusion protein	106	40
4731	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	133	57
4732	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	76
4733	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	114	43
4734	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	72
4735	M76546	Helianthus annuus	hydroxyproline-rich protein	113	43
4736	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	99	59
4737	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	92	47
4738	AP000616	Oryza sativa	similar to RING-H2 finger protein	133	73

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			RHA1a (AF078683)		
4739	AF044205	Gossypium hirsutum	proline-rich protein precursor	105	42
4740	S78854	Oryctolagus cuniculus	alpha-tropomyosin	159	87
4741	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	151	79
4742	B01372	Homo sapiens	Neuron-associated protein.	159	85
4743	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	122	100
4744	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	82
4745	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	154	78
4746	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	164	80
4747	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	100
4748	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	117	53
4749	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	208	93
4750	AF155232	Pisum sativum	extensin	172	40
4751	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	117	76
4752	AF130079	Homo sapiens	PRO2852	104	70
4753	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	154	50
4754	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	167	50
4755	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	138	100
4756	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	163	66
4757	M11901	Rattus norvegicus	proline-rich salivary protein	102	45
4758	D38112	Homo sapiens	NADH dehydrogenase subunit 5	242	94
4759	AF046935	Homo sapiens	PCF11p homolog	244	94
4760	M76546	Helianthus annuus	hydroxyproline-rich protein	165	41
4761	Y30681	Homo sapiens	Splice variant ZAP-1B protein of the human tumor suppressor gene ZAP-1.	115	60
4762	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	178	84
4763	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	134	84
4764	R95913	Homo sapiens	Neural thread protein.	136	70
4765	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	139	69
4766	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	102	56
4767	U63159	Mus musculus	transaldolase	218	100
4768	AF230279	Caenorhabditis elegans	SWI3-like protein; PSA-1	106	38
4769	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	116	56
4770	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	136	67
4771	X92485	Plasmodium	pva1	85	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
4772	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	95	80
4773	AC002398	Homo sapiens	F25965_3	96	39
4774	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	110	75
4775	AF120151	Homo sapiens	cytokine receptor-like molecule 9	112	100
4776	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	141	74
4777	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	108	75
4778	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	117	55
4779	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	101	55
4780	AB007860	Homo sapiens	KIAA0400	119	88
4781	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	122	88
4782	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	98	84
4783	M22334	Homo sapiens	unknown protein	611	93
4784	Y36203	Homo sapiens	Human secreted protein #75.	350	76
4785	K02401	Homo sapiens	chorionic somatomammotropin	188	97
4786	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	152	64
4787	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	102	67
4788	M38451	Homo sapiens	growth hormone	264	94
4789	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	77
4790	K02401	Homo sapiens	chorionic somatomammotropin	250	96
4791	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	127	88
4792	Y36112	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 497.	125	78
4793	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	131	51
4794	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	124	57
4795	M18095	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	103	34
4796	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	131	69
4797	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	160	77
4798	AL132841	Caenorhabditis elegans	Y15E3A.3	120	51
4799	AL009146	Drosophila melanogaster	alternatively spliced form	79	94
4800	S74221	Homo sapiens	IK factor=cytokine down-regulating HLA class II	108	80
4801	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	121	100
4802	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	94	90
4803	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	101	90

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4804	R95913	Homo sapiens	Neural thread protein.	139	71
4805	X61045	Hydra sp.	mini-collagen	126	68
4806	X12544	Homo sapiens	3 HLA-DR B protein precursor (AA - 29 to 267)	114	56
4807	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	160	84
4808	D38112	Homo sapiens	NADH dehydrogenase subunit 6	277	94
4809	L26953	Homo sapiens	chromosomal protein	90	60
4810	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	108	76
4811	L26953	Homo sapiens	chromosomal protein	121	62
4812	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	124	71
4813	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	78	46
4814	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	100	78
4815	AF152961	Homo sapiens	chromatin-specific transcription elongation factor FACT 140 kDa subunit	152	96
4816	U93569	Homo sapiens	putative p150	334	82
4817	AB014575	Homo sapiens	KIAA0675 protein	125	67
4818	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	114	90
4819	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	129	45
4820	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	134	48
4821	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	129	61
4822	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	137	83
4823	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	126	55
4824	AF113685	Homo sapiens	PRO0974	110	54
4825	U63542	Homo sapiens	FAP protein	136	70
4826	X83413	Human herpesvirus 6	U88	130	54
4827	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	152	76
4828	U76609	Homo sapiens	ribosomal L5 protein	134	89
4829	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	110	57
4830	AC006161	Arabidopsis thaliana	putative CENP-B/ARS-binding protein-like protein	141	31
4831	G03556	Homo sapiens	Human secreted protein, SEQ ID NO: 7637.	143	71
4832	U94189	Rattus norvegicus	Duo	158	79
4833	J04031	Homo sapiens	MDMCSF (EC 1.5.1.5; EC 3.5.4.9; EC 6.3.4.3)	193	97
4834	Y13397	Homo sapiens	Amino acid sequence of protein PRO334.	654	97
4835	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	107	53
4836	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	464	93
4837	AF272833	Homo sapiens	misato	413	87
4838	AF130089	Homo sapiens	PRO2550	132	71
4839	G00333	Homo sapiens	Human secreted protein, SEQ ID NO:	116	54

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4414.		
4840	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	89	80
4841	W77354	Homo sapiens	Human telomere repeat binding factor 2 truncated protein.	106	100
4842	AF090942	Homo sapiens	PRO0657	160	75
4843	AF090944	Homo sapiens	PRO0663	202	80
4844	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	167	81
4845	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	166	74
4846	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	228	97
4847	U12690	Homo sapiens	cytochrome oxidase subunit II	198	95
4848	AB023485	Mus musculus	transcription factor CA150b	118	42
4849	Z70684	Caenorhabditis elegans	F28D1.8	98	42
4850	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	106	45
4851	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	179	92
4852	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	145	82
4853	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	123	77
4854	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	112	55
4855	U66464	Homo sapiens	hematopoietic progenitor kinase	110	81
4856	AC011708	Arabidopsis thaliana	putative RING zinc finger protein	121	43
4857	M81321	Macaca fascicularis	proline-rich protein	126	35
4858	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	104	40
4859	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	195	75
4860	X65165	Volvox carteri	extensin	248	55
4861	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	106	79
4862	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	185	92
4863	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	142	75
4864	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	100
4865	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	163	63
4866	AB023229	Homo sapiens	KIAA1012 protein	208	92
4867	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	144	80
4868	L26953	Homo sapiens	chromosomal protein	126	70
4869	U63542	Homo sapiens	FAP protein	134	40
4870	D86853	Catharanthus roseus	extensin	102	48
4871	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	152	69
4872	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	136	55
4873	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	156	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4874	Y17832	Human endogenous retrovirus K	env protein	219	67
4875	AF217517	Homo sapiens	uncharacterized bone marrow protein BM041	81	38
4876	L27428	Homo sapiens	reverse transcriptase	105	91
4877	M64792	Rattus norvegicus	salivary proline-rich protein	146	46
4878	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	99	38
4879	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	105	77
4880	R58816	Homo sapiens	Human c-myc far upstream element (FUSE) binding protein (FBP) variant from PBL clone 31-10.	87	39
4881	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	150	67
4882	AF175223	Drosophila melanogaster	SANT domain protein SMRTER	84	89
4883	AF174482	Homo sapiens	polycomb 3	136	57
4884	Y54324	Homo sapiens	Amino acid sequence of a human gastric cancer antigen protein.	147	66
4885	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	141	71
4886	U55376	Caenorhabditis elegans	F16H11.2 gene product	95	100
4887	AF261918	Homo sapiens	disintegrin metalloproteinase with thrombospondin repeats	262	72
4888	J02459	bacteriophage lambda	K (tail component;199)	610	100
4889	Y95435	Homo sapiens	Human calcium channel SOC-2/CRAC-1.	219	89
4890	B01372	Homo sapiens	Neuron-associated protein.	134	80
4891	X64712	Gallus gallus	collagen-alpha-3 type IX	112	41
4892	K02401	Homo sapiens	chorionic somatomammotropin	556	87
4893	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	108	55
4894	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	62
4895	L26953	Homo sapiens	chromosomal protein	93	81
4896	AJ277740	Homo sapiens	RPB11b1beta protein	102	66
4897	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	145	87
4898	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	131	67
4899	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	153	64
4900	U90304	Homo sapiens	iroquois-class homeodomain protein IRX-2a	109	41
4901	D29956	Homo sapiens	This gene is similar to tre oncogene(X63547).	120	73
4902	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	116	70
4903	Y69166	Homo sapiens	A mature human N-acetylglycosaminyl transferase protein.	102	82
4904	AF119900	Homo sapiens	PRO2822	157	57
4905	U93565	Homo sapiens	putative p150	146	55
4906	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	120	67
4907	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	160	76
4908	Y86248	Homo sapiens	Human secreted protein HCHPF68,	136	55

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			SEQ ID NO:163.		
4909	AF155232	Pisum sativum	extensin	98	43
4910	U15647	Mus musculus	reverse transcriptase	196	50
4911	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	144	56
4912	AF225419	Homo sapiens	HSCARG	248	61
4913	M76546	Helianthus annuus	hydroxyproline-rich protein	110	47
4914	AL117382	Homo sapiens	dJ881L22.2 (novel protein)	312	100
4915	AB037814	Homo sapiens	KIAA1393 protein	192	68
4916	D38112	Homo sapiens	NADH dehydrogenase subunit 4	169	89
4917	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	105	90
4918	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	116	86
4919	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	132	100
4920	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	183	65
4921	AF090944	Homo sapiens	PRO0663	141	57
4922	AF090931	Homo sapiens	PRO0483	159	55
4923	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	81
4924	U09500	Homo sapiens	cytochrome b	276	94
4925	AB002377	Homo sapiens	KIAA0379 protein	304	98
4926	M22334	Homo sapiens	unknown protein	201	62
4927	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	142	65
4928	AF130089	Homo sapiens	PRO2550	116	82
4929	U21123	Drosophila melanogaster	ena polypeptide	94	41
4930	W75159	Homo sapiens	Human secreted protein encoded by gene 45 clone HTD54.	294	82
4931	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	96	74
4932	G02460	Homo sapiens	Human secreted protein, SEQ ID NO: 6541.	101	57
4933	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	142	70
4934	AF130087	Homo sapiens	PRO2411	137	80
4935	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	132	56
4936	AB032604	Mus musculus	MIWI (piwi)	313	50
4937	X74987	Homo sapiens	2'-5' oligoadenylate binding protein	144	96
4938	AF054658	Homo sapiens	kappa 1 immunoglobulin light chain variable region	120	87
4939	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	134	67
4940	U22230	Felis catus	ribosomal protein S17	118	100
4941	AB028956	Homo sapiens	KIAA1033 protein	527	88
4942	G00429	Homo sapiens	Human secreted protein, SEQ ID NO: 4510.	281	86
4943	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	71
4944	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	108	95
4945	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	170	76
4946	AF090895	Homo sapiens	PRO0117	125	65
4947	D13866	Homo sapiens	alpha-catenin	575	100
4948	L01664	Homo sapiens	lysophospholipase	166	96

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4949	AF118085	Homo sapiens	PRO1975	572	96
4950	AK024455	Homo sapiens	FLJ00047 protein	95	81
4951	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	58
4952	AB011142	Homo sapiens	KIAA0570 protein	120	88
4953	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	108	39
4954	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	175	69
4955	AK024455	Homo sapiens	FLJ00047 protein	119	64
4956	AF116715	Homo sapiens	PRO2829	142	75
4957	M31520	Homo sapiens	ribosomal protein S24	158	100
4958	D38113	Pan troglodytes	ATPase subunit 8	98	64
4959	AF130089	Homo sapiens	PRO2550	156	75
4960	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	136	95
4961	S61950	Oryctolagus cuniculus	alpha 2(I) procollagen, alpha 2(I) {C-terminal}	159	93
4962	AF070540	Homo sapiens	putative nuclear protein	513	93
4963	S61950	Oryctolagus cuniculus	alpha 2(I) procollagen, alpha 2(I) {C-terminal}	159	93
4964	AF146191	Homo sapiens	FRG1	343	92
4965	Y16624	Homo sapiens	Human phosphoprotein 32 (pp32) protein sequence.	114	100
4966	X67813	Canis familiaris	signal recognition particle, 72 kDa subunit	127	100
4967	S79410	Mus musculus	nuclear localization signal binding protein	127	63
4968	U83303	Homo sapiens	line-1 reverse transcriptase	117	69
4969	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	101	80
4970	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	173	69
4971	D38112	Homo sapiens	ATPase subunit 6	112	91
4972	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	209	97
4973	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	162	80
4974	AL050399	Arabidopsis thaliana	putative proline-rich protein	75	91
4975	L11668	Bos taurus	cyclophilin-40	134	100
4976	M55169	Homo sapiens	tripeptidyl peptidase II	385	90
4977	AF090944	Homo sapiens	PRO0663	154	88
4978	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	102	62
4979	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	128	70
4980	G00721	Homo sapiens	Human secreted protein, SEQ ID NO: 4802.	104	95
4981	R54656	Homo sapiens	Prostaglandin I2 production stimulating protein B.	101	100
4982	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	124	38
4983	AF273053	Homo sapiens	CTCL tumor antigen se89-1	281	96
4984	M15530	Homo sapiens	B-cell growth factor	117	58
4985	D13641	Homo sapiens	mitochondrial outer membrane protein 19	534	94
4986	L11316	Mus musculus	ect2	528	92
4987	X51755	Homo sapiens	open reading frame (458 AA)	108	90
4988	M61877	Homo sapiens	erythroid alpha spectrin	129	87

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
4989	X57316	Saccharomyces cerevisiae	carboxypeptidase s	134	50
4990	G00338	Homo sapiens	Human secreted protein, SEQ ID NO: 4419.	151	78
4991	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	173	61
4992	M34019	Bos taurus	beta-adrenergic receptor kinase	172	100
4993	L26953	Homo sapiens	chromosomal protein	135	86
4994	X97675	Homo sapiens	plakophilin 2b	124	63
4995	Y36112	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 497.	153	77
4996	AF130089	Homo sapiens	PRO2550	175	48
4997	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	95	68
4998	Y86214	Homo sapiens	Nuclear transport protein clone hfb341 protein sequence.	312	98
4999	G03681	Homo sapiens	Human secreted protein, SEQ ID NO: 7762.	100	95
5000	AF152961	Homo sapiens	chromatin-specific transcription elongation factor FACT 140 kDa subunit	127	96
5001	U70063	Homo sapiens	acid ceramidase	315	96
5002	AF041373	Rattus norvegicus	clathrin assembly protein short form	163	63
5003	AK001841	Homo sapiens	unnamed protein product	468	83
5004	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	143	61
5005	S79410	Mus musculus	nuclear localization signal binding protein	116	47
5006	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	107	55
5007	G00338	Homo sapiens	Human secreted protein, SEQ ID NO: 4419.	151	76
5008	Z15005	Homo sapiens	CENP-E	281	84
5009	AF130089	Homo sapiens	PRO2550	122	75
5010	AL049698	Homo sapiens	dJ470B24.1.1 (myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6) (isoform 1))	77	33
5011	G02382	Homo sapiens	Human secreted protein, SEQ ID NO: 6463.	90	62
5012	AL023780	Schizosaccharomyces pombe	DNA binding protein	145	36
5013	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	93	46
5014	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	104	43
5015	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	104	55
5016	U15647	Mus musculus	expressed in select embryonal carcinoma cells and testicular cells; similar to Swiss-Prot Accession Number P11260	119	35
5017	B10545	Homo sapiens	Human aspartate protease psn-like4 protein.	649	98
5018	AF089745	Homo sapiens	FK506-binding protein	656	98
5019	AF081484	Homo sapiens	alpha-tubulin isoform 1	634	97
5020	AF081484	Homo sapiens	alpha-tubulin isoform 1	603	92
5021	AF081484	Homo sapiens	alpha-tubulin isoform 1	623	94
5022	AF081484	Homo sapiens	alpha-tubulin isoform 1	671	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5023	AF130089	Homo sapiens	PRO2550	109	71
5024	AB013452	Homo sapiens	ATPasell	208	77
5025	R27654	Homo sapiens	Human calcium channel 27980/16.	183	100
5026	Y36156	Homo sapiens	Human secreted protein #28.	114	64
5027	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	74
5028	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	149	59
5029	S74728	Homo sapiens	antiquitin=26g turgor protein homolog	652	98
5030	L41498	Homo sapiens	longation factor 1-alpha 1	592	87
5031	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N-acetyl-galactosaminyltransferase	454	70
5032	AJ223948	Homo sapiens	RNA helicase	574	84
5033	AF021935	Rattus norvegicus	mytonic dystrophy kinase-related Cdc42-binding kinase	670	97
5034	AF150755	Mus musculus	microtubule-actin crosslinking factor	526	80
5035	AF150755	Mus musculus	microtubule-actin crosslinking factor	602	89
5036	AF081484	Homo sapiens	alpha-tubulin isoform 1	598	89
5037	U09823	Oryctolagus cuniculus	elongation factor 1 alpha	708	96
5038	AE003621	Drosophila melanogaster	CG13384 gene product	279	45
5039	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	107	68
5040	AF047469	Homo sapiens	arsenite translocating ATPase	650	94
5041	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	109	41
5042	AJ007798	Homo sapiens	stromal antigen 3, (STAG3)	288	100
5043	L26953	Homo sapiens	chromosomal protein	124	67
5044	AB005047	Homo sapiens	SH3 binding protein	105	88
5045	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	143	78
5046	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	164	83
5047	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	121	63
5048	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	153	64
5049	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	120	59
5050	Z25535	Homo sapiens	nuclear pore complex protein hnup153	115	88
5051	J03176	Bradyrhizobium japonicum	cytochrome b/c1 precursor	97	35
5052	X85995	Homo sapiens	immunoglobulin light chain	200	100
5053	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	164	76
5054	B01372	Homo sapiens	Neuron-associated protein.	109	80
5055	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	209	54
5056	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	110	51
5057	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	93	39
5058	X92474	Homo sapiens	ch-TOG	147	100
5059	L27428	Homo sapiens	reverse transcriptase	264	75
5060	S79410	Mus musculus	nuclear localization signal binding protein	119	44
5061	L25616	Homo sapiens	CG1 protein'	119	77
5062	G03790	Homo sapiens	Human secreted protein, SEQ ID NO:	99	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7871.		
5063	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	164	59
5064	AF118082	Homo sapiens	PRO1902	175	53
5065	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	84	51
5066	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	108	100
5067	AF155232	Pisum sativum	extensin	137	45
5068	X63005	Mus musculus	proline-rich protein	98	35
5069	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	307	56
5070	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	173	89
5071	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	153	68
5072	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	164	73
5073	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	109	73
5074	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	121	80
5075	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	113	72
5076	U12690	Homo sapiens	cytochrome oxidase subunit II	151	88
5077	AF090944	Homo sapiens	PRO0663	138	78
5078	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	150	74
5079	X97675	Homo sapiens	plakophilin 2b	179	93
5080	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	123	76
5081	AF240630	Mus musculus	IQ motif containing GTPase activating protein 1	176	59
5082	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	100	54
5083	S79410	Mus musculus	nuclear localization signal binding protein	99	59
5084	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	101	57
5085	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	118	77
5086	AB047600	Macaca fascicularis	hypothetical protein	93	69
5087	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	88	80
5088	AF000298	Caenorhabditis elegans	weak similarity to collagens; glycine- and proline-rich	112	57
5089	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	87	61
5090	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	74	61
5091	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	83	78
5092	AF065484	Homo sapiens	sorting nexin 1A	172	81
5093	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	139	90
5094	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	164	78
5095	U02313	Mus musculus	protein kinase	147	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5096	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	129	67
5097	U64849	Caenorhabditis elegans	Contains similarity to Pfam domain: PF00646 (F-box), Score=28.7, E-value=4.3e-05, N=1	197	39
5098	AF006010	Homo sapiens	progesterone induced protein	174	86
5099	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	119	55
5100	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	132	82
5101	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	159	77
5102	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	99	70
5103	J02459	bacteriophage lambda	J (tail:host specificity;1132)	485	96
5104	J02459	bacteriophage lambda	H (tail component;853)	823	98
5105	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	106	42
5106	AF130089	Homo sapiens	PRO2550	121	35
5107	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	135	81
5108	P92219	Homo sapiens (human)	CR1 protein.	123	88
5109	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	83	78
5110	U41751	Mus musculus	EI24	560	83
5111	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	69
5112	AF130089	Homo sapiens	PRO2550	164	88
5113	G03084	Homo sapiens	Human secreted protein, SEQ ID NO: 7165.	160	72
5114	AF052831	Trypanosoma cruzi	unknown	107	70
5115	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna; complete virion genome.	128	68
5116	X55684	Lycopersicon esculentum	extensin (class I)	60	29
5117	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	124	64
5118	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	115	60
5119	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	112	79
5120	X65718	Prunus dulcis	extensin	94	33
5121	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	100
5122	AJ007714	Homo sapiens	lysine-ketoglutarate reductase /saccharopine dehydrogenase	154	96
5123	AJ007714	Homo sapiens	lysine-ketoglutarate reductase /saccharopine dehydrogenase	158	80
5124	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	109	44
5125	AF130089	Homo sapiens	PRO2550	112	46
5126	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	129	60
5127	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	99	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5128	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	143	57
5129	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	140	55
5130	J02459	bacteriophage lambda	H (tail component;853)	378	100
5131	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	123	78
5132	J04088	Homo sapiens	DNA topoisomerase II (EC 5.99.1.3)	163	96
5133	AL132841	Caenorhabditis elegans	Y15E3A.3	147	85
5134	D90827	Escherichia coli	Serine/Threonine protein phosphatase (EC 3.1.3.16).	329	46
5135	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	159	62
5136	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	161	91
5137	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	136	96
5138	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	129	67
5139	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	93	31
5140	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	141	46
5141	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	166	67
5142	AF003535	Homo sapiens	ORF2-like protein	168	50
5143	AF259792	Homo sapiens	SWI1Lbeta protein	684	98
5144	Y36203	Homo sapiens	Human secreted protein #75.	130	63
5145	AF130089	Homo sapiens	PRO2550	151	76
5146	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	52
5147	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	129	85
5148	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	101	67
5149	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	118	56
5150	AF130051	Homo sapiens	PRO0898	80	72
5151	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene preoduct.	165	63
5152	X56832	Homo sapiens	muscle specific enolase	573	90
5153	X76930	Homo sapiens	hepatocyte nuclear factor 4	544	91
5154	U12919	Mus musculus	adenylyl cyclase type VII	156	75
5155	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	91	76
5156	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	133	50
5157	Y08387	Homo sapiens	mu-adaptin-related protein 2	252	86
5158	R13556	Homo sapiens	Protein encoded downstream of hhcm_M oncoprotein.	126	66
5159	AF090942	Homo sapiens	PRO0657	139	77
5160	AF090942	Homo sapiens	PRO0657	120	70
5161	D67066	Bos taurus	N-WASP	135	42
5162	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	115	73
5163	AF044496	Canis familiaris	acidic ribosomal phosphoprotein P0	112	78
5164	W48351	Homo sapiens	Human breast cancer related protein	106	58

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCRB2.		
5165	AJ250095	Bordetella bronchiseptica	pertactin (P.68)	119	64
5166	U96411	Mus musculus	otogelin; MLEMP	609	90
5167	AF116238	Homo sapiens	pseudouridine synthase 1	237	87
5168	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	151	78
5169	AL050342	Homo sapiens	dJ655K7.1 (novel protein)	263	100
5170	AK024455	Homo sapiens	FLJ00047 protein	177	72
5171	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	94	100
5172	L38908	Nicotiana tabacum	extensin	101	47
5173	AF055904	Myxococcus xanthus	unknown	107	36
5174	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	143	59
5175	Y00337	Homo sapiens	Human secreted protein encoded by gene 81.	123	86
5176	AJ010957	Hippopotamus amphibius	NADH1	212	90
5177	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	84	76
5178	U83280	Leishmania donovani	39 kDa antigen	128	90
5179	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	183	45
5180	L27428	Homo sapiens	reverse transcriptase	106	46
5181	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	144	45
5182	R83119	Homo sapiens	Human cisplatin resistance protein.	142	96
5183	R95330	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 1TU).	475	71
5184	AF090930	Homo sapiens	PRO0478	121	57
5185	AF193613	Homo sapiens	cell recognition molecule Caspr2	338	50
5186	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	102	36
5187	AL031118	Homo sapiens	dJ153G14.3 (novel C2H2 type Zinc Finger protein)	465	62
5188	AF183144	Mus musculus	left-right dynein	199	83
5189	J02459	bacteriophage lambda	J (tail:host specificity;1132)	748	95
5190	AF193613	Homo sapiens	cell recognition molecule Caspr2	229	50
5191	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	135	65
5192	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	84
5193	Y00311	Homo sapiens	Human secreted protein encoded by gene 54.	112	49
5194	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	126	56
5195	AF104261	Mus musculus	Pax transcription activation domain interacting protein PTP	487	72
5196	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	132	65
5197	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	130	80
5198	X55777	Homo sapiens	52kD protein	106	30
5199	AF092170	Homo sapiens	polycystic kidney disease 2 related	122	91

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			protein		
5200	AF092170	Homo sapiens	polycystic kidney disease 2 related protein	138	96
5201	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	107	67
5202	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	81
5203	R95913	Homo sapiens	Neural thread protein.	96	61
5204	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	83	55
5205	AF319476	Homo sapiens	GKAP42	705	100
5206	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	78	62
5207	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	119	75
5208	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	166	50
5209	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	139	39
5210	AF090931	Homo sapiens	PRO0483	94	90
5211	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	114	74
5212	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	116	70
5213	U53209	Homo sapiens	transformer-2 alpha	124	95
5214	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	130	58
5215	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	151	49
5216	L26953	Homo sapiens	chromosomal protein	95	52
5217	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	66
5218	AF220264	Homo sapiens	MOST-1	151	65
5219	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	125	53
5220	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	138	65
5221	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	129	66
5222	AF194537	Homo sapiens	NAG13	120	60
5223	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	115	60
5224	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	144	58
5225	AF000996	Homo sapiens	ubiquitous TPR motif, Y isoform	164	70
5226	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	125	73
5227	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	164	69
5228	M34451	Caenorhabditis elegans	collagen (rol-6)	100	41
5229	X16396	Homo sapiens	precursor polypeptide (AA -29 to 315)	306	88
5230	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	112	69
5231	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	157	75
5232	D86982	Homo sapiens	similar to human ankyrin 1(S08275)	201	100
5233	AF116712	Homo sapiens	PRO2738	135	49
5234	AL049758	Homo sapiens	dI437M21.1 (novel protein)	184	70

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5235	AB014527	Homo sapiens	KIAA0627 protein	164	100
5236	AF194537	Homo sapiens	NAG13	183	64
5237	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene preduct.	170	43
5238	AF135439	Mus musculus	formin binding protein 11	230	100
5239	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	137	69
5240	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	168	63
5241	AF116661	Homo sapiens	PRO1438	152	58
5242	L27428	Homo sapiens	reverse transcriptase	193	53
5243	AF130089	Homo sapiens	PRO2550	141	60
5244	AF118086	Homo sapiens	PRO1992	135	71
5245	AJ228863	Mus musculus	CLIP-115	195	97
5246	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	81
5247	AC007887	Arabidopsis thaliana	F1504.29	76	93
5248	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	151	75
5249	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	66
5250	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	136	70
5251	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	80
5252	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	54
5253	AF090944	Homo sapiens	PRO0663	177	62
5254	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	132	57
5255	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	129	74
5256	D38112	Homo sapiens	NADH dehydrogenase subunit 2	157	91
5257	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	160	78
5258	U16296	Homo sapiens	TIAM1 protein	133	100
5259	AL160371	Leishmania major	probable (bhv-6) u1102, variant a DNA, complete virion genome	92	93
5260	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	324	78
5261	AK024455	Homo sapiens	FLJ00047 protein	100	50
5262	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	217	100
5263	AB047600	Macaca fascicularis	hypothetical protein	125	57
5264	U83246	Homo sapiens	copine I	199	86
5265	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	150	72
5266	U91329	Homo sapiens	kinesin-like motor protein KIF1C	132	93
5267	J00672	Oryctolagus cuniculus	beta-myosin	109	100
5268	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	74	43
5269	AF119851	Homo sapiens	PRO1722	96	61
5270	AF090930	Homo sapiens	PRO0478	113	91
5271	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	123	62
5272	B01372	Homo sapiens	Neuron-associated protein.	122	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5273	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	116	78
5274	AF090931	Homo sapiens	PRO0483	144	67
5275	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	117	68
5276	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	111	58
5277	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	147	67
5278	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	67
5279	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	69
5280	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	196	45
5281	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	115	73
5282	A18812	Brassica napus	extensin	120	38
5283	Z68747	Homo sapiens	imogen 38	291	75
5284	X77816	Rattus norvegicus	PR-Vbeta1	97	37
5285	AF130089	Homo sapiens	PRO2550	181	73
5286	AF130089	Homo sapiens	PRO2550	147	67
5287	AF090942	Homo sapiens	PRO0657	90	50
5288	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	116	74
5289	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	143	64
5290	D86972	Homo sapiens	similar to E.coli hypothetical 29.6 KD protein(P1:YIGW_ECOLI)	111	100
5291	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	145	57
5292	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	131	65
5293	Y08061	Homo sapiens	Human c-myb protein fragment.	213	76
5294	AF090895	Homo sapiens	PRO0117	134	52
5295	AF017635	Homo sapiens	DCHT	145	100
5296	G02558	Homo sapiens	Human secreted protein, SEQ ID NO: 6639.	136	60
5297	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	118	67
5298	AK024455	Homo sapiens	FLJ00047 protein	67	80
5299	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	164	75
5300	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	129	55
5301	R14643	Homo sapiens	Gamma interferon receptor.	107	82
5302	V00662	Homo sapiens	URF 4 (NADH dehydrogenase subunit)	238	90
5303	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	205	68
5304	AF130089	Homo sapiens	PRO2550	100	77
5305	R13556	Homo sapiens	Protein encoded downstream of hbc_M oncoprotein.	117	44
5306	X92485	Plasmodium vivax	pva1	128	61
5307	G02597	Homo sapiens	Human secreted protein, SEQ ID NO: 6678.	77	57
5308	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	140	42
5309	Y91577	Homo sapiens	Human secreted protein sequence	489	78

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			encoded by gene 2 SEQ ID NO:250.		
5310	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	138	65
5311	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	129	65
5312	AF119851	Homo sapiens	PRO1722	97	65
5313	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	160	90
5314	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	113	81
5315	AF071310	Mus musculus	OPA-containing protein 1	228	53
5316	AF090942	Homo sapiens	PRO0657	162	70
5317	U83303	Homo sapiens	line-1 reverse transcriptase	109	83
5318	AF090894	Homo sapiens	PRO0113	125	63
5319	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	129	66
5320	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	130	75
5321	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	138	81
5322	L27428	Homo sapiens	reverse transcriptase	139	52
5323	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	109	83
5324	AF118082	Homo sapiens	PRO1902	107	70
5325	M81321	Macaca fascicularis	proline-rich protein	114	37
5326	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	112	79
5327	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	99	72
5328	AF090930	Homo sapiens	PRO0478	152	73
5329	L27428	Homo sapiens	reverse transcriptase	267	65
5330	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	140	82
5331	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	164	54
5332	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	135	52
5333	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	124	76
5334	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	97	56
5335	AP000060	Aeropyrum pernix	103aa long hypothetical protein	71	50
5336	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	75
5337	Z93784	Homo sapiens	dJ398C22.1 (novel protein, ortholog of mouse brain protein E46)	280	68
5338	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	132	64
5339	AF210651	Homo sapiens	NAG18	160	56
5340	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	133	80
5341	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	151	75
5342	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	105	50
5343	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	103	75
5344	G03021	Homo sapiens	Human secreted protein, SEQ ID NO:	132	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7102.		
5345	Y87103	Homo sapiens	Human secreted protein sequence SEQ ID NO:142.	92	48
5346	AL121891	Homo sapiens	dJ1187M17.2 (KIAA0552 protein)	148	43
5347	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	130	33
5348	AF090944	Homo sapiens	PRO0663	205	72
5349	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	135	57
5350	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	101	37
5351	AF265578	Homo sapiens	orphan neurotransmitter transporter NTT5	121	39
5352	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	105	75
5353	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	167	69
5354	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSIW18.	97	60
5355	G00590	Homo sapiens	Human secreted protein, SEQ ID NO: 4671.	113	80
5356	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	123	67
5357	W88609	Homo sapiens	Secreted protein encoded by gene 76 clone HKIXL73.	94	79
5358	AC004450	Arabidopsis thaliana	putative extensin	110	37
5359	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	79
5360	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	199	74
5361	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	174	97
5362	AB017437	Gallus gallus	avens	98	44
5363	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	93
5364	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	181	70
5365	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	159	68
5366	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	94	60
5367	X52022	Homo sapiens	collagen type VI, alpha 3 chain	150	33
5368	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	120	77
5369	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	145	75
5370	X97675	Homo sapiens	plakophilin 2b	170	85
5371	AF130079	Homo sapiens	PRO2852	103	95
5372	L26953	Homo sapiens	chromosomal protein	117	54
5373	AF210651	Homo sapiens	NAG18	137	67
5374	Y30681	Homo sapiens	Splice variant ZAP-1B protein of the human tumor suppressor gene ZAP-1.	106	76
5375	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	109	70
5376	AL109819	Arabidopsis thaliana	extensin-like protein	123	34
5377	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	127	79
5378	AF036170	Dictyostelium	homeobox-containing protein Wariar	93	83

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		discoideum			
5379	AF130089	Homo sapiens	PRO2550	134	75
5380	AF161384	Homo sapiens	HSPC266	663	96
5381	AF130051	Homo sapiens	PRO0898	147	77
5382	AF090944	Homo sapiens	PRO0663	118	83
5383	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	129	55
5384	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	110	68
5385	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	53
5386	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	145	96
5387	U54788	Mus musculus	Wiskott-Aldrich Syndrome Protein	108	51
5388	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	104	89
5389	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	70
5390	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	103	72
5391	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	119	85
5392	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	120	65
5393	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	131	78
5394	G01552	Homo sapiens	Human secreted protein, SEQ ID NO: 5633.	159	90
5395	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	110	65
5396	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	85	59
5397	X86681	Homo sapiens	HNP36 protein	248	71
5398	L27428	Homo sapiens	reverse transcriptase	133	62
5399	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	132	54
5400	AL080196	Homo sapiens	hypothetical protein	164	96
5401	D38112	Homo sapiens	NADH dehydrogenase subunit 5	119	75
5402	AF090944	Homo sapiens	PRO0663	99	64
5403	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	93	58
5404	U42471	Mus musculus	Wiskott-Aldrich Syndrome protein homolog	103	37
5405	W05278	Homo sapiens	Tumour necrosis factor-related gene product CL6.5.40.	137	80
5406	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	102	69
5407	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	102	69
5408	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	142	69
5409	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	139	63
5410	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	65	47
5411	AF181626	Drosophila melanogaster	BcDNA.GH03694	171	53
5412	U93565	Homo sapiens	putative p150	195	70
5413	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	170	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5414	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	126	61
5415	X83572	Homo sapiens	ARSD	133	100
5416	D86853	Catharanthus roseus	extensin	113	41
5417	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	139	60
5418	G03472	Homo sapiens	Human secreted protein, SEQ ID NO: 7553.	175	77
5419	R32010	Homo sapiens	Rp15-TIA-1.	140	83
5420	D67066	Bos taurus	N-WASP	153	41
5421	U42391	Homo sapiens	myosin-IXb	203	100
5422	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	116	74
5423	AF220264	Homo sapiens	MOST-1	94	78
5424	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	128	63
5425	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	131	57
5426	AF130089	Homo sapiens	PRO2550	120	58
5427	Z70204	Caenorhabditis elegans	contains similarity to Pfam domain: PF00628 (PHD-finger), Score=63.1, E-value=1.9e-15, N=1-cDNA EST EMBL:T00556 comes from this gene-cDNA EST yk344f7.5 comes from this gene	131	55
5428	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	158	51
5429	AF130089	Homo sapiens	PRO2550	112	73
5430	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	161	52
5431	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	131	72
5432	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	152	79
5433	AF090942	Homo sapiens	PRO0657	109	67
5434	AE003588	Drosophila melanogaster	CG2839 gene product	141	50
5435	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	154	79
5436	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	128	41
5437	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	143	63
5438	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	117	84
5439	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	112	76
5440	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	42
5441	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	124	64
5442	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	193	56
5443	X07495	Homo sapiens	translated region (AA 1-264)	108	41
5444	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	135	62
5445	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	130	41
5446	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	136	71

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5447	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	123	62
5448	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	101	45
5449	U13866	unidentified cloning vector	non-functional lacZ alpha peptide	106	57
5450	X01469	Plasmodium lophurae	histidine-rich protein	162	56
5451	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	130	88
5452	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	155	68
5453	AF119900	Homo sapiens	PRO2822	162	63
5454	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	120	51
5455	AC007204	Homo sapiens	BC273239.1	1485	69
5456	L27428	Homo sapiens	reverse transcriptase	122	41
5457	M18094	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	141	39
5458	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	118	68
5459	AF090930	Homo sapiens	PRO0478	144	64
5460	AF130089	Homo sapiens	PRO2550	124	60
5461	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	135	69
5462	X97675	Homo sapiens	plakophilin 2b	103	72
5463	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	137	69
5464	AF229067	Homo sapiens	PADI-H protein	146	65
5465	AF116715	Homo sapiens	PRO2829	83	71
5466	AF090930	Homo sapiens	PRO0478	146	52
5467	U93574	Homo sapiens	putative p150	203	52
5468	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	89	50
5469	AF191838	Homo sapiens	TANK binding kinase TBK1	121	95
5470	AF130079	Homo sapiens	PRO2852	146	69
5471	AF090944	Homo sapiens	PRO0663	90	66
5472	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	106	63
5473	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	127	60
5474	AF064553	Mus musculus	NSD1 protein	269	100
5475	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	132	65
5476	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	130	86
5477	U11271	Homo sapiens	thromboxane A2 receptor	118	67
5478	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	143	60
5479	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	113	75
5480	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	119	74
5481	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	103	85
5482	AF238235	Entamoeba histolytica	diaphanous protein	108	35
5483	AF090930	Homo sapiens	PRO0478	120	55
5484	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5485	M61883	Sus scrofa	apomucin	252	55
5486	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	107	77
5487	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	110	46
5488	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	88	62
5489	AF025467	Caenorhabditis elegans	contains similarity to drosophila DNA-binding protein K10 (NID:g8148)	124	47
5490	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	220	71
5491	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	195	65
5492	M76546	Helianthus annuus	hydroxyproline-rich protein	116	38
5493	AF118086	Homo sapiens	PRO1992	135	82
5494	AF090930	Homo sapiens	PRO0478	105	74
5495	Y94451	Homo sapiens	Human inflammation associated protein #8.	170	61
5496	G03465	Homo sapiens	Human secreted protein, SEQ ID NO: 7546.	72	65
5497	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	152	78
5498	X56123	Mus musculus	talin	594	88
5499	AL035652	Homo sapiens	dJ1J6.1 (topoisomerase (DNA) I)	105	86
5500	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
5501	Y45389	Homo sapiens	Human secreted protein fragment encoded from gene 31.	161	93
5502	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	119	60
5503	X03145	Homo sapiens	pot. ORF I	215	79
5504	AF240630	Mus musculus	IQ motif containing GTPase activating protein 1	180	61
5505	AL390212	Homo sapiens	dJ29M10B.1.2 (protein kinase C binding protein 1 (isoform 2))	1282	93
5506	AF118086	Homo sapiens	PRO1992	146	61
5507	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	116	74
5508	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	165	50
5509	D38112	Homo sapiens	NADH dehydrogenase subunit 5	211	95
5510	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	114	69
5511	AF090944	Homo sapiens	PRO0663	125	58
5512	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	125	53
5513	Y36156	Homo sapiens	Human secreted protein #28.	110	68
5514	AF118086	Homo sapiens	PRO1992	128	76
5515	Z22866	Mus musculus	skelemin	218	95
5516	Z22866	Mus musculus	skelemin	218	95
5517	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	127	71
5518	AL133380	Homo sapiens	dJ862P8.3 (Similar to MAP3K10 (mitogen-activated protein kinase kinase kinase 10))	603	77
5519	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	187	78
5520	AF090901	Homo sapiens	PRO0195	115	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5521	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	180	53
5522	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	155	73
5523	W90847	Homo sapiens	Human lymphocyte targeted peptide #15.	149	100
5524	X97675	Homo sapiens	plakophilin 2b	153	70
5525	D37793	Mus musculus	synaptotagminII/IP4BP	651	84
5526	M32319	Homo sapiens	HLA protein allele B51	754	94
5527	AF130051	Homo sapiens	PRO0898	93	64
5528	X92485	Plasmodium vivax	pva1	88	66
5529	AJ131890	Homo sapiens	DNA polymerase lambda	205	100
5530	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	132	68
5531	Y02926	Homo sapiens	Fragment of human secreted protein encoded by gene 101.	87	59
5532	AF090931	Homo sapiens	PRO0483	133	75
5533	AF090942	Homo sapiens	PRO0657	122	66
5534	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	145	56
5535	D38112	Homo sapiens	NADH dehydrogenase subunit 5	569	91
5536	K02401	Homo sapiens	chorionic somatomammotropin	375	98
5537	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	136	68
5538	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	130	44
5539	S62928	Homo sapiens	PRBIM protein precursor	104	40
5540	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	127	70
5541	AE000463	Escherichia coli K12	putative glycosidase	254	100
5542	J02459	bacteriophage lambda	H (tail component;853)	761	100
5543	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICEL) protein sequence.	119	58
5544	U59185	Homo sapiens	putative monocarboxylate transporter	233	87
5545	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	187	65
5546	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	556	84
5547	X92485	Plasmodium vivax	pva1	110	67
5548	AB023233	Homo sapiens	KIAA1016 protein	246	97
5549	U16359	Rattus norvegicus	nitric oxide synthase	95	64
5550	AC002044	Homo sapiens	Alpha-fetoprotein enhancer binding protein (3' partial)	111	38
5551	AF026802	Homo sapiens	alpha-3 type IX collagen	117	47
5552	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	85	88
5553	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	91	88
5554	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	104	71
5555	AF130089	Homo sapiens	PRO2550	172	86
5556	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	105	72
5557	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	160	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5558	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	131	68
5559	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	112	67
5560	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	159	73
5561	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	141	67
5562	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	150	71
5563	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	146	80
5564	AF090942	Homo sapiens	PRO0657	157	73
5565	M64793	Rattus norvegicus	salivary proline-rich protein	169	43
5566	AL035526	Arabidopsis thaliana	extensin-like protein	103	40
5567	AF130089	Homo sapiens	PRO2550	132	67
5568	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	129	83
5569	X67337	Homo sapiens	Human pre-mRNA cleavage factor I 68 kDa subunit	153	42
5570	AF068266	Homo sapiens	EHT protein	169	91
5571	W48927	Homo sapiens	Schwannomin-binding protein C-terminal fragment.	113	42
5572	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	112	68
5573	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	122	71
5574	L20450	Mus musculus	DNA-binding protein	283	61
5575	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	95
5576	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	140	71
5577	Y20648	Homo sapiens	Human neurofilament-L wild type protein fragment 38.	66	37
5578	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	112	41
5579	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	142	74
5580	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	142	77
5581	AF153606	Homo sapiens	angiopoietin-related protein	737	95
5582	AF090930	Homo sapiens	PRO0478	149	77
5583	X52493	Glycine max	DNA-directed RNA polymerase	140	46
5584	M76546	Helianthus annuus	hydroxyproline-rich protein	101	51
5585	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	66	47
5586	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	130	72
5587	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	148	56
5588	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	148	66
5589	AC006014	Homo sapiens	similar to KIAA0618 and nuclear envelope protein POM 121; alternatively spliced product; similar to PID:g3327050 and P52591 (PID:g1709213)	108	84
5590	R13556	Homo sapiens	Protein encoded downstream of hhc M	122	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			oncoprotein.		
5591	AB001684	Chlorella vulgaris	ORF74	61	47
5592	AF090930	Homo sapiens	PRO0478	123	70
5593	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	120	57
5594	W80406	Homo sapiens	A secreted protein encoded by clone dh40.3.	124	59
5595	L26953	Homo sapiens	chromosomal protein	116	62
5596	L26953	Homo sapiens	chromosomal protein	115	67
5597	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	157	55
5598	Y71213	Homo sapiens	Human irritable bowel disease related polypeptide IMX39.	131	44
5599	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	125	45
5600	AF130089	Homo sapiens	PRO2550	142	62
5601	AY014404	Homo sapiens	kinesin-like protein RBKIN2	297	98
5602	AF210651	Homo sapiens	NAG18	113	71
5603	AF090931	Homo sapiens	PRO0483	129	71
5604	X01060	Homo sapiens	put. transferrin receptor (aa 1-760)	226	80
5605	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	455	75
5606	M64793	Rattus norvegicus	salivary proline-rich protein	119	42
5607	A31039	Nicotiana glauca	PRP3	92	36
5608	AF090944	Homo sapiens	PRO0663	147	64
5609	G00552	Homo sapiens	Human secreted protein, SEQ ID NO: 4633.	64	46
5610	X01065	Cairina moschata	histone H5	88	40
5611	U03413	Dictyostelium discoideum	calcium binding protein	104	40
5612	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	144	37
5613	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	127	65
5614	G01218	Homo sapiens	Human secreted protein, SEQ ID NO: 5299.	196	97
5615	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	122	68
5616	AB029309	Homo sapiens	Npw38-binding protein NpwBP	312	78
5617	X03145	Homo sapiens	pot. ORF III	101	80
5618	AF090930	Homo sapiens	PRO0478	159	78
5619	D88461	Rattus rattus	N-WASP	107	40
5620	W48927	Homo sapiens	Schwannomin-binding protein C-terminal fragment.	104	38
5621	Y36156	Homo sapiens	Human secreted protein #28.	134	50
5622	AF090894	Homo sapiens	PRO0113	119	65
5623	AF130089	Homo sapiens	PRO2550	130	69
5624	AF130089	Homo sapiens	PRO2550	140	78
5625	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	162	49
5626	AF130089	Homo sapiens	PRO2550	152	80
5627	AF151837	Homo sapiens	CGI-79 protein	127	78
5628	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	122	84
5629	AJ237981	Vitis vinifera	putative proline-rich cell wall protein	93	50
5630	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	110	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5631	AF130089	Homo sapiens	PRO2550	151	62
5632	U47661	Lupinus luteus	proline-rich protein PRP2 precursor	67	28
5633	Y08061	Homo sapiens	Human c-myb protein fragment.	93	61
5634	AL133215	Homo sapiens	bA108L7.6 (semaphorin 4G (sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain))	323	100
5635	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	138	67
5636	AF090942	Homo sapiens	PRO0657	184	67
5637	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	95	80
5638	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	139	83
5639	AF119900	Homo sapiens	PRO2822	143	62
5640	AL390114	Leishmania major	extremely cysteine/valine rich protein	151	61
5641	Y36243	Homo sapiens	Human secreted protein encoded by gene 20.	118	72
5642	AF090895	Homo sapiens	PRO0117	140	56
5643	Y51611	Homo sapiens	Human HSGT1 protein.	611	96
5644	AF162692	Homo sapiens	putative voltage-gated calcium channel gamma-4 subunit	172	73
5645	Z98883	Homo sapiens	c407A10.1 (GPII (N-acetylglucosaminyl transferase component))	229	100
5646	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	117	80
5647	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	159	78
5648	AF217517	Homo sapiens	uncharacterized bone marrow protein BM041	97	49
5649	AF210651	Homo sapiens	NAG18	149	58
5650	AK000385	Homo sapiens	unnamed protein product	125	36
5651	U02313	Mus musculus	protein kinase	143	96
5652	AF090944	Homo sapiens	PRO0663	95	43
5653	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	131	61
5654	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	100	58
5655	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	157	70
5656	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	100
5657	M64793	Rattus norvegicus	salivary proline-rich protein	123	47
5658	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	159	46
5659	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	163	60
5660	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	105	46
5661	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	125	71
5662	D87744	Mus musculus	DRPLA protein	89	40
5663	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	65
5664	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	87	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5665	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	71	44
5666	A18812	Brassica napus	extensin	98	41
5667	AF130089	Homo sapiens	PRO2550	128	74
5668	AF090930	Homo sapiens	PRO0478	136	54
5669	X52634	Mus musculus	t1m protein	169	59
5670	AB001684	Chlorella vulgaris	ORF49b	70	62
5671	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	153	66
5672	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	123	78
5673	AF090942	Homo sapiens	PRO0657	150	60
5674	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	123	78
5675	M22332	Homo sapiens	unknown protein	121	43
5676	W40353	Homo sapiens	Human unspecified protein from US5702907.	128	72
5677	AL049868	Homo sapiens	dJ927M24.2 (KIAA1219)	403	95
5678	U31785	Human papillomavirus type 36	putative	103	44
5679	G02409	Homo sapiens	Human secreted protein, SEQ ID NO: 6490.	101	73
5680	AF068229	Homo sapiens	lysyl hydroxylase 3	148	92
5681	Y00358	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	209	81
5682	AB008515	Homo sapiens	RanBPM	142	100
5683	AB010692	Arabidopsis thaliana	contains similarity to endo-beta-N-acetylglucosaminidase-gene_id:K18I2.3.27	148	45
5684	J02459	bacteriophage lambda	J (tail:host specificity;1132)	746	100
5685	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	194	69
5686	AB049054	Homo sapiens	brain link protein-1	160	100
5687	AF229067	Homo sapiens	PADI-H protein	144	68
5688	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	120	70
5689	AP001313	Arabidopsis thaliana	contains similarity to pherophorin-gene_id:T5M7.14	106	47
5690	M76976	Drosophila melanogaster	dorsal-ventral patterning protein	167	37
5691	L24559	Homo sapiens	DNA polymerase alpha	175	100
5692	AF071777	Mus musculus	IRE1	604	85
5693	AF061741	Homo sapiens	retinal short-chain dehydrogenase/reductase retSDR1	704	99
5694	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	178	66
5695	AF092092	Homo sapiens	AP-3 adaptor complex mu3A subunit	653	92
5696	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	106	86
5697	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	132	75
5698	M64793	Rattus norvegicus	salivary proline-rich protein	116	40
5699	AF161361	Homo sapiens	HSPC098	128	56
5700	U21123	Drosophila melanogaster	ena polypeptide	106	57

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5701	AF119901	Homo sapiens	PRO2831	113	76
5702	K02576	Homo sapiens	salivary proline-rich protein 1	101	49
5703	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	105	78
5704	AF130089	Homo sapiens	PRO2550	122	75
5705	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	136	72
5706	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	113	75
5707	AF229067	Homo sapiens	PADI-H protein	134	81
5708	W40353	Homo sapiens	Human unspecified protein from US5702907.	129	65
5709	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	137	81
5710	AK024455	Homo sapiens	FLJ00047 protein	108	54
5711	Y76381	Homo sapiens	Fragment of human secreted protein encoded by gene 75.	247	93
5712	AF116715	Homo sapiens	PRO2829	118	75
5713	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	154	71
5714	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	141	79
5715	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	91	80
5716	AF090944	Homo sapiens	PRO0663	136	56
5717	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	153	65
5718	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	109	70
5719	AF130089	Homo sapiens	PRO2550	140	86
5720	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	144	67
5721	AF130089	Homo sapiens	PRO2550	146	58
5722	AF118086	Homo sapiens	PRO1992	130	58
5723	D21230	Homo sapiens	alpha 1(XV) collagen chain	390	78
5724	AL049569	Homo sapiens	dJ37C10.5 (KIAA0445)	266	93
5725	X04412	Homo sapiens	plasma gelsolin	761	95
5726	A21853	synthetic construct	serine protease inhibitor	206	100
5727	Y16610	Homo sapiens	paraplegin	218	95
5728	AF132021	Homo sapiens	myosin X	613	87
5729	AL163491	Arabidopsis thaliana	putative protein	236	46
5730	L19704	Homo sapiens	alternative first exon	561	86
5731	D83703	Homo sapiens	peroxisome assembly factor-2	240	84
5732	AB007936	Homo sapiens	KIAA0467 protein	189	77
5733	L38622	Mus musculus	mSin3B gene product	280	94
5734	AF051944	Gallus gallus	Xin	460	68
5735	B07857	Homo sapiens	Amino acid sequence of Smad1 interactor protein clone S1+12-5.	172	67
5736	Z14020	Nicotiana tabacum	Pistil extensin like protein, partial CDS only	105	44
5737	L17308	Gossypium hirsutum	proline-rich cell wall protein	145	34
5738	Y76141	Homo sapiens	Human secreted protein encoded by gene 18.	109	72
5739	AF178534	Homo sapiens	talin	583	82
5740	D13435	Homo sapiens	PIG-F	143	100
5741	AC005578	Homo sapiens	F20887_1, partial CDS	584	86

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5742	AC005578	Homo sapiens	F20887_1, partial CDS	470	85
5743	AJ010479	Homo sapiens	kinesin-like protein	102	23
5744	M19419	Mus musculus	proline-rich salivary protein	107	42
5745	U29377	Caenorhabditis elegans	lysine-rich	97	44
5746	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	90	67
5747	D84223	Homo sapiens	leucyl tRNA synthetase	165	83
5748	J04990	Homo sapiens	cathepsin G	165	100
5749	Y36203	Homo sapiens	Human secreted protein #75.	122	77
5750	V00488	Homo sapiens	alpha globin	181	94
5751	M18642	Homo sapiens	lactoferrin	122	96
5752	W15286	Homo sapiens	Soluble type I insulin-like growth factor receptor.	481	87
5753	Z98595	Schizosaccharomyces pombe	coronin-like protein	192	38
5754	AL035683	Homo sapiens	dJ1063B2.1 (Beta-1,4-galactosyltransferase)	239	100
5755	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	170	61
5756	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	105	61
5757	D49490	Homo sapiens	protein disulfide isomerase-related protein (PDIR)	669	96
5758	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	175	72
5759	X61451	Mus musculus	F41	130	100
5760	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	91	61
5761	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	130	76
5762	AF130079	Homo sapiens	PRO2852	126	61
5763	AF143946	Homo sapiens	transcriptional activator SRCAP	288	40
5764	M80627	Homo sapiens	helix-loop-helix protein	127	88
5765	AF038007	Homo sapiens	FIC1	290	47
5766	G01881	Homo sapiens	Human secreted protein, SEQ ID NO: 5962.	427	97
5767	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	172	75
5768	B12884	Homo sapiens	Human alpha-bradeion protein sequence.	465	70
5769	Y66645	Homo sapiens	Membrane-bound protein PRO1310.	347	100
5770	AB033168	Mus musculus	nuclear protein ZAP	115	39
5771	X83575	Cricetulus griseus	CHO1 antigen	113	57
5772	AF135422	Homo sapiens	GDP-mannose pyrophosphorylase A	764	91
5773	L38644	Rattus norvegicus	karyopherin beta	121	68
5774	AB020746	Arabidopsis thaliana	protein kinase-like protein	107	33
5775	Y17920	Drosophila melanogaster	CALO protein	128	31
5776	AK000309	Homo sapiens	unnamed protein product	988	98
5777	AF010404	Homo sapiens	ALR	469	97
5778	AB045131	Homo sapiens	NADPH-dependent retinol dehydrogenase/reductase	126	92
5779	AF197927	Homo sapiens	AF5q31 protein	530	95
5780	X79198	Homo sapiens	host cell factor	119	74
5781	X69838	Homo sapiens	G9a	157	41

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5782	Y94450	Homo sapiens	Human inflammation associated protein #7.	227	44
5783	AF216804	Rattus norvegicus	nuclear matrix transcription factor	1539	98
5784	R06463	Homo sapiens	Derived protein of clone ICA13 (ATCC 40553).	638	91
5785	AF000149	Mus musculus	ATP-binding cassette transporter	292	41
5786	D89974	Homo sapiens	glycosylphosphatidyl inositol-anchored protein GPI-80	490	78
5787	AF090942	Homo sapiens	PRO0657	132	63
5788	X56932	Homo sapiens	23 kD highly basic protein	286	100
5789	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	114	63
5790	Z97211	Schizosaccharomyces pombe	kinesin-like protein	346	60
5791	AF134707	Homo sapiens	disintegrin and metalloproteinase domain 19	144	95
5792	Z19550	Homo sapiens	N-acetylglucosaminide beta-1,6-N-acetylglucosaminyltransferase	547	76
5793	AF090930	Homo sapiens	PRO0478	103	80
5794	Y59879	Homo sapiens	Human normal uterus tissue derived protein 42.	407	97
5795	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	149	72
5796	AF077208	Homo sapiens	HSPC022	682	100
5797	D42138	Homo sapiens	PIG-B	597	86
5798	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	151	75
5799	M29487	Homo sapiens	integrin alpha subunit precursor	160	80
5800	D87438	Homo sapiens	Similar to a C.elegans protein in cosmid C14H10	354	85
5801	W54282	Homo sapiens	Protein sequence of the di-alpha haemoglobin gene contained in pSS1.	195	97
5802	AB030176	Homo sapiens	peptidylarginine deiminase type II	107	100
5803	D38441	Homo sapiens	acylamino acid-releasing enzyme	156	71
5804	Y55939	Homo sapiens	Human GEK2 protein.	157	96
5805	X89626	Bos taurus	240K protein of rod photoreceptor cng-channel	92	42
5806	AC006963	Homo sapiens	similar to Kelch proteins; similar to BAA77027 (PID:g4650844)	177	38
5807	Y86275	Homo sapiens	Human secreted protein HSRGW16, SEQ ID NO:190.	436	77
5808	D50577	Mesocricetus auratus	carboxylesterase precursor	328	55
5809	AF272148	Homo sapiens	KRAB zinc finger protein	593	68
5810	W57260	Homo sapiens	Human semaphorin Y.	651	96
5811	AF202893	Mus musculus	Kif21b	491	82
5812	AC006963	Homo sapiens	similar to Kelch proteins; similar to BAA77027 (PID:g4650844)	219	38
5813	AB017114	Homo sapiens	AD 3	142	57
5814	AC007954	Homo sapiens	unknown	678	100
5815	AF124726	Homo sapiens	acinusL	790	93
5816	AB015330	Homo sapiens	HRIHFB2007	167	36
5817	AB020684	Homo sapiens	KIAA0877 protein	699	57
5818	Z15025	Homo sapiens	Bat2	172	49
5819	X95761	Mus musculus	new:Rhobin	549	79
5820	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	166	68
5821	X55126	Mus musculus	Zfp-29	633	93
5822	Y99366	Homo sapiens	Human PRO1475 (UNQ746) amino	452	98

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			acid sequence SEQ ID NO:88.		
5823	AB040801	Homo sapiens	SREB3	611	95
5824	M27878	Homo sapiens	DNA binding protein	462	64
5825	Y13620	Homo sapiens	BCL9	140	40
5826	AF152510	Homo sapiens	protocadherin gamma A3 short form protein	525	92
5827	M23451	Achlya ambisexualis	steroid receptor	337	61
5828	AJ011305	Homo sapiens	guanine nucleotide exchange factor, delta subunit	132	100
5829	Y85565	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/2) sequence.	710	96
5830	U03277	Drosophila melanogaster	cloned by ability to arrest the cell cycle when expressed in the fission yeast Schizosaccharomyces pombe	258	46
5831	AF193342	Mus musculus	GCN2alpha	469	85
5832	AF279265	Homo sapiens	putative anion transporter 1	240	91
5833	AK023998	Homo sapiens	unnamed protein product	687	97
5834	AK023998	Homo sapiens	unnamed protein product	674	96
5835	AF071059	Mus musculus	zinc finger RNA binding protein	243	100
5836	AF178534	Homo sapiens	talin	463	62
5837	J04569	Homo sapiens	glial fibrillary acidic protein	102	55
5838	AF068625	Mus musculus	DNA cytosine-5 methyltransferase 3A	130	89
5839	AB037739	Homo sapiens	KIAA1318 protein	644	97
5840	R86865	Homo sapiens	Human protocadherin pc3.	660	96
5841	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	117	84
5842	X51486	Gallus gallus	cNFI-A1 protein (AA 1-522)	590	86
5843	U65785	Homo sapiens	150 kDa oxygen-regulated protein ORP150	200	95
5844	U16126	Homo sapiens	EAA4	679	97
5845	AL035071	Homo sapiens	dJ1085F17.1.3 (ortholog of mouse DNMT3B (DNA Cytosine-5 Methyltransferase 3B3) (isoform 3))	717	100
5846	Y13620	Homo sapiens	BCL9	505	81
5847	AC004812	Homo sapiens	similar to human HsGCN1 U77700 (PID:g2282576); similar to yeast translation activator GCN1 (PID:g462168)	316	100
5848	M77246	Rattus norvegicus	beta-chain clathrin associated protein complex AP-2	611	89
5849	AF007833	Homo sapiens	kruppel-related zinc finger protein hcKrox	569	79
5850	AF056617	Homo sapiens	BWSCR2 associated zinc-finger protein BAZ1	175	32
5851	D38548	Homo sapiens	The ha0936 gene product is novel.	409	65
5852	G00528	Homo sapiens	Human secreted protein, SEQ ID NO: 4609.	166	55
5853	D87071	Homo sapiens	similar to C.elegans protein encoded in cosmid T20D3 (Z68220).	188	76
5854	M64979	Homo sapiens	glial factor-1	557	83
5855	G01480	Homo sapiens	Human secreted protein, SEQ ID NO: 5561.	400	82
5856	X06345	Xenopus laevis	lamin A (AA 1-265)	109	68
5857	AB017499	Oryctolagus cuniculus	Lipoprotein Receptor Related Protein 5	196	40
5858	D43633	Oryzias latipes	G protein-coupled seven-transmembrane receptor	281	50
5859	AF067165	Homo sapiens	zinc finger protein 3	669	87

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5860	AL031118	Homo sapiens	dJ153G14.3 (novel C2H2 type Zinc Finger protein)	218	38
5861	U13897	Homo sapiens	homolog of Drosophila discs large protein, isoform 1	130	35
5862	M74002	Homo sapiens	arginine-rich nuclear protein	80	23
5863	X67855	Oryctolagus cuniculus	brain calcium channel BII-1	147	66
5864	U35376	Homo sapiens	repressor transcriptional factor	475	67
5865	AF251038	Homo sapiens	GAP-like protein	325	58
5866	L46815	Mus musculus	DNA binding protein Rc	409	66
5867	S68944	Rattus sp.	Na+/Cl(-)-dependent neurotransmitter transporter	582	95
5868	X97675	Homo sapiens	plakophilin 2b	159	93
5869	AF152478	Homo sapiens	protocadherin alpha 13 short form protein	680	100
5870	AF118082	Homo sapiens	PRO1902	130	48
5871	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	149	49
5872	A61971	unidentified	MCSP	621	82
5873	Z54206	Bovine herpesvirus 1	UL51	104	33
5874	AF069765	Homo sapiens	signal recognition particle 72	674	97
5875	AF179428	Homo sapiens	DNA polymerase zeta catalytic subunit variant 1	692	100
5876	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	119	48
5877	Y94990	Homo sapiens	Human secreted protein vb21_1, SEQ ID NO:20.	446	98
5878	L08811	Drosophila melanogaster	adherin	264	42
5879	D86983	Homo sapiens	similar to D.melanogaster peroxidase(U11052)	429	100
5880	AF152508	Homo sapiens	protocadherin gamma A2 short form protein	664	100
5881	AF152508	Homo sapiens	protocadherin gamma A2 short form protein	660	98
5882	AF190018	Mus musculus	K-Cl cotransporter	199	88
5883	AB023229	Homo sapiens	KIAA1012 protein	107	83
5884	U53420	Rattus norvegicus	sodium-calcium exchanger form 3	595	98
5885	AF039019	Homo sapiens	zinc finger DNA binding protein 89 kDa	608	92
5886	AF207661	Homo sapiens	sodium bicarbonate cotransporter-like protein	701	100
5887	AF130051	Homo sapiens	PRO0898	115	74
5888	AF152508	Homo sapiens	protocadherin gamma A2 short form protein	720	100
5889	AF251079	Homo sapiens	heptacellular carcinoma novel gene-3 protein	741	98
5890	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	118	51
5891	AF157326	Homo sapiens	TIP120 protein	571	85
5892	AF129170	Homo sapiens	apolipoprotein E receptor 2	630	99
5893	X05561	Homo sapiens	alpha-1 chain precursor (AA -27 to 917) (2953 is 2nd base in codon)	197	45
5894	AJ238374	Homo sapiens	putative protein TH1	641	96
5895	X63526	Homo sapiens	homologue to elongation factor 1-gamma from A.salina	709	97
5896	Y11651	Homo sapiens	phosphate cyclase	521	80

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5897	Y18448	Homo sapiens	Bassoon protein	681	100
5898	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	138	63
5899	AF152473	Homo sapiens	protocadherin alpha C1 short form protein	733	100
5900	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	133	66
5901	R06463	Homo sapiens	Derived protein of clone ICA13 (ATCC 40553).	522	99
5902	X12928	Triticum aestivum	HMW glutenin subunit 5 (AA 1-848)	169	25
5903	X61048	Hydra sp.	mini-collagen	88	33
5904	AF118082	Homo sapiens	PRO1902	247	60
5905	A00279	synthetic construct	Human serum albumin	482	84
5906	T14722_cd1	Homo sapiens	01-DEC-1992 Human CD27 antigen cDNA.	431	94
5907	Y73475	Homo sapiens	Human secreted protein clone ye7_1 protein sequence SEQ ID NO:172.	271	94
5908	AF175265	Homo sapiens	vacuolar sorting protein 35	645	92
5909	Y12713	Mus musculus	Pro-Pol-dUTPase polypeptide	125	50
5910	G00360	Homo sapiens	Human secreted protein, SEQ ID NO: 4441.	115	58
5911	W88762	Homo sapiens	Polypeptide fragment encoded by gene 20.	152	50
5912	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	154	68
5913	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	209	71
5914	AB046048	Macaca fascicularis	unnamed portein product	143	49
5915	S80644	Sus scrofa	glutaminase; GA	338	85
5916	AF213393	Mus musculus	ATP-binding cassette protein	92	95
5917	X52622	Mus musculus	integrase (409 AA)	425	45
5918	U49973	Homo sapiens	ORF2: function unknown	114	64
5919	S71403	Mus musculus	m33-A isoform	120	42
5920	AF090931	Homo sapiens	PRO0483	94	89
5921	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	99	36
5922	AJ006770	Cicer arietinum	extensin	96	32
5923	AJ250193	Mus musculus	muscle protein 637	730	72
5924	AF229067	Homo sapiens	PADI-H protein	278	63
5925	X92485	Plasmodium vivax	pva1	99	50
5926	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	84	66
5927	AF130089	Homo sapiens	PRO2550	114	64
5928	J00126	Homo sapiens	MHC factor B	237	100
5929	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	251	79
5930	AF090895	Homo sapiens	PRO0117	63	62
5931	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	147	37
5932	U83857	Homo sapiens	Aac11	209	80
5933	AF068294	Homo sapiens	HDCMB45P	144	50
5934	X92485	Plasmodium vivax	pva1	135	69
5935	L07545	Leishmania tarentolae	A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to	127	36

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gel compression		
5936	R95913	Homo sapiens	Neural thread protein.	276	58
5937	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	130	65
5938	Y16781	Homo sapiens	Human secreted protein (clone bh157_7).	1258	100
5939	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	167	68
5940	U93570	Homo sapiens	putative p150	103	41
5941	G03472	Homo sapiens	Human secreted protein, SEQ ID NO: 7553.	189	74
5942	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	110	47
5943	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	122	90
5944	AF130089	Homo sapiens	PRO2550	101	48
5945	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	162	86
5946	X92485	Plasmodium vivax	pval	104	70
5947	M29622	Mus musculus	open reading frame 2	132	64
5948	AF130089	Homo sapiens	PRO2550	131	60
5949	AF130089	Homo sapiens	PRO2550	151	60
5950	AF130079	Homo sapiens	PRO2852	117	52
5951	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	185	62
5952	U49973	Homo sapiens	ORF2: function unknown	160	62
5953	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	145	55
5954	M22332	Homo sapiens	unknown protein	169	41
5955	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	133	72
5956	U70935	Peromyscus maniculatus	reverse transcriptase	100	36
5957	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	105	63
5958	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	112	48
5959	Z49944	Canis familiaris	CDC42 GTP-binding protein	120	40
5960	AF118082	Homo sapiens	PRO1902	158	61
5961	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	91	65
5962	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	121	62
5963	AF118082	Homo sapiens	PRO1902	113	60
5964	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	65
5965	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	120	57
5966	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	306	77
5967	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7305.	80	41
5968	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	109	75
5969	AF119855	Homo sapiens	PRO1847	162	72
5970	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	146	46
5971	M19155	Plasmodium falciparum	S-antigen precursor	122	37
5972	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	121	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
5973	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	107	60
5974	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	83	68
5975	G00497	Homo sapiens	Human secreted protein, SEQ ID NO: 4578.	111	47
5976	U93572	Homo sapiens	p40	112	33
5977	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	107	58
5978	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	120	70
5979	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	106	54
5980	M64792	Rattus norvegicus	salivary proline-rich protein	105	31
5981	X66285	Mus musculus	HC1 ORF	86	36
5982	M64793	Rattus norvegicus	salivary proline-rich protein	110	43
5983	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	131	60
5984	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	110	60
5985	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	107	47
5986	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	160	77
5987	AF130079	Homo sapiens	PRO2852	272	77
5988	U93570	Homo sapiens	putative p150	87	46
5989	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	202	89
5990	AF130089	Homo sapiens	PRO2550	238	74
5991	AF118082	Homo sapiens	PRO1902	119	41
5992	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	60
5993	L27428	Homo sapiens	reverse transcriptase	110	60
5994	S79410	Mus musculus	nuclear localization signal binding protein	98	45
5995	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	90
5996	X58236	Homo sapiens	36/8-8 fusion protein with epitope for anti-lectin antibody	78	68
5997	Y08061	Homo sapiens	Human c-myb protein fragment.	97	63
5998	AP002460	Arabidopsis thaliana	gene_id:F1D9,26~unknown protein	100	38
5999	U93569	Homo sapiens	p40	103	52
6000	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	100	63
6001	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	121	51
6002	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	115	64
6003	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	105	40
6004	AF130089	Homo sapiens	PRO2550	122	63
6005	R95913	Homo sapiens	Neural thread protein.	235	56
6006	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	173	58
6007	X92485	Plasmodium vivax	pval	96	53

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6008	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	236	62
6009	Y17832	Human endogenous retrovirus K	env protein	103	66
6010	AF119900	Homo sapiens	PRO2822	91	50
6011	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	155	55
6012	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	201	91
6013	Y36156	Homo sapiens	Human secreted protein #28.	253	70
6014	AF130079	Homo sapiens	PRO2852	119	36
6015	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	137	63
6016	AF130089	Homo sapiens	PRO2550	110	40
6017	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	142	57
6018	AF116661	Homo sapiens	PRO1438	147	69
6019	AF130089	Homo sapiens	PRO2550	169	71
6020	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	208	60
6021	AF119851	Homo sapiens	PRO1722	147	65
6022	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	139	47
6023	AF130089	Homo sapiens	PRO2550	142	66
6024	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	91	76
6025	M18093	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	103	48
6026	D86853	Catharanthus roseus	extensin	97	46
6027	AF130089	Homo sapiens	PRO2550	95	47
6028	X92485	Plasmodium vivax	pval	102	61
6029	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	149	53
6030	G00643	Homo sapiens	Human secreted protein, SEQ ID NO: 4724.	96	76
6031	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	144	44
6032	AB011483	Arabidopsis thaliana	contains similarity to root cap protein-gene_id:MUF9.16	117	37
6033	X92485	Plasmodium vivax	pval	85	40
6034	AF118082	Homo sapiens	PRO1902	112	58
6035	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	121	59
6036	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	65
6037	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	107	71
6038	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	140	65
6039	X92485	Plasmodium vivax	pval	84	78
6040	AF130051	Homo sapiens	PRO0898	107	69
6041	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	113	58
6042	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	209	75

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6043	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	98	56
6044	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	126	43
6045	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	65
6046	Y36156	Homo sapiens	Human secreted protein #28.	93	62
6047	AF130079	Homo sapiens	PRO2852	205	83
6048	R95913	Homo sapiens	Neural thread protein.	148	45
6049	D38112	Homo sapiens	cytochrome c oxidase subunit 3	234	86
6050	D38113	Pan troglodytes	NADH dehydrogenase subunit 5	403	61
6051	M11901	Rattus norvegicus	proline-rich salivary protein	96	42
6052	AF130089	Homo sapiens	PRO2550	348	73
6053	AF119851	Homo sapiens	PRO1722	109	68
6054	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	168	66
6055	AF161356	Homo sapiens	HSPC093	83	58
6056	X92485	Plasmodium vivax	pval	155	55
6057	G04000	Homo sapiens	Human secreted protein, SEQ ID NO: 8081.	520	100
6058	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	148	65
6059	W03626	Homo sapiens	Human thyrotropin GPR N-terminal sequence.	163	53
6060	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	300	68
6061	U93563	Homo sapiens	putative p150	389	37
6062	AF090895	Homo sapiens	PRO0117	66	78
6063	X92485	Plasmodium vivax	pval	110	86
6064	AF130089	Homo sapiens	PRO2550	166	71
6065	M22332	Homo sapiens	unknown protein	188	48
6066	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	101	52
6067	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	107	41
6068	G00528	Homo sapiens	Human secreted protein, SEQ ID NO: 4609.	99	75
6069	M22332	Homo sapiens	unknown protein	153	80
6070	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	109	82
6071	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	123	73
6072	AF130079	Homo sapiens	PRO2852	143	60
6073	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	132	55
6074	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	158	65
6075	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	157	68
6076	AF116712	Homo sapiens	PRO2738	102	41
6077	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	102	69
6078	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	109	60
6079	AF118082	Homo sapiens	PRO1902	196	61
6080	AF118082	Homo sapiens	PRO1902	165	59
6081	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	153	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6082	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	188	71
6083	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	109	60
6084	V00672	Pan troglodytes	reading frame protein 4	185	85
6085	AF130051	Homo sapiens	PRO0898	307	67
6086	AF130079	Homo sapiens	PRO2852	96	72
6087	D38112	Homo sapiens	NADH dehydrogenase subunit 1	171	82
6088	AF090895	Homo sapiens	PRO0117	110	67
6089	U43360	Peromyscus maniculatus	reverse transcriptase	101	46
6090	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	114	36
6091	Y02925	Homo sapiens	Fragment of human secreted protein encoded by gene 101.	111	46
6092	G00366	Homo sapiens	Human secreted protein, SEQ ID NO: 4447.	137	54
6093	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	176	59
6094	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	199	50
6095	U70935	Peromyscus maniculatus	reverse transcriptase	216	44
6096	X71442	Rattus norvegicus	ORF 1; putative	109	53
6097	AF119855	Homo sapiens	PRO1847	88	71
6098	L27428	Homo sapiens	reverse transcriptase	104	45
6099	AF090895	Homo sapiens	PRO0117	119	61
6100	U52077	Homo sapiens	mariner transposase	295	67
6101	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	156	73
6102	M22332	Homo sapiens	unknown protein	132	44
6103	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	140	56
6104	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	64	47
6105	M64791	Rattus norvegicus	salivary proline-rich protein	123	41
6106	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	139	69
6107	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	75	58
6108	AF068294	Homo sapiens	HDCMB45P	141	43
6109	AF118086	Homo sapiens	PRO1992	160	77
6110	M63819	Plasmodium falciparum	malaria antigen	62	46
6111	G03093	Homo sapiens	Human secreted protein, SEQ ID NO: 7174.	130	65
6112	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	282	70
6113	AF119851	Homo sapiens	PRO1722	156	63
6114	AF229067	Homo sapiens	PADI-H protein	134	48
6115	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	143	44
6116	D38112	Homo sapiens	cytochrome c oxidase subunit 1	201	80
6117	AF285567	Microcebus griseorufus	cytochrome b	185	58
6118	AL138636	Arabidopsis thaliana	extensin precursor-like protein	141	28
6119	X92485	Plasmodium vivax	pva1	165	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6120	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	164	84
6121	M13100	Rattus norvegicus	unknown protein	176	49
6122	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	177	50
6123	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	83	71
6124	AF130089	Homo sapiens	PRO2550	109	85
6125	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	129	70
6126	AF144054	Homo sapiens	apoptosis related protein APR-4	149	54
6127	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	138	70
6128	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	236	77
6129	U93564	Homo sapiens	putative p150	152	53
6130	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	129	57
6131	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	127	56
6132	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	195	67
6133	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	92	42
6134	AK000496	Homo sapiens	unnamed protein product	158	59
6135	X92485	Plasmodium vivax	pval	146	55
6136	Y36203	Homo sapiens	Human secreted protein #75.	133	57
6137	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	148	68
6138	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	106	36
6139	AF130051	Homo sapiens	PRO0898	77	65
6140	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	222	73
6141	AF119851	Homo sapiens	PRO1722	107	63
6142	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	117	57
6143	R95913	Homo sapiens	Neural thread protein.	114	70
6144	AF068294	Homo sapiens	HDCMB45P	123	56
6145	AF118082	Homo sapiens	PRO1902	113	32
6146	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	105	42
6147	Y30731	Homo sapiens	Amino acid sequence of a human secreted protein.	938	100
6148	U93574	Homo sapiens	putative p150	99	47
6149	AF090894	Homo sapiens	PRO0113	145	55
6150	AF130079	Homo sapiens	PRO2852	125	49
6151	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	91	48
6152	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7305.	89	60
6153	Y01398	Homo sapiens	Secreted protein encoded by gene 16 clone HNGFR75.	90	82
6154	X92485	Plasmodium vivax	pval	110	42
6155	S79410	Mus musculus	nuclear localization signal binding protein	118	48
6156	G01495	Homo sapiens	Human secreted protein, SEQ ID NO:	170	89

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			5576.		
6157	X92485	Plasmodium vivax	pval	157	52
6158	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	108	58
6159	U36794	Coturnix japonica	Cytochrome oxidase subunit I	70	73
6160	AF118082	Homo sapiens	PRO1902	119	66
6161	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	154	64
6162	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	107	37
6163	M22332	Homo sapiens	unknown protein	125	51
6164	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	163	59
6165	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	235	64
6166	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	108	36
6167	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	139	59
6168	D38112	Homo sapiens	cytochrome c oxidase subunit 3	562	85
6169	D38113	Pan troglodytes	NADH dehydrogenase subunit 4	296	51
6170	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	95	85
6171	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	329	73
6172	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	136	53
6173	K03206	Homo sapiens	salivary proline-rich protein precursor	104	36
6174	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	136	75
6175	U93569	Homo sapiens	p40	192	40
6176	X70343	Nicotiana glauca	extensin	94	35
6177	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	140	81
6178	AF119855	Homo sapiens	PRO1847	114	43
6179	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	98	68
6180	X03717	Homo sapiens	pot. unidentified reading frame	112	42
6181	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	204	76
6182	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	110	73
6183	D38112	Homo sapiens	NADH dehydrogenase subunit 3	240	88
6184	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	102	47
6185	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	99	49
6186	Y36156	Homo sapiens	Human secreted protein #28.	196	75
6187	AF169387	Mus musculus	alpha 3 collagen IV	111	38
6188	AF194537	Homo sapiens	NAG13	138	37
6189	X91836	Vigna unguiculata	extensin class 1 protein	167	33
6190	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	175	63
6191	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	123	46
6192	X92485	Plasmodium	pval	115	54

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
6193	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	345	65
6194	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	82	54
6195	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	214	56
6196	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	87	79
6197	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	118	41
6198	X62691	Homo sapiens	ribosomal protein homologous to yeast S24	215	73
6199	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	100	46
6200	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	143	73
6201	V00711	Mus musculus	cytochrome oxidase I	435	92
6202	U93572	Homo sapiens	putative p150	99	63
6203	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	109	45
6204	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	163	39
6205	M15530	Homo sapiens	B-cell growth factor	113	60
6206	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	128	50
6207	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	181	72
6208	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	123	75
6209	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	120	62
6210	Y36203	Homo sapiens	Human secreted protein #75.	169	81
6211	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	130	52
6212	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	123	48
6213	D86854	Catharanthus roseus	extensin	120	44
6214	G02754	Homo sapiens	Human secreted protein, SEQ ID NO: 6835.	117	100
6215	W33698	Homo sapiens	AL-2-long (AL-2l) protein.	262	100
6216	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	102	62
6217	U40342	Mus musculus	ninein	77	72
6218	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	174	49
6219	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	234	54
6220	X92485	Plasmodium vivax	pva1	107	46
6221	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	104	40
6222	X86029	Vigna unguiculata	extensin-like protein	140	35
6223	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	216	59
6224	AF068294	Homo sapiens	HDCMB45P	164	60
6225	Y50797	Homo sapiens	Human calmodulin/NEF protein binding inhibitor 2.	135	50
6226	AE003859	Xylella fastidiosa	hypothetical protein	139	41
6227	G00637	Homo sapiens	Human secreted protein, SEQ ID NO:	103	58

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4718.		
6228	AF130089	Homo sapiens	PRO2550	126	43
6229	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	190	88
6230	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	124	77
6231	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	174	79
6232	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	168	78
6233	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	164	67
6234	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	288	94
6235	AF113685	Homo sapiens	PRO0974	114	46
6236	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	150	40
6237	AL096844	Streptomyces coelicolor A3(2)	putative integral membrane protein	88	39
6238	AF130079	Homo sapiens	PRO2852	167	50
6239	AF130089	Homo sapiens	PRO2550	365	85
6240	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	212	69
6241	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	102	54
6242	AF109907	Homo sapiens	S164	146	90
6243	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	132	52
6244	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	138	52
6245	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	113	32
6246	AF130089	Homo sapiens	PRO2550	154	77
6247	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	91	40
6248	Y36156	Homo sapiens	Human secreted protein #28.	105	43
6249	AF116661	Homo sapiens	PRO1438	131	60
6250	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	132	68
6251	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	70	73
6252	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	106	42
6253	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	247	68
6254	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	75
6255	V00662	Homo sapiens	cytochrome oxidase I	355	78
6256	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	131	65
6257	D38112	Homo sapiens	cytochrome c oxidase subunit I	176	86
6258	AF061340	Artibeus jamaicensis	cytochrome c oxidase subunit III	308	63
6259	AF016099	Mus musculus	endonuclease/reverse transcriptase	114	43
6260	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	179	78
6261	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	192	75
6262	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	146	71
6263	U09116	Homo sapiens	ORF1, encodes a 40 kDa product	114	37
6264	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	88	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6265	U49974	Homo sapiens	mariner transposase	206	71
6266	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	71	72
6267	AF097473	Mus musculus	ORF1	86	40
6268	X70343	Nicotiana sylvestris	extensin	95	33
6269	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	94	84
6270	L27428	Homo sapiens	reverse transcriptase	132	48
6271	AF118082	Homo sapiens	PRO1902	153	53
6272	U12690	Homo sapiens	cytochrome oxidase subunit II	222	91
6273	X03145	Homo sapiens	pot. ORF V	89	35
6274	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	90	71
6275	U93572	Homo sapiens	p40	83	43
6276	AF058700	Bos taurus	ubiquitin-S27a fusion protein	148	70
6277	AF016099	Mus musculus	endonuclease/reverse transcriptase	96	65
6278	AF130079	Homo sapiens	PRO2852	179	86
6279	AF161356	Homo sapiens	HSPC093	108	57
6280	X77816	Rattus norvegicus	PR-Vbeta1	109	51
6281	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	130	58
6282	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	81	69
6283	AF068294	Homo sapiens	HDCMB45P	98	37
6284	AF116715	Homo sapiens	PRO2829	112	68
6285	X92485	Plasmodium vivax	pva1	92	64
6286	U93570	Homo sapiens	p40	90	38
6287	Y36203	Homo sapiens	Human secreted protein #75.	225	62
6288	Z11793	Homo sapiens	selenoprotein P	220	65
6289	X92485	Plasmodium vivax	pva1	125	70
6290	X52634	Mus musculus	tlm protein	114	45
6291	M11901	Rattus norvegicus	proline-rich salivary protein	94	36
6292	AF116661	Homo sapiens	PRO1438	144	46
6293	L27428	Homo sapiens	reverse transcriptase	81	44
6294	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	152	51
6295	AF130089	Homo sapiens	PRO2550	137	35
6296	L27428	Homo sapiens	reverse transcriptase	96	53
6297	B01372	Homo sapiens	Neuron-associated protein.	134	69
6298	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	110	58
6299	AF130089	Homo sapiens	PRO2550	110	61
6300	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	136	63
6301	AF220264	Homo sapiens	MOST-1	172	90
6302	AF130079	Homo sapiens	PRO2852	311	71
6303	AF068294	Homo sapiens	HDCMB45P	136	53
6304	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	110	62
6305	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	113	45
6306	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	166	58

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6307	S85655	Homo sapiens	prohibitin	664	91
6308	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	155	64
6309	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	73
6310	AF119851	Homo sapiens	PRO1722	160	67
6311	L27428	Homo sapiens	reverse transcriptase	91	50
6312	AF130089	Homo sapiens	PRO2550	140	55
6313	AF130089	Homo sapiens	PRO2550	211	68
6314	X15917	Paramecium aurelia	ORF4 protein (AA 1-156)	97	38
6315	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	94	51
6316	Y36203	Homo sapiens	Human secreted protein #75.	124	65
6317	L27428	Homo sapiens	reverse transcriptase	117	56
6318	M11900	Mus musculus	15-kDa proline-rich salivary protein	105	41
6319	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	175	69
6320	U92673	Eurythenes sp. 'AUS-3F'	cytochrome oxidase I	59	37
6321	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	283	72
6322	AK000496	Homo sapiens	unnamed protein product	206	70
6323	AB047934	Macaca fascicularis	hypothetical protein	173	68
6324	AB023485	Mus musculus	transcription factor CA150b	131	43
6325	AF020262	Bos taurus	general protein transport factor p16	76	67
6326	U22376	Homo sapiens	alternatively spliced product using exon 13A	98	57
6327	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	115	60
6328	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	100	57
6329	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	115	67
6330	U43360	Peromyscus maniculatus	reverse transcriptase	82	63
6331	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	138	57
6332	K01664	Drosophila melanogaster	Bkm-like protein	112	37
6333	M69297	Homo sapiens	ORF 3	70	43
6334	U15647	Mus musculus	reverse transcriptase	146	53
6335	AF090894	Homo sapiens	PRO0113	107	48
6336	AF130089	Homo sapiens	PRO2550	359	75
6337	AJ271872	Nicotiana glauca	extensin	134	32
6338	AJ132694	Homo sapiens	small GTPase rac1b	99	100
6339	AF119851	Homo sapiens	PRO1722	123	60
6340	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	215	56
6341	U83774	Pernis apivorus	cytochrome oxidase I	193	80
6342	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	139	62
6343	X92485	Plasmodium vivax	pva1	104	81
6344	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	110	64
6345	U93572	Homo sapiens	p40	79	48
6346	X92485	Plasmodium	pva1	156	55

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
6347	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	104	85
6348	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	158	77
6349	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	89	64
6350	AF130089	Homo sapiens	PRO2550	187	69
6351	U56732	Rattus norvegicus	KRAB/zinc finger suppressor protein 1	161	64
6352	U70932	Peromyscus leucopus	reverse transcriptase	126	61
6353	X55687	Lycopersicon esculentum	extensin (class II)	89	44
6354	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	107	57
6355	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	88	76
6356	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	98	61
6357	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	165	51
6358	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	214	58
6359	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	75	88
6360	X07882	Homo sapiens	Po protein	151	47
6361	Z11592	Phytophthora parasitica	cytochrome c oxidase subunit 3	78	76
6362	AF090944	Homo sapiens	PRO0663	130	46
6363	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	117	39
6364	AF229067	Homo sapiens	PADI-H protein	155	75
6365	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	100	55
6366	AK024501	Homo sapiens	FLJ00110 protein	282	100
6367	AF118082	Homo sapiens	PRO1902	157	57
6368	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	151	63
6369	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	161	96
6370	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	124	63
6371	AF130079	Homo sapiens	PRO2852	297	77
6372	X92485	Plasmodium vivax	pval	129	42
6373	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	122	63
6374	AF119851	Homo sapiens	PRO1722	251	65
6375	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	139	73
6376	X70343	Nicotiana glauca	extensin	104	35
6377	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7305.	70	52
6378	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	97	69
6379	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	109	51
6380	Z38128	Mus musculus	histone H1	113	36
6381	U93573	Homo sapiens	p40	212	43

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6382	K02576	Homo sapiens	salivary proline-rich protein 1	109	40
6383	AL096744	Homo sapiens	hypothetical protein	164	49
6384	AF220264	Homo sapiens	MOST-1	119	56
6385	X92485	Plasmodium vivax	pval	108	65
6386	X53581	Rattus norvegicus	ORF4	148	36
6387	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	116	52
6388	M13100	Rattus norvegicus	unknown protein	119	48
6389	AB047948	Macaca fascicularis	hypothetical protein	80	33
6390	X53581	Rattus norvegicus	ORF4	139	55
6391	AK025947	Homo sapiens	unnamed protein product	166	52
6392	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	244	75
6393	M22332	Homo sapiens	unknown protein	166	39
6394	AF229067	Homo sapiens	PADI-H protein	128	59
6395	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	80	70
6396	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	95	44
6397	M26361	Mus musculus	LINE/Ig H-chain fusion protein	97	61
6398	AF118082	Homo sapiens	PRO1902	93	48
6399	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	116	89
6400	U93570	Homo sapiens	putative p150	88	43
6401	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	147	61
6402	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	77	56
6403	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	156	47
6404	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	155	56
6405	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	88	39
6406	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	84	68
6407	G00560	Homo sapiens	Human secreted protein, SEQ ID NO: 4641.	244	90
6408	L27428	Homo sapiens	reverse transcriptase	108	42
6409	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	136	58
6410	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	106	44
6411	U70935	Peromyscus maniculatus	reverse transcriptase	154	40
6412	AF090931	Homo sapiens	PRO0483	99	85
6413	AL031186	Homo sapiens	bK984G1.1 (supported by FGENES)	249	78
6414	AF130089	Homo sapiens	PRO2550	100	55
6415	AB047963	Macaca fascicularis	hypothetical protein	165	57
6416	M22332	Homo sapiens	unknown protein	111	42
6417	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	140	50
6418	AF016099	Mus musculus	endonuclease/reverse transcriptase	147	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6419	D38112	Homo sapiens	NADH dehydrogenase subunit 1	194	84
6420	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	144	81
6421	U49973	Homo sapiens	ORF2: function unknown--	91	62
6422	G02754	Homo sapiens	Human secreted protein, SEQ ID NO: 6835.	135	96
6423	AF072508	Homo sapiens	envelope protein	128	49
6424	AK000385	Homo sapiens	unnamed protein product	161	54
6425	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	148	54
6426	X92485	Plasmodium vivax	pval	103	75
6427	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	183	80
6428	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	97	46
6429	AF016099	Mus musculus	endonuclease/reverse transcriptase	100	51
6430	Y36203	Homo sapiens	Human secreted protein #75.	139	58
6431	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	112	47
6432	X92485	Plasmodium vivax	pval	83	72
6433	Y35984	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 233.	121	59
6434	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	66	43
6435	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	152	51
6436	D89501	Homo sapiens	similar to salivary proline-rich protein P-B	88	38
6437	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	113	58
6438	X99467	Medicago truncatula	ENOD20	110	37
6439	Y86574	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:491.	129	58
6440	X92485	Plasmodium vivax	pval	114	46
6441	AK024455	Homo sapiens	FLJ00047 protein	173	57
6442	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	85	51
6443	Y36203	Homo sapiens	Human secreted protein #75.	104	56
6444	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	138	50
6445	M24732	Homo sapiens	lamin-like protein	71	45
6446	AF119851	Homo sapiens	PRO1722	163	69
6447	AF126163	Homo sapiens	HHLA3 protein	98	53
6448	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	151	58
6449	AF200187	cercopithecine herpesvirus 15	EBNA2-like protein	125	38
6450	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	107	52
6451	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	114	54
6452	AF090942	Homo sapiens	PRO0657	129	65
6453	M19503	Homo sapiens	ORF1; putative	86	39
6455	X92485	Plasmodium vivax	pval	99	40

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6456	X86030	Vigna unguiculata	extensin-like protein	115	36
6457	Y08061	Homo sapiens	Human c-myc protein fragment.	113	61
6458	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	90	37
6459	AF119851	Homo sapiens	PRO1722	243	66
6460	J05497	Rattus norvegicus	snRNP-associated polypeptide N	101	31
6461	AF130089	Homo sapiens	PRO2550	183	76
6462	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	93	53
6463	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	122	72
6464	Y36156	Homo sapiens	Human secreted protein #28.	85	52
6465	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	120	40
6466	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	94	36
6467	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	96	58
6468	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	121	67
6469	X92485	Plasmodium vivax	pva1	89	72
6470	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	128	56
6471	AF130089	Homo sapiens	PRO2550	155	83
6472	U93569	Homo sapiens	putative p150	131	42
6473	AF130079	Homo sapiens	PRO2852	111	54
6474	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	115	51
6475	AF220264	Homo sapiens	MOST-1	111	58
6476	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	137	45
6477	AF016099	Mus musculus	endonuclease/reverse transcriptase	106	35
6478	X92485	Plasmodium vivax	pva1	220	55
6480	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	112	61
6481	U49973	Homo sapiens	ORF2: function unknown	96	42
6482	U15647	Mus musculus	reverse transcriptase	111	61
6483	X92485	Plasmodium vivax	pva1	181	49
6484	L27428	Homo sapiens	reverse transcriptase	135	50
6485	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	144	52
6486	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	174	63
6487	U93569	Homo sapiens	p40	176	53
6488	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	72	42
6489	L26953	Homo sapiens	chromosomal protein	93	33
6490	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	125	57
6491	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	155	70
6492	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	251	75
6493	U15647	Mus musculus	reverse transcriptase	100	40

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6494	AK027208	Homo sapiens	unnamed protein product	109	68
6495	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	52
6496	AF130089	Homo sapiens	PRO2550	230	69
6497	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	237	62
6498	AF090894	Homo sapiens	PRO0113	140	68
6499	Y03000	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	138	84
6500	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	123	69
6501	M69297	Homo sapiens	ORF 3	87	58
6502	M22332	Homo sapiens	unknown protein	81	44
6503	X92485	Plasmodium vivax	pval	111	52
6504	AF090895	Homo sapiens	PRO0117	131	60
6505	Y73932	Homo sapiens	Human prostate tumor EST fragment derived protein #119.	97	69
6506	U93568	Homo sapiens	putative p150	122	32
6507	X86029	Vigna unguiculata	extensin-like protein	177	32
6508	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	282	60
6509	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	142	61
6510	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	93	35
6511	U52077	Homo sapiens	mariner transposase	372	73
6512	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	81	50
6513	AF090928	Homo sapiens	PRO0470	97	39
6514	AF134827	Monodelphis domestica	small nuclear ribonucleoprotein B'	108	47
6515	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	82	44
6516	AF068754	Homo sapiens	heat shock factor binding protein 1 HSBP1	118	69
6517	AF130089	Homo sapiens	PRO2550	207	69
6518	M22332	Homo sapiens	unknown protein	154	55
6519	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	95	39
6520	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	65	37
6521	AK023563	Homo sapiens	unnamed protein product	268	58
6522	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	181	61
6523	AF210651	Homo sapiens	NAG18	85	85
6524	AF130079	Homo sapiens	PRO2852	127	51
6525	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	113	51
6526	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	85	62
6527	U42471	Mus musculus	Wiscott-Aldrich Syndrome protein homolog	115	48
6528	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	86	60
6529	R59842	Homo sapiens	ApoE4L1 protease.	92	58
6530	R59842	Homo sapiens	ApoE4L1 protease.	135	77
6531	W48351	Homo sapiens	Human breast cancer related protein	88	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCRB2.		
6532	AF119851	Homo sapiens	PRO1722	121	61
6533	AF063866	Melanoplus sanguinipes entomopoxvirus	ORF MSV233 hypothetical protein	85	35
6534	G02469	Homo sapiens	Human secreted protein, SEQ ID NO: 6550.	123	59
6535	R95913	Homo sapiens	Neural thread protein.	132	67
6536	AF130079	Homo sapiens	PRO2852	113	58
6537	AB047600	Macaca fascicularis	hypothetical protein	159	60
6538	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	279	68
6539	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	112	55
6540	AF130089	Homo sapiens	PRO2550	124	56
6541	U93574	Homo sapiens	putative p150	159	39
6542	AF118082	Homo sapiens	PRO1902	114	45
6543	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	78	50
6544	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	118	44
6545	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	138	62
6546	AF116661	Homo sapiens	PRO1438	162	59
6547	S62928	Homo sapiens	PRB1M protein precursor	116	48
6548	AB030192	Mus musculus	homologue of S70447 F1Fo-ATP synthase complex Fo membrane domain f subunit	174	63
6549	AK025116	Homo sapiens	unnamed protein product	136	56
6550	X92485	Plasmodium vivax	pva1	105	56
6551	AF130079	Homo sapiens	PRO2852	172	91
6552	U70935	Peromyscus maniculatus	reverse transcriptase	84	42
6553	S79410	Mus musculus	nuclear localization signal binding protein	100	55
6554	M76546	Helianthus annuus	hydroxyproline-rich protein	110	39
6555	AF130089	Homo sapiens	PRO2550	205	64
6556	AF130079	Homo sapiens	PRO2852	165	48
6557	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene preduct.	160	74
6558	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	133	49
6559	X92485	Plasmodium vivax	pva1	121	78
6560	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	76	45
6561	AF217374	Acanthaster planci	cytochrome oxidase subunit I	234	85
6562	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	61
6563	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	134	84
6564	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	66	47
6565	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	180	49

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6566	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	96	57
6567	X92485	Plasmodium vivax	pval	96	58
6568	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	103	73
6569	AF119851	Homo sapiens	PRO1722	81	60
6570	AF289098	Cladastis kentukea	ENOD2	110	36
6571	AF118086	Homo sapiens	PRO1992	115	65
6572	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	142	57
6573	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	89	41
6574	M22332	Homo sapiens	unknown protein	95	34
6575	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	98	64
6576	AK021848	Homo sapiens	unnamed protein product	131	41
6577	AF161356	Homo sapiens	HSPC093	155	57
6578	AF116909	Homo sapiens	unknown	75	76
6579	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	95	53
6580	AF130089	Homo sapiens	PRO2550	276	74
6581	K02576	Homo sapiens	salivary proline-rich protein 1	119	33
6582	U49973	Homo sapiens	ORF2: function unknown	94	62
6583	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	90	65
6584	AJ249395	Globodera pallida	NADH-ubiquinone oxidoreductase subunit 4	99	41
6585	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	75	62
6586	U49973	Homo sapiens	ORF2: function unknown	134	58
6587	Y08061	Homo sapiens	Human c-myb protein fragment.	112	47
6588	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	217	53
6589	K02576	Homo sapiens	salivary proline-rich protein 1	147	41
6590	U43627	Arabidopsis thaliana	extensin	103	31
6591	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	71	34
6592	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	177	66
6593	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	100	72
6594	M69297	Homo sapiens	ORF 3	137	43
6595	X68101	Rattus norvegicus	trg	372	89
6596	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	81	62
6597	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	99	43
6598	Z99714	Homo sapiens	bK1048E9.5 (novel protein)	1642	98
6599	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	162	59
6600	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	132	65
6601	AK000385	Homo sapiens	unnamed protein product	187	74
6602	AF130051	Homo sapiens	PRO0898	137	54
6603	S58722	Homo sapiens	X-linked retinopathy protein {C-	88	48

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			terminal, clone XEH.8c}		
6604	X61047	Hydra sp.	mini-collagen	116	45
6605	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	109	71
6606	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	212	66
6607	AF232673	Homo sapiens	B17 long form	1272	99
6608	AF118082	Homo sapiens	PRO1902	77	52
6609	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	132	74
6610	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	70	61
6611	Y36203	Homo sapiens	Human secreted protein #75.	140	62
6612	X92485	Plasmodium vivax	pval	157	72
6613	U52077	Homo sapiens	mariner transposase	260	67
6614	AF161392	Homo sapiens	HSPC274	138	45
6615	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	93	65
6616	AF119851	Homo sapiens	PRO1722	147	49
6617	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	101	63
6618	AL390114	Leishmania major	extremely cysteine/valine rich protein	117	39
6619	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	105	58
6620	U15647	Mus musculus	reverse transcriptase	106	38
6621	AF130089	Homo sapiens	PRO2550	171	52
6622	X92485	Plasmodium vivax	pval	139	44
6623	AF090895	Homo sapiens	PRO0117	161	58
6624	M63730	Homo sapiens	BPAG2	107	32
6625	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	183	61
6626	AF078860	Homo sapiens	PTD007	69	73
6627	AL080253	Arabidopsis thaliana	putative snRNP protein	101	37
6628	AK000385	Homo sapiens	unnamed protein product	140	57
6629	W60652	Homo sapiens	Human DVic-1 (alternative transcript).	218	51
6630	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	152	66
6631	AB046048	Macaca fascicularis	unnamed portein product	118	65
6632	X92485	Plasmodium vivax	pval	119	88
6633	X03145	Homo sapiens	pot. ORF V	98	39
6634	K02576	Homo sapiens	salivary proline-rich protein 1	165	41
6635	X59448	Drosophila melanogaster	dynammin	111	39
6636	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	162	50
6637	AF130089	Homo sapiens	PRO2550	141	75
6638	AF118082	Homo sapiens	PRO1902	108	63
6639	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	144	60
6640	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	104	47
6641	AF118082	Homo sapiens	PRO1902	121	53
6642	AF118082	Homo sapiens	PRO1902	195	68
6643	R95913	Homo sapiens	Neural thread protein.	212	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6644	AF090928	Homo sapiens	PRO0470	81	65
6645	AF130079	Homo sapiens	PRO2852	151	69
6646	AF003535	Homo sapiens	ORF2-like protein	140	35
6647	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	169	61
6648	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	100	42
6649	M15530	Homo sapiens	B-cell growth factor	121	76
6650	AF090942	Homo sapiens	PRO0657	119	53
6651	AF118082	Homo sapiens	PRO1902	130	52
6652	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	143	87
6653	AF130089	Homo sapiens	PRO2550	143	63
6654	AF119851	Homo sapiens	PRO1722	285	70
6655	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	103	75
6656	AF119855	Homo sapiens	PRO1847	61	60
6657	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	107	36
6658	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	84	61
6659	AF119851	Homo sapiens	PRO1722	177	54
6660	X92485	Plasmodium vivax	pva1	104	55
6661	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	116	57
6662	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	68
6663	L22029	Glycine max	hydroxyproline-rich glycoprotein	115	35
6664	D00570	Mus musculus	open reading frame (251 AA)	126	35
6665	AF130051	Homo sapiens	PRO0898	129	77
6666	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	108	42
6667	G02851	Homo sapiens	Human secreted protein, SEQ ID NO: 6932.	71	41
6668	AF130079	Homo sapiens	PRO2852	110	59
6669	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	113	66
6670	G00527	Homo sapiens	Human secreted protein, SEQ ID NO: 4608.	98	73
6671	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	80	51
6672	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	113	36
6673	V01201	Simian sarcoma virus	coding sequence of pol	143	47
6674	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	159	78
6675	G00648	Homo sapiens	Human secreted protein, SEQ ID NO: 4729.	64	56
6676	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	96	48
6677	AF130089	Homo sapiens	PRO2550	100	75
6678	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	94	68
6679	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	105	71
6680	G03812	Homo sapiens	Human secreted protein, SEQ ID NO: 7893.	218	53
6681	G00352	Homo sapiens	Human secreted protein, SEQ ID NO:	115	53

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4433.		
6682	AF161356	Homo sapiens	HSPC093	163	47
6683	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	78	72
6684	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	87	42
6685	S79410	Mus musculus	nuclear localization signal binding protein	98	43
6686	U93564	Homo sapiens	p40	96	41
6687	AF119855	Homo sapiens	PRO1847	137	67
6688	U52077	Homo sapiens	mariner transposase	268	81
6689	X92485	Plasmodium vivax	pva1	97	58
6690	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	133	56
6691	M63274	Plasmodium falciparum	malaria antigen	61	46
6692	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	147	80
6693	M11901	Rattus norvegicus	proline-rich salivary protein	115	40
6694	G02451	Homo sapiens	Human secreted protein, SEQ ID NO: 6532.	131	50
6695	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	174	66
6696	AF068294	Homo sapiens	HDCMB45P	154	59
6697	X55685	Lycopersicon esculentum	extensin (class I)	112	41
6698	M83293	Simian immunodeficiency virus	vpx protein	85	41
6699	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	169	88
6700	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	121	58
6701	AF118080	Homo sapiens	PRO1880	127	59
6702	X92485	Plasmodium vivax	pva1	106	58
6703	AF161356	Homo sapiens	HSPC093	155	53
6704	X92485	Plasmodium vivax	pva1	164	54
6705	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	172	59
6706	AK025326	Homo sapiens	unnamed protein product	146	50
6707	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	112	43
6708	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	119	71
6709	AF176531	Mus musculus	F-box protein FBX16	324	60
6710	X92485	Plasmodium vivax	pva1	96	64
6711	AF130089	Homo sapiens	PRO2550	203	67
6712	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	150	59
6713	AF090944	Homo sapiens	PRO0663	114	43
6714	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	110	47
6715	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	131	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6716	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	103	65
6717	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	115	46
6718	G01222	Homo sapiens	Human secreted protein, SEQ ID NO: 5303.	54	100
6719	Y36203	Homo sapiens	Human secreted protein #75.	129	78
6720	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	107	64
6721	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICEL) protein sequence.	130	61
6722	Y36203	Homo sapiens	Human secreted protein #75.	167	72
6723	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	116	46
6724	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	133	42
6725	U80761	Homo sapiens	CTG26 alternate open reading frame	88	76
6726	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	218	61
6727	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	399	81
6728	U01877	Homo sapiens	p300 protein	119	27
6729	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	107	51
6730	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	130	58
6731	X66285	Mus musculus	HC1 ORF	79	38
6732	K02576	Homo sapiens	salivary proline-rich protein 1	114	38
6733	AF057352	Homo sapiens	hepatocellular carcinoma autoantigen	148	81
6734	AF090895	Homo sapiens	PRO0117	152	57
6735	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	164	61
6736	X92485	Plasmodium vivax	pval	92	89
6737	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	112	49
6738	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	278	72
6739	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	191	47
6740	AF118082	Homo sapiens	PRO1902	83	49
6741	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	83	43
6742	Y36708	Homo sapiens	Fragment of human secreted protein encoded by gene 62.	71	64
6743	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	177	70
6744	Y91475	Homo sapiens	Human secreted protein sequence encoded by gene 25 SEQ ID NO:148.	159	50
6745	X92485	Plasmodium vivax	pval	112	39
6746	Z82268	Caenorhabditis elegans	predicted using Genefinder--contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=73.8, E-value=1.2e-18, N=2; PF01484 (Nematode cuticle collagen N-terminal domain), Score=37.5, E-value=1e-07, N=1--cDNA EST yk92f1.5 comes from this gene--cDNA EST yk55f6.5 comes from this gene--cDNA EST yk65b7.3 comes from this gene--cDNA EST	108	36

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			yk58f3.5 comes from this gene-cDNA EST yk72h5.5 comes from this gene-cDNA EST yk55c4.5 comes from this gene-cDNA EST yk58h1.5 comes from this gene-cDNA EST yk65a12.5 comes from this gene-cDNA EST yk94f4.5 comes from this gene		
6747	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	113	38
6748	R95913	Homo sapiens	Neural thread protein.	108	56
6749	U57747	Mus musculus	platelet-activating factor acetylhydrolase isoform Ib beta subunit	209	69
6750	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	159	65
6751	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	96	48
6752	AF090895	Homo sapiens	PRO0117	115	56
6753	AF217973	Homo sapiens	unknown	105	66
6754	AF119851	Homo sapiens	PRO1722	156	55
6755	AF119855	Homo sapiens	PRO1847	189	66
6756	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	163	55
6757	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	123	57
6758	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	156	70
6759	AF130051	Homo sapiens	PRO0898	98	68
6760	M36914	Zea mays	cell wall protein (put.); putative	75	28
6761	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	98	85
6762	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	88	62
6763	M19756	Homo sapiens	MHC HLA-Bw47 precursor	580	92
6764	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	115	52
6765	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	321	51
6766	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	124	59
6767	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	303	64
6768	AF061340	Artibeus jamaicensis	cytochrome c oxidase subunit II	213	67
6769	T71265_cd1	Homo sapiens	19-JAN-1996 Neuronal apoptosis inhibitor protein (NAIP) cDNA.	188	59
6770	B01390	Homo sapiens	Neuron-associated protein.	92	55
6771	AF017777	Drosophila melanogaster	la costa	114	50
6772	Z34955	Sus scrofa	protein phosphatase 2A 65 kDa regulatory subunit, alpha isoform	331	93
6773	X61296	Rattus norvegicus	open reading frame 2	101	37
6774	AL117345	Homo sapiens	dJ416F21.2 (novel protein)	639	91
6775	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	110	61
6776	AJ007798	Homo sapiens	stromal antigen 3, (STAG3)	238	76
6777	AB029065	Mus musculus	Ser/Thr kinase KKIAMRE-beta	165	66
6778	M37400	Homo sapiens	aspartate aminotransferase	208	68
6779	AF130089	Homo sapiens	PRO2550	127	52
6780	AF130079	Homo sapiens	PRO2852	332	81

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6781	AL049748	Homo sapiens	dJ41P2.2 (RNA binding motif protein 9 (isoform 1))	264	60
6782	L11007	Rattus norvegicus	cyclin-dependent kinase 4	239	75
6783	AF319938	Thermus thermophilus	competence factor ComEA	115	36
6784	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	119	44
6785	L16864	African swine fever virus	cd2 homologue	152	34
6786	Y36203	Homo sapiens	Human secreted protein #75.	99	44
6787	AF130087	Homo sapiens	PRO2411	172	65
6788	AF208846	Homo sapiens	BM-004	664	100
6789	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	90	83
6790	AP000059	Aeropyrum pernix	120aa long hypothetical protein	81	43
6791	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	53
6792	Y12961	Homo sapiens	Amino acid sequence of a human secreted peptide.	175	65
6793	Y73442	Homo sapiens	Human secreted protein clone ya66_1 protein sequence SEQ ID NO:106.	565	93
6794	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	136	50
6795	AC004022	Homo sapiens	serum paraoxonase/esterase 3	137	93
6796	AF009668	multiple sclerosis associated retrovirus	polyprotein	194	60
6797	R59842	Homo sapiens	ApoE4L1 protease.	121	92
6798	U88167	Caenorhabditis elegans	contains similarity to C2 domains	171	73
6799	AF293024	Homo sapiens	steroid receptor RNA activator isoform 1	767	97
6800	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	123	65
6801	B01203	Homo sapiens	Human GTPase associated protein-28.	313	87
6802	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	125	47
6803	AF078036	Homo sapiens	RelA associated inhibitor; NF-kappaB subunit p65 binding protein	1275	95
6804	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	131	53
6805	Y57946	Homo sapiens	Human transmembrane protein HTPN-70.	1128	100
6806	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	81	81
6807	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	129	52
6808	AB046048	Macaca fascicularis	unnamed protein product	273	63
6809	K02401	Homo sapiens	chorionic somatomammotropin	446	95
6810	AF130089	Homo sapiens	PRO2550	150	56
6811	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	123	65
6812	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	93	38
6813	AF090930	Homo sapiens	PRO0478	103	65
6814	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	138	54

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6815	B24423	Homo sapiens	Human PRO1244 protein sequence SEQ ID NO:193.	484	95
6816	M11901	Rattus norvegicus	proline-rich salivary protein	105	43
6817	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	96	56
6818	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	102	48
6819	U82303	Homo sapiens	unknown	105	57
6820	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	113	45
6821	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	97	39
6822	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	146	86
6823	U52077	Homo sapiens	mariner transposase	192	78
6824	AC004237	Homo sapiens	KIF3	129	86
6825	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	138	66
6826	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	112	64
6827	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	108	68
6828	U49974	Homo sapiens	mariner transposase	103	86
6829	AF119851	Homo sapiens	PRO1722	115	53
6830	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	82	62
6831	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	94	73
6832	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	131	53
6833	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	74	50
6834	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	168	61
6835	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	140	60
6836	X92485	Plasmodium vivax	pval	99	58
6837	AB046048	Macaca fascicularis	unnamed portein product	147	42
6838	AB047600	Macaca fascicularis	hypothetical protein	134	52
6839	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	141	60
6840	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	126	73
6841	AF130089	Homo sapiens	PRO2550	167	63
6842	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	140	56
6843	AF090894	Homo sapiens	PRO0113	148	62
6844	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	119	51
6845	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	75	61
6846	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	65	44
6847	AF130089	Homo sapiens	PRO2550	160	76
6848	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	132	68
6849	AF116715	Homo sapiens	PRO2829	123	67
6850	Y01437	Homo sapiens	Secreted protein encoded by gene 55	142	96

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			clone HLMBP18.		
6851	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	110	76
6852	AF068294	Homo sapiens	HDCMB45P	161	56
6853	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	111	57
6854	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	165	72
6855	AF130051	Homo sapiens	PRO0898	117	61
6856	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	138	72
6857	X55685	Lycopersicon esculentum	extensin (class I)	190	45
6858	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	164	69
6859	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	90	52
6860	AF119851	Homo sapiens	PRO1722	331	73
6861	G00418	Homo sapiens	Human secreted protein, SEQ ID NO: 4499.	130	67
6862	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	114	53
6863	X92485	Plasmodium vivax	pval	105	63
6864	AF068294	Homo sapiens	HDCMB45P	206	61
6865	AF068294	Homo sapiens	HDCMB45P	128	46
6866	L00016	Homo sapiens	urf4	157	58
6867	X92485	Plasmodium vivax	pval	95	89
6868	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	77
6869	AF130089	Homo sapiens	PRO2550	162	67
6870	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	257	65
6871	X71972	Mus musculus	ribosomal protein S24	211	85
6872	M28016	Homo sapiens	cytochrome b	72	93
6873	M24069	Homo sapiens	DNA-binding protein A	1662	79
6874	AF130051	Homo sapiens	PRO0898	163	76
6875	AF006061	Homo sapiens	placental growth hormone isoform hGH-V3	263	90
6876	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	94	80
6877	AF130079	Homo sapiens	PRO2852	130	76
6878	S80905	Homo sapiens	Con1	148	38
6879	X55683	Lycopersicon esculentum	extensin (class I)	70	35
6880	U16359	Rattus norvegicus	nitric oxide synthase	106	94
6881	AK025047	Homo sapiens	unnamed protein product	167	50
6882	X92485	Plasmodium vivax	pval	110	63
6883	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	185	46
6884	AK024455	Homo sapiens	FLJ00047 protein	81	64
6885	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	113	47
6886	AF014008	Bos taurus	myocardial vascular inhibition factor	158	96
6887	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	183	83
6888	Y45382	Homo sapiens	Human secreted protein fragment	199	49

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			encoded from gene 28.		
6889	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	140	67
6890	AF130051	Homo sapiens	PRO0898	135	65
6891	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	147	65
6892	X72963	Nicotiana tabacum	pAP8 product	80	44
6893	AF073957	Homo sapiens	CXC chemokine BRAK	399	82
6894	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	160	80
6895	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	150	70
6896	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	178	85
6897	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	142	62
6898	AF118082	Homo sapiens	PRO1902	144	53
6899	AF130051	Homo sapiens	PRO0898	187	72
6900	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	121	85
6901	AF130089	Homo sapiens	PRO2550	100	63
6902	Z29446	Hepatitis C virus	core region	60	36
6903	AF107406	Homo sapiens	GW128	71	63
6904	W03627	Homo sapiens	Human follicle stimulating hormone GPR N-terminal sequence.	173	64
6905	AF130089	Homo sapiens	PRO2550	88	65
6906	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	78	84
6907	U93569	Homo sapiens	p40	145	48
6908	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	186	50
6909	AF130089	Homo sapiens	PRO2550	244	77
6910	M18093	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	119	38
6911	AF130089	Homo sapiens	PRO2550	139	47
6912	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	146	60
6913	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	131	70
6914	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	106	74
6915	AF161361	Homo sapiens	HSPC098	79	66
6916	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	207	60
6917	AF130051	Homo sapiens	PRO0898	258	61
6918	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	108	65
6919	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	58
6920	G02635	Homo sapiens	Human secreted protein, SEQ ID NO: 6716.	168	80
6921	AF116661	Homo sapiens	PRO1438	71	48
6922	AF090940	Homo sapiens	PRO0644	72	85
6923	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	186	70
6924	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	89	55
6925	AF229067	Homo sapiens	PADI-H protein	122	72

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
6926	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	105	37
6927	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	173	60
6928	X56603	Mus musculus	mouse 57-KD Calcium-binding protein (MCaBP)	103	52
6929	AF119851	Homo sapiens	PRO1722	148	76
6930	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	96	61
6931	AF077208	Homo sapiens	HSPC022	155	72
6932	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	111	62
6933	M22332	Homo sapiens	unknown protein	154	77
6934	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	146	60
6935	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	168	63
6936	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	124	50
6937	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	99	77
6938	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	111	68
6939	AF118082	Homo sapiens	PRO1902	120	54
6940	AF090942	Homo sapiens	PRO0657	149	72
6941	M22332	Homo sapiens	unknown protein	96	51
6942	AF130087	Homo sapiens	PRO2411	132	58
6943	M15530	Homo sapiens	B-cell growth factor	97	52
6944	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	87	52
6945	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	73	66
6946	Z10561_cdl	Homo sapiens	12-MAR-1998 DNA encoding G protein-coupled receptor protein designated SREB2.	330	96
6947	W53869	Homo sapiens	Gravin polypeptide fragment, residues 1526-1780.	170	89
6948	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	164	86
6949	AF118086	Homo sapiens	PRO1992	117	86
6950	AF090928	Homo sapiens	PRO0470	115	58
6951	AF130089	Homo sapiens	PRO2550	124	69
6952	Y38397	Homo sapiens	Human secreted protein encoded by gene No. 12.	94	64
6953	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	132	55
6954	X92485	Plasmodium vivax	pval	108	64
6955	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	117	85
6956	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	93	53
6957	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	106	50
6958	AF130089	Homo sapiens	PRO2550	127	67
6959	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	119	49
6960	J02459	bacteriophage lambda	U (tail component;131)	492	92
6961	G03133	Homo sapiens	Human secreted protein, SEQ ID NO:	180	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7214.		
6962	Z66490	Salmo trutta	slow myotomal muscle tropomyosin	182	72
6963	AF130089	Homo sapiens	PRO2550	108	73
6964	W21733	Homo sapiens	NIP-1 encoded by clone 59.	131	69
6965	AF161356	Homo sapiens	HSPC093	58	48
6966	AB047934	Macaca fascicularis	hypothetical protein	146	58
6967	X92485	Plasmodium vivax	pval	116	55
6968	AF118082	Homo sapiens	PRO1902	85	65
6969	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	176	63
6970	AF116712	Homo sapiens	PRO2738	101	56
6971	X96667	Homo sapiens	beta-galactoside alpha-2,3-sialyltransferase	172	97
6972	Y86574	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:491.	150	82
6973	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	176	58
6974	AF162149	Mycoplasma bovis	variable surface lipoprotein	143	40
6975	W17971	Homo sapiens	RAC protein kinase C-terminal binding protein C-terminal region.	135	81
6976	AF130089	Homo sapiens	PRO2550	345	78
6977	AF130089	Homo sapiens	PRO2550	195	63
6978	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	75
6979	M60510	Mus musculus	beta-D-galactosidase fusion protein	96	47
6980	AF118086	Homo sapiens	PRO1992	131	64
6981	AF130089	Homo sapiens	PRO2550	132	64
6982	L27428	Homo sapiens	reverse transcriptase	128	35
6983	U93566	Homo sapiens	p40	98	31
6984	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	138	78
6985	L27428	Homo sapiens	reverse transcriptase	133	67
6986	AF090895	Homo sapiens	PRO0117	139	62
6987	G00528	Homo sapiens	Human secreted protein, SEQ ID NO: 4609.	212	60
6988	Y36203	Homo sapiens	Human secreted protein #75.	189	73
6989	AF116712	Homo sapiens	PRO2738	87	42
6990	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	128	63
6991	AF090930	Homo sapiens	PRO0478	154	52
6992	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	102	76
6993	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	151	48
6994	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	113	47
6995	J02974	Acanthamoeba castellanii	myosin IB heavy chain	120	43
6996	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	151	69
6997	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	153	60
6998	Y12961	Homo sapiens	Amino acid sequence of a human secreted peptide.	114	66
6999	AF113685	Homo sapiens	PRO0974	88	58
7000	AF130089	Homo sapiens	PRO2550	146	58

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7001	U93565	Homo sapiens	putative p150	96	46
7002	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFTU96.	146	57
7003	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	206	92
7004	AF130089	Homo sapiens	PRO2550	104	50
7005	AL137472	Homo sapiens	hypothetical protein	179	55
7006	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	379	98
7007	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	121	38
7008	AF119851	Homo sapiens	PRO1722	136	63
7009	AF218028	Homo sapiens	unknown	104	52
7010	AF130079	Homo sapiens	PRO2852	129	60
7011	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	110	54
7012	X03145	Homo sapiens	pot. ORF VI	130	65
7013	AF090944	Homo sapiens	PRO0663	171	75
7014	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	122	65
7015	M26460	Homo sapiens	retinoblastoma 1	113	37
7016	X92485	Plasmodium vivax	pval	112	56
7017	X92485	Plasmodium vivax	pval	144	57
7018	AF130079	Homo sapiens	PRO2852	224	74
7019	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	129	43
7020	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	58
7021	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	106	69
7022	AF090901	Homo sapiens	PRO0195	103	88
7023	AF116661	Homo sapiens	PRO1438	120	47
7024	AP002460	Arabidopsis thaliana	gene_id:F1D9.26-unknown protein	325	60
7025	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	126	63
7026	AF119900	Homo sapiens	PRO2822	111	70
7027	AF130051	Homo sapiens	PRO0898	133	44
7028	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	179	68
7029	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	72	60
7030	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	130	50
7031	J03941	Mus musculus	ferritin heavy chain	124	57
7032	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	157	59
7033	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	120	65
7034	Y36156	Homo sapiens	Human secreted protein #28.	164	48
7035	U80761	Homo sapiens	CTG26 alternate open reading frame	116	48
7036	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	130	52
7037	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	113	55
7038	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	78	68
7039	AF130089	Homo sapiens	PRO2550	121	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7040	AF119855	Homo sapiens	PRO1847	158	65
7041	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	116	62
7042	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	117	54
7043	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	123	80
7044	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	144	63
7045	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	86	44
7046	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	80	72
7047	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	100	57
7048	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	152	66
7049	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	94	72
7050	AF176323	Macropus eugenii	small nuclear ribonucleoprotein B'	103	41
7051	AF255446	Cryptosporidium parvum	Dip1-associated protein C	127	38
7052	M64792	Rattus norvegicus	salivary proline-rich protein	149	42
7053	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	147	69
7054	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	109	54
7055	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	185	86
7056	U60269	Homo sapiens	putative envelope protein; orf similar to env of Type A and Type B retroviruses and to class II HERVs	125	65
7057	AF068294	Homo sapiens	HDCMB45P	264	73
7058	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	190	95
7059	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	140	62
7060	AF090894	Homo sapiens	PRO0113	185	62
7061	AF107406	Homo sapiens	GW128	66	80
7062	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	86	46
7063	AF119851	Homo sapiens	PRO1722	117	74
7064	X92485	Plasmodium vivax	pval	123	66
7065	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	79	59
7066	L23545	Homo sapiens	putative	135	44
7067	AF119851	Homo sapiens	PRO1722	301	69
7068	AF130079	Homo sapiens	PRO2852	118	71
7069	AF119851	Homo sapiens	PRO1722	150	64
7070	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	138	48
7071	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	94	39
7072	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	145	62
7073	G00397	Homo sapiens	Human secreted protein, SEQ ID NO:	155	44

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4478.		
7074	AF130089	Homo sapiens	PRO2550	146	60
7075	U49974	Homo sapiens	mariner transposase	198	83
7076	AF236085	Homo sapiens	CYP4F11	427	79
7077	AF130089	Homo sapiens	PRO2550	159	52
7078	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	206	85
7079	D32202	Homo sapiens	alpha 1C adrenergic receptor isoform 2	152	71
7080	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	88	62
7081	AB046048	Macaca fascicularis	unnamed portein product	135	46
7082	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	142	75
7083	X53581	Rattus norvegicus	ORF4	119	64
7084	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	111	62
7085	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	64
7086	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	71	66
7087	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	81	54
7088	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	148	50
7089	U08021	Homo sapiens	nicotinamide N-methyltransferase	116	100
7090	U93569	Homo sapiens	p40	199	82
7091	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	124	56
7092	X92485	Plasmodium vivax	pval	125	60
7093	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	109	62
7094	AF118082	Homo sapiens	PRO1902	191	50
7095	X92485	Plasmodium vivax	pval	129	67
7096	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	80	66
7097	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	162	67
7098	AF116715	Homo sapiens	PRO2829	123	63
7099	L27428	Homo sapiens	reverse transcriptase	189	50
7100	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	84	48
7101	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	104	65
7102	D85030	Schizosaccharomyces pombe	ribosomal protein S33 homolog	139	85
7103	G03021	Homo sapiens	Human secreted protein, SEQ ID NO: 7102.	177	77
7104	U72543	Sus scrofa	ubiquitin-like/S30 ribosomal fusion protein	129	100
7105	AC007787	AA 187-502	NFI-X3=transcription factor	190	84
7106	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	110	38
7107	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	157	56
7108	Z69381	Saccharomyces cerevisiae	N1114	450	91

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7109	V49572_cd1	Homo sapiens	13-NOV-1996 Human stomach cancer clone HP10122 cDNA #1.	353	70
7110	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	99	45
7111	AF068294	Homo sapiens	HDCMB45P	132	55
7112	AB033020	Homo sapiens	KIAA1194 protein	850	100
7113	AB019692	Homo sapiens	protein kinase PKNbeta	792	87
7114	M12140	Homo sapiens	envelope protein	154	79
7115	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	88	62
7116	AF124491	Homo sapiens	ARF GTPase-activating protein GIT2	1216	100
7117	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	153	54
7118	AF130089	Homo sapiens	PRO2550	184	64
7119	AF130079	Homo sapiens	PRO2852	144	68
7120	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	112	51
7121	AF032384	Xenopus laevis	metalloprotease-disintegrin	304	76
7122	K01664	Drosophila melanogaster	Bkm-like protein	99	71
7123	AJ238706	Drosophila melanogaster	monocarboxylate transporter 1 homologue	161	38
7124	X92485	Plasmodium vivax	pva1	127	54
7125	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	80	65
7126	AF116712	Homo sapiens	PRO2738	118	53
7127	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	115	64
7128	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	90	62
7129	AF118090	Homo sapiens	PRO2044	280	80
7130	AF129085	Homo sapiens	carboxy terminus of Hsp70-interacting protein	593	91
7131	AF054840	Homo sapiens	tetraspan TM4SF; Tspan-3	513	83
7132	L27428	Homo sapiens	reverse transcriptase	156	51
7133	AK001647	Homo sapiens	unnamed protein product	2334	99
7134	AF130051	Homo sapiens	PRO0898	142	84
7135	X53581	Rattus norvegicus	ORF4	213	46
7136	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	101	86
7137	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	194	68
7138	U21634	Onychomys torridus	cytochrome c oxidase subunit III	111	84
7139	X60592	Homo sapiens	CDw40	201	95
7140	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	141	63
7141	M76979	Homo sapiens	pigment epithelial-differentiating factor	458	93
7142	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	142	54
7143	Y27677	Homo sapiens	Human secreted protein encoded by gene No. 111.	323	90
7144	AF116712	Homo sapiens	PRO2738	132	60
7145	AB024057	Homo sapiens	vascular Rab-GAP/TBC-containing protein	121	45
7146	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	144	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7147	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	141	76
7148	R06400	Homo sapiens	Lambda gt10ch2 encoded C-terminal alpha amidating enzyme.	337	85
7149	S87759	Homo sapiens	protein phosphatase 2C alpha, PP2Calpha	427	78
7150	M12140	Homo sapiens	envelope protein	541	64
7151	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	106	85
7152	X55683	Lycopersicon esculentum	extensin (class I)	70	38
7153	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	194	61
7154	AF130089	Homo sapiens	PRO2550	89	60
7155	AF100742	Homo sapiens	M-phase phosphoprotein homolog	714	94
7156	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	143	78
7157	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	174	79
7158	AL031230	Homo sapiens	dJ73M23.3 (KIAA0319)	214	45
7159	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	155	37
7160	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	129	46
7161	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	150	53
7162	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	107	55
7163	M13043	Mus musculus	alpha-1 (IV) collagen	80	42
7164	AB011004	Homo sapiens	UDP-N-acetylglucosamine pyrophosphorylase	257	90
7165	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	111	47
7166	AF119851	Homo sapiens	PRO1722	279	61
7167	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	136	51
7168	W73327	Homo sapiens	Bipolar affective disorder associated gene fsh16 product.	287	63
7169	Y35946	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 195.	1231	99
7170	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	132	76
7171	U83303	Homo sapiens	line-1 reverse transcriptase	184	60
7172	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	141	64
7173	AF129507	Homo sapiens	transcription factor ICBP90	245	55
7174	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	131	56
7175	AF161356	Homo sapiens	HSPC093	107	55
7176	AF218028	Homo sapiens	unknown	116	55
7177	G02654	Homo sapiens	Human secreted protein, SEQ ID NO: 6735.	117	52
7178	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	94	38
7179	AF130089	Homo sapiens	PRO2550	124	47
7180	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	109	66
7181	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	65
7182	Y36156	Homo sapiens	Human secreted protein #28.	127	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7183	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	121	75
7184	X92485	Plasmodium vivax	pval	129	60
7185	AF130089	Homo sapiens	PRO2550	116	53
7186	AF130089	Homo sapiens	PRO2550	137	64
7187	X51760	Homo sapiens	zinc finger protein (583 AA)	236	56
7188	X92485	Plasmodium vivax	pval	131	50
7189	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	152	57
7190	AF068294	Homo sapiens	HDCMB45P	163	50
7191	AF119855	Homo sapiens	PRO1847	55	50
7192	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	142	57
7193	M15530	Homo sapiens	B-cell growth factor	106	53
7194	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	121	41
7195	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	124	60
7196	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	94	68
7197	U60315	Molluscum contagiosum virus subtype 1	MC054L	116	36
7198	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	116	67
7199	M15530	Homo sapiens	B-cell growth factor	146	59
7200	AF090894	Homo sapiens	PRO0113	165	65
7201	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	160	57
7202	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	129	53
7203	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	92	65
7204	AF126163	Homo sapiens	HHLA3 protein	131	78
7205	X92485	Plasmodium vivax	pval	116	42
7206	AF090931	Homo sapiens	PRO0483	136	83
7207	Y36156	Homo sapiens	Human secreted protein #28.	127	49
7208	Y12961	Homo sapiens	Amino acid sequence of a human secreted peptide.	158	55
7209	Y36203	Homo sapiens	Human secreted protein #75.	124	56
7210	M69008	Homo sapiens	alpha-1 type XIII collagen	90	34
7211	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	144	71
7212	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	133	60
7213	AF130089	Homo sapiens	PRO2550	163	86
7214	AF130089	Homo sapiens	PRO2550	111	52
7215	AF118082	Homo sapiens	PRO1902	150	63
7216	Y53663	Homo sapiens	A human B-cell growth factor related protein (BGFRP).	83	66
7217	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	141	68
7218	AF220264	Homo sapiens	MOST-1	123	66
7219	AF229067	Homo sapiens	PADI-H protein	121	52
7220	AF118086	Homo sapiens	PRO1992	130	61
7221	Y86248	Homo sapiens	Human secreted protein HCHPF68,	179	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			SEQ ID NO:163.		
7222	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	154	78
7223	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	200	95
7224	L27428	Homo sapiens	reverse transcriptase	127	55
7225	AB008227	Adiantum capillus-veneris	Extensin	121	43
7226	D38112	Homo sapiens	cytochrome c oxidase subunit 1	113	78
7227	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	153	96
7228	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	74
7229	M15530	Homo sapiens	B-cell growth factor	137	44
7230	AF004341	Homo sapiens	cytochrome c oxidase subunit III	140	87
7231	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	162	46
7232	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	90
7233	X15769	Mus musculus	UIRNA-associated 70-kDa protein	105	29
7234	M15530	Homo sapiens	B-cell growth factor	113	61
7235	AF194537	Homo sapiens	NAG13	249	65
7236	R20313	Homo sapiens	Gly(5) beta-globin mutant.	296	80
7237	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	123	50
7238	Y36156	Homo sapiens	Human secreted protein #28.	97	80
7239	D38112	Homo sapiens	NADH dehydrogenase subunit 3	395	81
7240	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	122	70
7241	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	90
7242	AF090942	Homo sapiens	PRO0657	118	47
7243	AF119851	Homo sapiens	PRO1722	112	62
7244	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	100	53
7245	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	144	66
7246	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	129	78
7248	X92485	Plasmodium vivax	pval	108	58
7249	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	170	74
7250	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	153	70
7251	U01849	Trypanosoma brucei	ORF2	93	39
7252	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	113	54
7253	G03473	Homo sapiens	Human secreted protein, SEQ ID NO: 7554.	110	83
7254	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	167	66
7255	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	179	83
7256	AF130079	Homo sapiens	PRO2852	147	70
7257	AF118082	Homo sapiens	PRO1902	80	45
7258	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	137	55
7259	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	90	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7260	X92485	Plasmodium vivax	pval	105	85
7261	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	162	76
7262	AF130089	Homo sapiens	PRO2550	98	43
7263	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	114	60
7264	AF116661	Homo sapiens	PRO1438	139	67
7265	AF104021	Bovine viral diarrhea virus-2	polyprotein	161	40
7266	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	116	43
7267	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	112	62
7268	M15530	Homo sapiens	B-cell growth factor	154	60
7269	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	95	54
7270	AF118082	Homo sapiens	PRO1902	139	62
7271	S52010	Mus sp.	orf1 5' of EpoR	93	33
7272	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	114	50
7273	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	166	61
7274	AF130089	Homo sapiens	PRO2550	124	43
7275	X92485	Plasmodium vivax	pval	147	44
7276	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	81	59
7277	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	146	67
7278	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	89	67
7279	AF130087	Homo sapiens	PRO2411	72	65
7280	Y40039	Homo sapiens	Peptide sequence derived from a human secreted protein.	130	69
7281	J03507	Homo sapiens	complement protein C7 precursor	357	81
7282	AF116661	Homo sapiens	PRO1438	117	48
7284	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	137	61
7285	AF116715	Homo sapiens	PRO2829	128	75
7286	AF130079	Homo sapiens	PRO2852	122	52
7287	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	120	50
7288	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	338	75
7289	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	114	72
7290	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	146	59
7291	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	156	58
7292	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	167	61
7293	X92485	Plasmodium vivax	pval	122	71
7294	AF130089	Homo sapiens	PRO2550	87	62
7295	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	140	50
7296	X92485	Plasmodium	pval	152	75

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
7297	AF090894	Homo sapiens	PRO0113	172	65
7298	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	121	61
7299	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	114	66
7300	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	228	80
7301	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	111	73
7302	U43360	Peromyscus maniculatus	reverse transcriptase	119	46
7303	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	168	76
7304	U58658	Homo sapiens	unknown	102	48
7305	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	118	53
7306	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	116	63
7307	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	149	58
7308	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	112	52
7309	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	115	54
7310	M15530	Homo sapiens	B-cell growth factor	131	54
7311	AF118082	Homo sapiens	PRO1902	168	46
7312	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	412	92
7313	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	326	74
7314	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	149	59
7315	AF289099	Maackia amurensis	ENOD2f	107	32
7316	U17009	Phytophthora infestans	SecY-independent transporter protein	135	41
7317	AF220264	Homo sapiens	MOST-1	133	72
7318	U49973	Homo sapiens	ORF2: function unknown	111	53
7319	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	274	80
7320	AB047600	Macaca fascicularis	hypothetical protein	79	56
7321	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	205	95
7322	AC005175	Homo sapiens	TA2R_HUMAN, BETA ISOFORM; TXA2-R; PROSTANOID TP RECEPTOR	127	57
7323	R48296	Homo sapiens	Human PGF-2/NT-3.	89	93
7324	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	157	60
7325	AF119855	Homo sapiens	PRO1847	172	66
7326	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	141	50
7327	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	156	56
7328	Y40039	Homo sapiens	Peptide sequence derived from a human secreted protein.	98	56
7329	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	161	64
7330	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	111	72

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7331	AF126163	Homo sapiens	HHLA3 protein	98	47
7332	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	122	61
7333	AF130079	Homo sapiens	PRO2852	136	54
7334	AK023563	Homo sapiens	unnamed protein product	265	73
7335	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	113	61
7336	M15530	Homo sapiens	B-cell growth factor	136	75
7337	D38112	Homo sapiens	cytochrome c oxidase subunit 1	168	81
7338	D38112	Homo sapiens	cytochrome c oxidase subunit 3	339	80
7339	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	170	74
7340	D38112	Homo sapiens	NADH dehydrogenase subunit 3	400	82
7341	L00016	Homo sapiens	urf4	295	72
7342	D38112	Homo sapiens	NADH dehydrogenase subunit 3	350	86
7343	M36647	Homo sapiens	mitochondrial hinge protein precursor	286	82
7344	X15917	Paramecium aurelia	ND2 protein (AA 1-193) (unusual start codon)	132	34
7345	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	136	82
7346	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	89	69
7347	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	133	69
7348	D38112	Homo sapiens	NADH dehydrogenase subunit 3	169	71
7349	D38112	Homo sapiens	cytochrome c oxidase subunit 1	347	83
7350	V00662	Homo sapiens	cytochrome oxidase I	325	85
7351	D38112	Homo sapiens	NADH dehydrogenase subunit 3	406	80
7352	D38112	Homo sapiens	NADH dehydrogenase subunit 3	224	79
7353	D38112	Homo sapiens	NADH dehydrogenase subunit 1	270	86
7354	D38112	Homo sapiens	NADH dehydrogenase subunit 3	167	90
7355	D38113	Pan troglodytes	cytochrome c oxidase subunit 1	120	87
7356	D38112	Homo sapiens	NADH dehydrogenase subunit 3	362	84
7357	D38112	Homo sapiens	NADH dehydrogenase subunit 3	188	72
7358	D38112	Homo sapiens	NADH dehydrogenase subunit 3	335	72
7359	U09500	Homo sapiens	cytochrome b	275	80
7360	D38112	Homo sapiens	NADH dehydrogenase subunit 3	209	73
7361	AF118078	Homo sapiens	PRO1848	95	58
7362	AB017116	Homo sapiens	AD 1	148	89
7363	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	146	42
7364	D38112	Homo sapiens	NADH dehydrogenase subunit 1	203	82
7365	D38112	Homo sapiens	NADH dehydrogenase subunit 1	206	84
7366	D38112	Homo sapiens	NADH dehydrogenase subunit 3	408	82
7367	D38112	Homo sapiens	NADH dehydrogenase subunit 3	456	86
7368	D38112	Homo sapiens	cytochrome c oxidase subunit 3	481	85
7369	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	150	53
7370	AB017116	Homo sapiens	AD 1	145	91
7371	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	173	85
7372	AF118082	Homo sapiens	PRO1902	122	54
7373	G00492	Homo sapiens	Human secreted protein, SEQ ID NO: 4573.	163	62
7374	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	53
7375	AF090894	Homo sapiens	PRO0113	128	64
7376	AK000241	Homo sapiens	unnamed protein product	131	67

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7377	AF119855	Homo sapiens	PRO1847	164	62
7379	AF016099	Mus musculus	endonuclease/reverse transcriptase	114	37
7380	U57362	Rattus norvegicus	collagen XII alpha 1	148	47
7381	D38112	Homo sapiens	ATPase subunit 6	423	76
7382	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	135	58
7383	AB040938	Homo sapiens	KIAA1505 protein	983	76
7384	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	102	48
7385	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	122	75
7386	U63295	Homo sapiens	seven in absentia homolog	260	85
7387	AB003499	Drosophila melanogaster	CG12706 gene product	103	32
7388	X03342	Homo sapiens	rpL32 (aa 1-135)	123	51
7389	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	129	58
7390	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	154	100
7391	AK026800	Homo sapiens	unnamed protein product	137	52
7392	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	117	73
7393	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	89	70
7394	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	80
7395	M15530	Homo sapiens	B-cell growth factor	98	57
7396	L10908	Mus musculus	Gcap1 gene product	105	51
7397	AF119851	Homo sapiens	PRO1722	127	55
7398	X99256	Hylobates lar	cytochrome oxidase subunit III	319	73
7399	D38112	Homo sapiens	cytochrome c oxidase subunit 3	497	77
7400	D38112	Homo sapiens	cytochrome c oxidase subunit 3	399	80
7401	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	170	83
7402	D38112	Homo sapiens	NADH dehydrogenase subunit 3	183	91
7403	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	88
7404	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	115	40
7405	D83006	Saccharomyces cerevisiae	gene required for phosphorylation of oligosaccharides/ has high homology with YJR061w	171	38
7406	AF144636	Gallus gallus	osteoblast regulatory factor 3A	108	44
7407	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	166	70
7408	D38112	Homo sapiens	cytochrome c oxidase subunit 3	407	93
7409	AF004341	Homo sapiens	cytochrome c oxidase subunit III	140	87
7410	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	111	59
7411	AF004341	Homo sapiens	cytochrome c oxidase subunit III	138	82
7412	D38112	Homo sapiens	NADH dehydrogenase subunit 3	431	82
7413	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	127	56
7414	AB036396	Rana nigromaculata	cytochrome b	109	87
7415	AF090930	Homo sapiens	PRO0478	121	76
7416	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	171	96
7417	D38112	Homo sapiens	NADH dehydrogenase subunit 3	446	91

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7418	AB018440	Echinococcus multilocularis	NADH dehydrogenase subunit 2	112	33
7419	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	123	66
7420	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	116	50
7421	AF155232	Pisum sativum	extensin	128	37
7422	AF161356	Homo sapiens	HSPC093	89	48
7423	D38115	Pongo pygmaeus	cytochrome c oxidase subunit 3	162	81
7424	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	171	79
7425	AF275953	synthetic construct	Cox8ND6gfp fusion protein	214	93
7426	D38112	Homo sapiens	cytochrome c oxidase subunit 1.	156	73
7427	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	130	59
7428	AK024455	Homo sapiens	FLJ00047 protein	82	66
7429	D38112	Homo sapiens	NADH dehydrogenase subunit 1	212	82
7430	S79410	Mus musculus	nuclear localization signal binding protein	124	48
7431	D38112	Homo sapiens	cytochrome c oxidase subunit 1	195	90
7432	D38112	Homo sapiens	cytochrome c oxidase subunit 1	217	84
7433	U87145	Toxoplasma gondii	ORF D	89	36
7434	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	213	72
7435	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	135	57
7436	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	151	82
7437	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	190	88
7438	D38112	Homo sapiens	NADH dehydrogenase subunit 1	141	78
7439	AF250284	Amsacta moorei entomopoxvirus	AMV012	88	31
7440	AF004341	Homo sapiens	cytochrome c oxidase subunit III	149	85
7441	U43360	Peromyscus maniculatus	reverse transcriptase	114	52
7442	AF275807	Homo sapiens	PNAS-110	157	48
7443	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	126	56
7444	D38112	Homo sapiens	NADH dehydrogenase subunit 4	475	95
7445	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	146	71
7446	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	130	60
7447	X92485	Plasmodium vivax	pval	153	45
7448	AF119851	Homo sapiens	PRO1722	96	55
7449	AF130079	Homo sapiens	PRO2852	153	73
7450	AF119851	Homo sapiens	PRO1722	238	52
7451	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	113	38
7452	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	147	57
7453	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	136	63
7454	R14163	Homo sapiens	Cellular DNA-binding protein RS1.	270	42
7455	X63526	Homo sapiens	homologue to elongation factor 1-	387	80

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gamma from A.salina		
7456	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	140	80
7457	AF119851	Homo sapiens	PRO1722	102	55
7458	G02756	Homo sapiens	Human secreted protein, SEQ ID NO: 6837.	83	55
7459	AF119851	Homo sapiens	PRO1722	132	64
7460	L10908	Mus musculus	Gcap1 gene product	106	64
7461	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	124	54
7462	X77816	Rattus norvegicus	PR-Vbeta1	142	51
7463	Y34068	Homo sapiens	Histone H1 isoform H1.5 pANCA-reactive fragment (residues 69-226).	96	35
7464	AB046048	Macaca fascicularis	unnamed poertin product	302	62
7465	X92485	Plasmodium vivax	pval	115	47
7466	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	116	65
7467	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	91	35
7468	AF161361	Homo sapiens	HSPC098	92	57
7469	AF216389	Homo sapiens	semaphorin Rs	288	88
7470	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	153	73
7471	AF130089	Homo sapiens	PRO2550	108	48
7472	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	159	58
7473	AF217536	Homo sapiens	truncated mevalonate kinase	115	71
7474	X61296	Rattus norvegicus	open reading frame 2	134	49
7475	U22376	Homo sapiens	alternatively spliced product using exon 13A	165	46
7476	AF119851	Homo sapiens	PRO1722	133	46
7477	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	127	69
7478	D38112	Homo sapiens	NADH dehydrogenase subunit 4	533	87
7479	S79410	Mus musculus	nuclear localization signal binding protein	122	59
7480	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	168	84
7481	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	181	80
7482	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	122	56
7483	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	132	37
7484	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	166	100
7485	D38112	Homo sapiens	cytochrome c oxidase subunit 1	277	72
7486	M29294	Rattus norvegicus	small nuclear ribonucleoparticle-associated protein	132	42
7487	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	140	50
7488	AF090901	Homo sapiens	PRO0195	101	62
7489	X97249	Homo sapiens	leucine-rich primary response protein	304	93
7490	D38112	Homo sapiens	NADH dehydrogenase subunit 3	447	84
7491	AK024455	Homo sapiens	FLJ00047 protein	122	63
7492	U87269	Homo sapiens	p120E4F transcription factor	244	66
7493	A31036	Nicotiana glauca	PRP2	87	31

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7494	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	206	97
7495	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	166	91
7496	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	66
7497	AK024455	Homo sapiens	FLJ00047 protein	67	61
7498	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	174	84
7499	X75438	Sus scrofa	homologue of proline/arginine rich antibacterial peptides	116	44
7500	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	166	89
7501	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	137	61
7502	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	213	60
7503	AB042770	Pteropus dasymallus	cytochrome c oxidase subunit 3	169	89
7504	AF126163	Homo sapiens	HHLA3 protein	110	62
7505	D38112	Homo sapiens	cytochrome c oxidase subunit 3	299	90
7506	D38112	Homo sapiens	cytochrome c oxidase subunit 3	194	88
7507	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	128	72
7508	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	86
7509	D38112	Homo sapiens	cytochrome c oxidase subunit 1	116	65
7510	L38908	Nicotiana tabacum	extensin	114	36
7512	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	273	73
7513	Y36156	Homo sapiens	Human secreted protein #28.	168	44
7514	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	171	96
7515	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	110	46
7516	D38115	Pongo pygmaeus	cytochrome c oxidase subunit 3	170	84
7517	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	105	43
7518	D38112	Homo sapiens	NADH dehydrogenase subunit 3	350	82
7519	D38114	Gorilla gorilla	NADH dehydrogenase subunit 3 (ND3)	141	84
7520	U12690	Homo sapiens	cytochrome oxidase subunit II	410	85
7521	D38112	Homo sapiens	cytochrome c oxidase subunit 1	112	71
7522	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhla.	96	46
7523	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	142	57
7524	AF220264	Homo sapiens	MOST-1	86	62
7525	AF130089	Homo sapiens	PRO2550	109	35
7526	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	106	79
7527	U49973	Homo sapiens	ORF2: function unknown	105	68
7528	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	122	62
7529	X05831	Rattus norvegicus	fibronectin precursor	100	64
7530	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	175	60
7531	X92485	Plasmodium	pval	120	59

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
7532	D38115	Pongo pygmaeus	cytochrome c oxidase subunit 3	383	75
7533	D38112	Homo sapiens	NADH dehydrogenase subunit 3	321	67
7534	AL359782	Trypanosoma brucei	possible (hhv-6) ul102, variant a dna, complete virion genome.	126	72
7535	AF119851	Homo sapiens	PRO1722	110	67
7536	D38112	Homo sapiens	cytochrome c oxidase subunit 3	531	81
7537	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	146	75
7538	X92485	Plasmodium vivax	pva1	141	48
7539	AF119900	Homo sapiens	PRO2822	86	42
7540	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	126	50
7541	M15530	Homo sapiens	B-cell growth factor	136	53
7542	X53581	Rattus norvegicus	ORF4	174	46
7543	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	138	74
7544	D38112	Homo sapiens	cytochrome c oxidase subunit 1	116	86
7545	M15530	Homo sapiens	B-cell growth factor	96	47
7546	X92485	Plasmodium vivax	pva1	149	58
7547	AF113685	Homo sapiens	PRO0974	110	48
7548	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	226	73
7549	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	316	73
7550	S79410	Mus musculus	nuclear localization signal binding protein	107	70
7551	AF130089	Homo sapiens	PRO2550	130	45
7552	R95913	Homo sapiens	Neural thread protein.	99	56
7553	U93569	Homo sapiens	putative p150	171	47
7554	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	111	75
7555	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	207	56
7556	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	59
7557	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	125	43
7558	Y86445	Homo sapiens	Human gene 42-encoded protein fragment, SEQ ID NO:360.	95	71
7559	X83413	Human herpesvirus 6	U88	108	32
7560	A18812	Brassica napus	extensin	125	38
7561	D38112	Homo sapiens	ATPase subunit 6	495	87
7562	AF130089	Homo sapiens	PRO2550	141	46
7563	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	106	61
7564	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	128	62
7565	U50191	Caenorhabditis elegans	C. elegans collagen dpy-10 gene (Levy, A.D., Yang, J. and Kramer, J.M. Mol. Biol Cell 4, 803-17, 1993)	101	37
7566	V00672	Pan troglodytes	reading frame protein 4	294	73
7567	A18812	Brassica napus	extensin	145	48
7568	D38112	Homo sapiens	cytochrome c oxidase subunit 3	241	69
7569	L00016	Homo sapiens	urf4	284	71
7570	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	115	50
7571	G00673	Homo sapiens	Human secreted protein, SEQ ID NO:	124	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4754.		
7572	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	126	65
7573	X92485	Plasmodium vivax	pval	157	49
7574	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	151	54
7575	AF130089	Homo sapiens	PRO2550	348	70
7576	R95913	Homo sapiens	Neural thread protein.	113	45
7577	L26953	Homo sapiens	chromosomal protein	148	38
7578	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	116	46
7579	AB047948	Macaca fascicularis	hypothetical protein	173	67
7580	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	149	57
7581	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	95	51
7582	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	125	85
7583	AC004079	Homo sapiens	human HOXA3; 95% similarity to e307530 (PID:g1888441)	127	100
7584	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	171	71
7585	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	141	80
7586	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	222	100
7587	D38112	Homo sapiens	cytochrome c oxidase subunit 1	194	71
7588	D38112	Homo sapiens	NADH dehydrogenase subunit 1	115	80
7589	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	127	77
7590	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhala.	112	60
7591	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	133	72
7592	A49807	Neisseria meningitidis	IGA-LPHA3	93	33
7593	Z67990	Caenorhabditis elegans	contains similarity to Pfam domain: PF01484 (Nematode cuticle collagen N-terminal domain), Score=27.5, E-value=0.0001, N=1	102	42
7594	U43627	Arabidopsis thaliana	extensin	99	44
7595	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	103	74
7596	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	112	49
7597	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	190	92
7598	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	96
7599	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	117	95
7600	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	192	85
7601	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	91
7602	D38112	Homo sapiens	NADH dehydrogenase subunit 3	333	71

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7603	D38112	Homo sapiens	cytochrome c oxidase subunit 3	190	86
7604	U09500	Homo sapiens	cytochrome b	279	93
7605	Z14016	Nicotiana tabacum	pistil extensin like protein, partial CDS	84	40
7606	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	108	71
7607	G03636	Homo sapiens	Human secreted protein, SEQ ID NO: 7717.	55	52
7608	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	114	54
7609	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	97	62
7610	D38112	Homo sapiens	NADH dehydrogenase subunit 3	434	87
7611	Y21418	Homo sapiens	Human high mobility group protein HMGI-C mutant fragment 2.	97	46
7613	X92485	Plasmodium vivax	pval	106	58
7614	AC003058	Arabidopsis thaliana	unknown protein	191	88
7615	S74221	Homo sapiens	IK factor=cytokine down-regulating HLA class II	153	65
7616	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	148	74
7617	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	169	56
7618	L35013	Homo sapiens	spliceosomal protein	95	55
7619	V00662	Homo sapiens	URF 3 (NADH dehydrogenase subunit)	441	85
7620	AF116638	Homo sapiens	PRO1546	172	42
7621	K03202	Homo sapiens	salivary proline-rich protein precursor	146	46
7622	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	145	72
7623	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	144	67
7624	U41031	Caenorhabditis elegans	proline-rich	92	59
7625	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	130	55
7626	L19098	Choristoneura fumiferana	cytochrome oxidase I	102	66
7627	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	99	76
7628	AF126163	Homo sapiens	HHLA3 protein	117	67
7629	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	69	53
7630	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	83	55
7631	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	87	64
7632	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	120	48
7633	R95913	Homo sapiens	Neural thread protein.	126	61
7634	V00662	Homo sapiens	cytochrome oxidase I	396	85
7635	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	205	84
7636	D38112	Homo sapiens	NADH dehydrogenase subunit 3	464	85
7637	D38112	Homo sapiens	NADH dehydrogenase subunit 2	165	94
7638	AF118086	Homo sapiens	PRO1992	120	68
7639	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7640	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	95	39
7641	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	143	68
7642	D38112	Homo sapiens	NADH dehydrogenase subunit 3	192	91
7643	D38112	Homo sapiens	NADH dehydrogenase subunit 3	416	80
7644	AF004341	Homo sapiens	cytochrome c oxidase subunit III	133	84
7645	U93570	Homo sapiens	putative p150	206	42
7646	D38112	Homo sapiens	ATPase subunit 6	192	80
7647	AF090942	Homo sapiens	PRO0657	128	71
7648	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	134	73
7649	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	115	52
7650	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	130	61
7651	X71442	Rattus norvegicus	ORF 1; putative	105	52
7652	L07545	Leishmania tarentolae	A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression	111	32
7653	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	89	53
7654	G02473	Homo sapiens	Human secreted protein, SEQ ID NO: 6554.	291	49
7655	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	165	63
7656	D38112	Homo sapiens	NADH dehydrogenase subunit 3	470	88
7657	D38112	Homo sapiens	NADH dehydrogenase subunit 3	367	80
7658	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	108	95
7659	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhala.	109	50
7660	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	77
7661	AP002460	Arabidopsis thaliana	gene_id:F1D9.26~unknown protein	121	40
7662	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	137	96
7663	AF217973	Homo sapiens	unknown	124	51
7664	X92485	Plasmodium vivax	pval	118	59
7665	AF118082	Homo sapiens	PRO1902	123	44
7666	AB014563	Homo sapiens	KIAA0663 protein	267	90
7667	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	114	49
7668	AF119855	Homo sapiens	PRO1847	152	72
7669	AK025116	Homo sapiens	unnamed protein product	127	65
7670	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	140	55
7671	R14847	Homo sapiens	Protein associated with biochemical pathway involving cAMP.	164	89
7672	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	93	68
7673	U37426	Homo sapiens	kinesin-like spindle protein HKSP	247	81
7674	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	125	75
7675	S67633	Homo sapiens	class I major histocompatibility antigen	103	59

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7676	AF126163	Homo sapiens	HHLA3 protein	146	72
7677	AC005192	Homo sapiens	similar to mouse interferon-related protein PC4; 96% identical to P19182 (PID:g135861)	143	87
7678	X07882	Homo sapiens	Po protein	126	39
7679	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	148	60
7680	AJ242540	Volvox carteri f. nagariensis	hydroxyproline-rich glycoprotein DZ-HRGP	177	37
7681	AF090930	Homo sapiens	PRO0478	80	58
7682	X55654	Homo sapiens	cytochrome C oxidase II subunit	115	65
7683	AB046048	Macaca fascicularis	unnamed portein product	145	67
7684	AF130079	Homo sapiens	PRO2852	117	60
7685	M13101	Rattus norvegicus	unknown protein	114	53
7686	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	134	74
7687	AF126163	Homo sapiens	HHLA3 protein	141	84
7688	Y36156	Homo sapiens	Human secreted protein #28.	120	61
7689	M37197	Homo sapiens	CCAAT-box-binding factor	104	95
7690	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	97	54
7691	AF220264	Homo sapiens	MOST-1	117	76
7692	AF063866	Melanoplus sanguinipes entomopoxvirus	ORF MSV233 hypothetical protein	94	31
7693	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	98	40
7694	AF118082	Homo sapiens	PRO1902	115	55
7695	G00517	Homo sapiens	Human secreted protein, SEQ ID NO: 4598.	116	56
7696	Y15163	Mus musculus	putative splice variant containing region C	133	51
7697	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	132	52
7698	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	155	77
7699	M15530	Homo sapiens	B-cell growth factor	106	79
7700	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	108	70
7701	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	166	62
7702	AF090931	Homo sapiens	PRO0483	125	68
7703	G03432	Homo sapiens	Human secreted protein, SEQ ID NO: 7513.	114	79
7704	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	175	63
7705	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	141	35
7706	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	58
7707	X92485	Plasmodium vivax	pval	126	42
7708	AK023563	Homo sapiens	unnamed protein product	217	72
7709	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	124	58
7710	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	124	56
7711	G03714	Homo sapiens	Human secreted protein, SEQ ID NO:	131	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7795.		
7712	D38112	Homo sapiens	NADH dehydrogenase subunit 1	116	72
7713	D38112	Homo sapiens	cytochrome c oxidase subunit 1	194	58
7714	X92485	Plasmodium vivax	pva1	123	68
7715	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	137	48
7716	AF119851	Homo sapiens	PRO1722	168	60
7717	U93570	Homo sapiens	putative p150	133	35
7718	AF116712	Homo sapiens	PRO2738	94	68
7719	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	107	55
7720	U49973	Homo sapiens	ORF2: function unknown	200	85
7721	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	234	73
7722	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	155	76
7723	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	140	65
7724	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	70	73
7725	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	94	55
7726	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	130	75
7727	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	94	78
7728	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	163	65
7729	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	111	63
7730	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	119	69
7731	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	113	84
7732	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	94	38
7733	U09500	Homo sapiens	cytochrome b	463	84
7734	D38112	Homo sapiens	cytochrome c oxidase subunit 3	334	92
7735	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	399	92
7736	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	128	55
7737	AC003058	Arabidopsis thaliana	unknown protein	167	66
7738	W48353	Homo sapiens	HUMAN breast cancer related protein BCFLT2.	86	70
7739	D86854	Catharanthus roseus	extensin	154	40
7740	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	122	57
7741	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	99	49
7742	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	117	35
7743	V00662	Homo sapiens	cytochrome oxidase I	568	89
7744	R63235	Homo sapiens	CNS neural thread protein HB4.	145	93
7745	R63235	Homo sapiens	CNS neural thread protein HB4.	154	100
7746	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7747	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	126	71
7748	D38112	Homo sapiens	cytochrome c oxidase subunit 3	327	92
7749	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	150	71
7750	AF130079	Homo sapiens	PRO2852	147	81
7751	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	104	49
7752	U43627	Arabidopsis thaliana	extensin	116	37
7753	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	71
7754	D38112	Homo sapiens	NADH dehydrogenase subunit 1	551	83
7755	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	88	56
7756	AF119851	Homo sapiens	PRO1722	97	56
7757	U80955	Caenorhabditis elegans	similar to RE repeat region of PIR:S27806 D. melanogaster homeotic protein BarH2 protein (dual bar protein)	89	100
7758	AC002045	Homo sapiens	Unknown protein product CIT987SK-A-589H1_1 splice form 2	97	94
7759	Y02775	Homo sapiens	Human secreted protein encoded by gene 12 clone HFTCU19.	288	98
7760	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	94	80
7761	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	199	76
7762	AF090931	Homo sapiens	PRO0483	153	84
7763	X92485	Plasmodium vivax	pval	114	62
7764	AF090931	Homo sapiens	PRO0483	107	86
7765	G02752	Homo sapiens	Human secreted protein, SEQ ID NO: 6833.	103	43
7766	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	168	73
7767	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	148	72
7768	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	222	83
7769	Y40039	Homo sapiens	Peptide sequence derived from a human secreted protein.	68	72
7770	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	156	62
7771	U93569	Homo sapiens	p40	188	43
7772	AL049934	Homo sapiens	hypothetical protein	113	47
7773	AF090931	Homo sapiens	PRO0483	86	65
7774	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	137	92
7775	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	143	65
7776	AF126163	Homo sapiens	HLA3 protein	141	71
7777	G00423	Homo sapiens	Human secreted protein, SEQ ID NO: 4504.	93	47
7778	AF090942	Homo sapiens	PRO0657	148	74
7779	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	194	83
7780	U14966	Homo sapiens	ribosomal protein L5	315	81

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7781	R59843	Homo sapiens	ApoE4Lx2 protease.	126	47
7782	AF119855	Homo sapiens	PRO1847	131	51
7783	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	79	53
7784	D38112	Homo sapiens	NADH dehydrogenase subunit 3	405	82
7785	G00331	Homo sapiens	Human secreted protein, SEQ ID NO: 4412.	64	42
7786	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	141	59
7787	AF118082	Homo sapiens	PRO1902	131	48
7788	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	88	64
7789	J03807	Strongylocentrotus purpuratus	histone H1-delta	111	43
7790	D38112	Homo sapiens	NADH dehydrogenase subunit 1	139	85
7791	V00662	Homo sapiens	cytochrome oxidase I	522	80
7792	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	153	72
7793	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	84	53
7794	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	82	46
7795	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	156	76
7796	D38112	Homo sapiens	ATPase subunit 8	166	77
7797	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	159	48
7798	AF090931	Homo sapiens	PRO0483	132	75
7799	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	97	57
7800	D21261	Homo sapiens	similar to human 22kDa, SM22 mRNA (HUM22SM).	99	84
7801	X64707	Homo sapiens	BBC1	232	77
7802	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	104	33
7803	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	50
7804	Y36203	Homo sapiens	Human secreted protein #75.	142	56
7805	AF119851	Homo sapiens	PRO1722	88	46
7806	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	149	57
7807	X68600	Hordeum vulgare	pZE40	90	37
7808	AK025047	Homo sapiens	unnamed protein product	138	54
7809	AF130089	Homo sapiens	PRO2550	375	71
7810	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	124	65
7811	R59842	Homo sapiens	ApoE4L1 protease.	156	58
7812	AF016446	Caenorhabditis elegans	similar to C. elegans cuticulin precursor CUT-2 (SP:P34682)	95	42
7813	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	154	65
7814	AK025047	Homo sapiens	unnamed protein product	165	71
7815	W34499	Homo sapiens	Obesity receptor C protein.	309	89
7816	AJ222673	Hepatitis C virus type 2c	core protein	95	42
7817	AB011483	Arabidopsis thaliana	contains similarity to root cap protein-gene_id:MUF9.16	104	61
7818	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	154	74

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7819	X92485	Plasmodium vivax	pval	112	61
7820	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	103	60
7821	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	174	65
7822	AF130089	Homo sapiens	PRO2550	107	67
7823	AF118086	Homo sapiens	PRO1992	143	73
7824	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	132	63
7825	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	142	59
7826	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	42
7827	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	128	65
7828	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	104	58
7829	AF132961	Homo sapiens	CGI-27 protein	154	49
7830	X70343	Nicotiana glauca	extensin	105	30
7831	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	100	62
7832	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	129	51
7833	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	99	46
7834	G02469	Homo sapiens	Human secreted protein, SEQ ID NO: 6550.	74	65
7835	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	163	55
7836	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	72	52
7837	AF090942	Homo sapiens	PRO0657	126	59
7838	Z33426	Human respiratory syncytial virus	glycoprotein	110	34
7839	D63480	Homo sapiens	The KIAA0146 gene product is novel.	158	89
7840	W48352	Homo sapiens	Human breast cancer related protein BCFLT1.	88	63
7841	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	156	60
7842	W90847	Homo sapiens	Human lymphocyte targeted peptide #15.	145	100
7843	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	127	66
7844	M28016	Homo sapiens	cytochrome b	214	78
7845	D38112	Homo sapiens	cytochrome c oxidase subunit 3	283	82
7846	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	94	73
7847	D38112	Homo sapiens	cytochrome b	525	83
7848	L27428	Homo sapiens	reverse transcriptase	210	67
7849	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	156	96
7850	X92485	Plasmodium vivax	pval	121	54
7851	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	147	59
7852	D38112	Homo sapiens	NADH dehydrogenase subunit 2	191	93

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7853	W48808	Homo sapiens	Homo sapiens clone CG109_1 protein.	72	69
7854	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	142	76
7855	U43627	Arabidopsis thaliana	extensin	124	35
7856	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	95
7857	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	95	57
7858	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	157	91
7859	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	108	45
7860	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	159	54
7861	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	155	63
7862	D38112	Homo sapiens	cytochrome c oxidase subunit 3	265	77
7863	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	145	56
7864	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	222	100
7865	D38112	Homo sapiens	cytochrome c oxidase subunit 1	409	87
7866	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	112	50
7867	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	169	74
7868	AL031004	Arabidopsis thaliana	RSZp22 splicing factor	127	35
7869	U83771	Accipiter superciliosus	cytochrome oxidase I	168	73
7870	U83771	Accipiter superciliosus	cytochrome oxidase I	186	81
7871	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	203	56
7872	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	130	71
7873	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	106	44
7874	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	138	69
7875	AF119855	Homo sapiens	PRO1847	174	70
7876	AF210651	Homo sapiens	NAG18	164	76
7877	Z93244	Homo sapiens	bK116F5.2 (PUTATIVE RhoGAP (CDC42 GTPase Activating Protein) LIKE protein)	111	45
7878	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	227	79
7879	AK024455	Homo sapiens	FLJ00047 protein	120	68
7880	Y36156	Homo sapiens	Human secreted protein #28.	85	68
7881	AF116661	Homo sapiens	PRO1438	138	61
7882	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	141	55
7883	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	111	63
7884	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	106	64
7885	AK022821	Homo sapiens	unnamed protein product	175	72
7886	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	59

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7887	L27428	Homo sapiens	reverse transcriptase	165	63
7888	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	139	61
7889	M15530	Homo sapiens	B-cell growth factor	132	74
7890	Y01181	Homo sapiens	Polypeptide fragment encoded by gene 12.	81	64
7891	AB046048	Macaca fascicularis	unnamed portein product	150	61
7892	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	154	73
7893	AF130089	Homo sapiens	PRO2550	224	61
7894	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	127	69
7895	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	142	62
7896	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	50
7897	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	108	68
7898	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	144	65
7899	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	105	83
7900	AF026689	Homo sapiens	prostate-specific transglutaminase	104	57
7901	X03717	Homo sapiens	pot. unidentified reading frame	105	46
7902	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	94	67
7903	X61046	Hydra sp.	mini-collagen	107	46
7904	AF124726	Homo sapiens	acinusL	111	44
7905	U77049	Ovis aries	bactinecin 11	116	38
7906	AF118086	Homo sapiens	PRO1992	130	73
7907	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	121	48
7908	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	124	83
7909	AC004450	Arabidopsis thaliana	putative extensin	167	34
7910	AF130079	Homo sapiens	PRO2852	110	42
7911	AF090942	Homo sapiens	PRO0657	144	66
7912	AF090931	Homo sapiens	PRO0483	96	80
7913	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	128	46
7914	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	87	68
7915	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	105	75
7916	X92485	Plasmodium vivax	pval	102	67
7917	AF090942	Homo sapiens	PRO0657	126	76
7918	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	108	47
7919	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	156	63
7920	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	138	61
7921	L26251	Trypanosoma brucei	CR5	95	37
7922	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	176	73

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7923	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	174	61
7924	L27428	Homo sapiens	reverse transcriptase	121	33
7925	Y36156	Homo sapiens	Human secreted protein #28.	137	67
7926	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	119	73
7927	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	138	65
7928	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	138	60
7929	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	166	61
7930	AF004341	Homo sapiens	cytochrome c oxidase subunit III	144	87
7931	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	176	53
7932	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	179	60
7933	V00662	Homo sapiens	URF 3 (NADH dehydrogenase subunit)	279	92
7934	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	132	63
7935	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	101	64
7936	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	159	55
7937	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	320	80
7938	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	159	71
7939	AF144054	Homo sapiens	apoptosis related protein APR-4	127	65
7940	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	314	73
7941	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	121	57
7942	AB040936	Homo sapiens	KIAA1503 protein	149	71
7943	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	107	83
7944	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	74	60
7945	Y13141	Bromheadia finlaysoniana	extensin	68	35
7946	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	126	50
7947	AP000735	Arabidopsis thaliana	extensin protein-like	214	40
7948	AF161356	Homo sapiens	HSPC093	134	75
7949	AF090942	Homo sapiens	PRO0657	110	48
7950	AJ249395	Globodera pallida	cytochrome b	117	36
7951	AF116661	Homo sapiens	PRO1438	135	49
7952	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	92
7953	M15530	Homo sapiens	B-cell growth factor	143	65
7954	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	137	68
7955	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	130	62
7956	AF130089	Homo sapiens	PRO2550	153	62
7957	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	99	48
7958	AF161356	Homo sapiens	HSPC093	154	56

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7959	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	131	57
7960	X92485	Plasmodium vivax	pval	107	53
7961	AF210651	Homo sapiens	NAG18	113	77
7962	AF130051	Homo sapiens	PRO0898	84	71
7963	R59842	Homo sapiens	ApoE4L1 protease.	116	68
7964	AF090931	Homo sapiens	PRO0483	129	56
7965	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	151	51
7966	R95913	Homo sapiens	Neural thread protein.	110	40
7967	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	180	50
7968	AF090894	Homo sapiens	PRO0113	104	58
7969	Y21040	Homo sapiens	Human glial fibrillary acidic protein GFAP mutant fragment 49.	285	100
7970	AK001452	Homo sapiens	unnamed protein product	346	56
7971	V00672	Pan troglodytes	reading frame protein 4	134	90
7972	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	48
7973	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	104	84
7974	AF116661	Homo sapiens	PRO1438	140	62
7975	AF119882	Homo sapiens	PRO2492	112	48
7976	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	80	63
7977	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	124	89
7978	M11901	Rattus norvegicus	proline-rich salivary protein	125	36
7979	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	149	68
7980	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	289	84
7981	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	59
7982	X77816	Rattus norvegicus	PR-Vbeta1	109	69
7983	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	149	73
7984	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	128	72
7985	R59842	Homo sapiens	ApoE4L1 protease.	130	82
7986	AF090895	Homo sapiens	PRO0117	83	58
7987	X07881	Homo sapiens	proline-rich protein G1	131	41
7988	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	123	53
7989	AF090894	Homo sapiens	PRO0113	104	61
7990	Z93244	Homo sapiens	bK116F5.2 (PUTATIVE RhoGAP (CDC42 GTPase Activating Protein) LIKE protein)	100	61
7991	AK024455	Homo sapiens	FLJ00047 protein	131	56
7992	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	136	61
7993	AF210651	Homo sapiens	NAG18	133	61
7994	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	92	42
7995	D38112	Homo sapiens	cytochrome c oxidase subunit 1	171	82
7996	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	113	54

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
7997	AF090928	Homo sapiens	PRO0470	86	76
7998	AJ251579	Arabidopsis thaliana	cef protein	113	37
7999	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	119	60
8000	R95913	Homo sapiens	Neural thread protein.	105	70
8001	AF229067	Homo sapiens	PADI-H protein	118	61
8002	W88609	Homo sapiens	Secreted protein encoded by gene 76 clone HKIXL73.	83	65
8003	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	85	61
8004	S79410	Mus musculus	nuclear localization signal binding protein	123	43
8005	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	93	68
8006	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	147	64
8007	AF016099	Mus musculus	endonuclease/reverse transcriptase	147	38
8008	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	72
8009	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	71
8010	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	92	54
8011	G00589	Homo sapiens	Human secreted protein, SEQ ID NO: 4670.	152	59
8012	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	123	66
8013	AF161356	Homo sapiens	HSPC093	185	64
8014	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	107	54
8015	G00413	Homo sapiens	Human secreted protein, SEQ ID NO: 4494.	71	65
8016	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	139	66
8017	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	94	77
8018	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	108	46
8019	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	178	61
8020	G03639	Homo sapiens	Human secreted protein, SEQ ID NO: 7720.	85	65
8021	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	108	51
8022	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	202	77
8023	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	195	68
8024	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	158	53
8025	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	133	58
8026	X92485	Plasmodium vivax	pval	128	56
8027	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	135	61
8028	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFU96.	105	66
8029	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	126	59

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8030	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	117	40
8031	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	126	72
8032	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	125	41
8033	Y40039	Homo sapiens	Peptide sequence derived from a human secreted protein.	113	69
8034	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	102	66
8035	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	221	95
8036	AF041330	Bodo, saltans	NADH dehydrogenase subunit 5	106	36
8037	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	113	55
8038	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	108	64
8039	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	110	68
8040	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	169	86
8041	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	170	56
8042	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	95	58
8043	AK024455	Homo sapiens	FLJ00047 protein	152	68
8044	AF220264	Homo sapiens	MOST-1	83	68
8045	AK024455	Homo sapiens	FLJ00047 protein	131	55
8046	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	181	78
8047	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	147	61
8048	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	102	43
8049	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	117	59
8050	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	154	56
8051	D00570	Mus musculus	open reading frame (196 AA)	127	59
8052	AF040964	Homo sapiens	unknown protein IT1	143	50
8053	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	168	83
8054	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	108	70
8055	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	134	62
8056	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	65
8057	AF090895	Homo sapiens	PRO0117	110	77
8058	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	124	90
8059	AF118082	Homo sapiens	PRO1902	117	50
8060	AK022217	Homo sapiens	unnamed protein product	145	53
8061	AF130089	Homo sapiens	PRO2550	160	76
8062	AF119851	Homo sapiens	PRO1722	177	54
8063	D38112	Homo sapiens	NADH dehydrogenase subunit 3	362	73
8064	D38112	Homo sapiens	NADH dehydrogenase subunit 3	426	85
8065	D38112	Homo sapiens	NADH dehydrogenase subunit 3	344	90
8066	AF068294	Homo sapiens	HDCMB45P	146	60
8067	V00662	Homo sapiens	URF 3 (NADH dehydrogenase subunit)	461	87
8068	D38112	Homo sapiens	NADH dehydrogenase subunit 4	504	90

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8069	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	97	40
8070	R59842	Homo sapiens	ApoE4L1 protease.	147	47
8071	AF119851	Homo sapiens	PRO1722	139	59
8072	X92485	Plasmodium vivax	pval	183	45
8073	AF116712	Homo sapiens	PRO2738	95	52
8074	AF213465	Homo sapiens	dual oxidase	184	80
8075	AF090895	Homo sapiens	PRO0117	153	57
8076	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	162	73
8077	T85403_cd1	Homo sapiens	19-APR-1993 Human cadherin-11 coding sequence.	284	98
8078	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	99	63
8079	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	162	73
8080	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	142	52
8081	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	130	37
8082	X05285	Drosophila melanogaster	fibrillarin	100	34
8083	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	142	65
8084	G02216	Homo sapiens	Human secreted protein, SEQ ID NO: 6297.	380	82
8085	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	64
8086	X92485	Plasmodium vivax	pval	138	64
8087	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	117	82
8088	D38112	Homo sapiens	NADH dehydrogenase subunit 5	180	79
8089	U27143	Homo sapiens	protein kinase C inhibitor-I	119	41
8090	AF119851	Homo sapiens	PRO1722	85	47
8091	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	112	73
8092	S79410	Mus musculus	nuclear localization signal binding protein	133	64
8093	AF119854	Homo sapiens	PRO1843	522	100
8094	X92485	Plasmodium vivax	pval	115	82
8095	D38112	Homo sapiens	NADH dehydrogenase subunit 1	598	86
8096	AF097473	Mus musculus	ORF1	109	46
8097	AF097473	Mus musculus	ORF1	109	46
8098	Y17833	Human endogenous retrovirus K	pol protein	281	73
8099	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	156	69
8100	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	126	42
8101	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	126	65
8102	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	145	70
8103	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	163	71

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8104	AF130089	Homo sapiens	PRO2550	130	42
8105	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	116	57
8106	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	132	61
8107	AF090942	Homo sapiens	PRO0657	123	41
8108	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	134	38
8109	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	101	77
8110	D38112	Homo sapiens	cytochrome c oxidase subunit 1	340	90
8111	AF130089	Homo sapiens	PRO2550	123	86
8112	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	122	90
8113	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	182	47
8114	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	101	77
8115	G00452	Homo sapiens	Human secreted protein, SEQ ID NO: 4533.	72	50
8116	D38112	Homo sapiens	NADH dehydrogenase subunit 3	459	88
8117	L17318	Rattus norvegicus	proline-rich proteoglycan	110	45
8118	S79410	Mus musculus	nuclear localization signal binding protein	125	62
8119	G03639	Homo sapiens	Human secreted protein, SEQ ID NO: 7720.	106	78
8120	D38112	Homo sapiens	NADH dehydrogenase subunit 1	106	84
8121	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	110	45
8122	D86854	Catharanthus roseus	extensin	142	35
8123	X92485	Plasmodium vivax	pva1	144	53
8124	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	138	59
8125	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	163	67
8126	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	145	62
8127	X07881	Homo sapiens	proline-rich protein G1	142	37
8128	X70343	Nicotiana glauca	extensin	102	29
8129	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	113	48
8130	AF090895	Homo sapiens	PRO0117	150	71
8131	D00570	Mus musculus	open reading frame (251 AA)	130	41
8132	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	106	61
8133	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	128	61
8134	AF130079	Homo sapiens	PRO2852	181	77
8135	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	109	58
8136	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	98	64
8137	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	112	43
8138	AF119900	Homo sapiens	PRO2822	113	57
8139	D38112	Homo sapiens	NADH dehydrogenase subunit 3	427	86

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8140	AF004341	Homo sapiens	cytochrome c oxidase subunit III	155	88
8141	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	163	58
8142	D70836	Homo sapiens	Zinc-finger protein	156	47
8143	AC002291	Arabidopsis thaliana	extensin	153	37
8144	X55683	Lycopersicon esculentum	extensin (class I)	85	34
8145	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	100	76
8146	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	108	63
8147	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	110	79
8148	M22332	Homo sapiens	unknown protein	156	40
8149	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	92	76
8150	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	131	66
8151	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	441	76
8152	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	155	67
8153	AF130089	Homo sapiens	PRO2550	129	42
8154	AF130089	Homo sapiens	PRO2550	173	50
8155	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	64
8156	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	171	82
8157	L27428	Homo sapiens	reverse transcriptase	181	50
8158	U11271	Homo sapiens	thromboxane A2 receptor	138	73
8159	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	145	53
8160	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	139	58
8161	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	155	59
8162	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	141	64
8163	AF161361	Homo sapiens	HSPC098	89	66
8164	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	117	58
8165	AF130089	Homo sapiens	PRO2550	121	63
8166	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	148	85
8167	X92485	Plasmodium vivax	pval	97	56
8168	X92485	Plasmodium vivax	pval	115	57
8169	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	124	61
8170	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	123	60
8171	X92485	Plasmodium vivax	pval	105	44
8172	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	75	64
8173	S79410	Mus musculus	nuclear localization signal binding protein	106	65
8174	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	108	44

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8175	Y36203	Homo sapiens	Human secreted protein #75.	150	51
8176	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	114	41
8177	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	135	68
8178	AF090928	Homo sapiens	PRO0470	119	72
8179	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	141	75
8180	AF220264	Homo sapiens	MOST-1	94	61
8181	AF119851	Homo sapiens	PRO1722	143	73
8182	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	134	64
8183	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	143	59
8184	X92485	Plasmodium vivax	pval	127	72
8185	X92485	Plasmodium vivax	pval	130	65
8186	AF119851	Homo sapiens	PRO1722	285	64
8187	AF090942	Homo sapiens	PRO0657	137	38
8188	AF090931	Homo sapiens	PRO0483	154	66
8189	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	148	43
8190	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	268	79
8191	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	110	43
8192	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	129	78
8193	AF113685	Homo sapiens	PRO0974	86	52
8194	Y36203	Homo sapiens	Human secreted protein #75.	132	61
8195	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	225	77
8196	S80119	Rattus sp.	reverse transcriptase homolog	105	40
8197	X86031	Sus scrofa	homologue of proline/arginine-rich antibacterial protein	124	39
8198	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	121	60
8199	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	91	68
8200	Y36203	Homo sapiens	Human secreted protein #75.	131	56
8201	Y36203	Homo sapiens	Human secreted protein #75.	136	44
8202	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	166	48
8203	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	125	50
8204	Y36203	Homo sapiens	Human secreted protein #75.	127	58
8205	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	139	61
8206	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	190	92
8207	AF090931	Homo sapiens	PRO0483	160	87
8208	AF126163	Homo sapiens	HHLA3 protein	107	67
8209	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	93	41
8210	Y36156	Homo sapiens	Human secreted protein #28.	100	62
8211	AF161356	Homo sapiens	HSPC093	73	60
8212	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	107	34
8213	AB046048	Macaca	unnamed portein product	146	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		fascicularis			
8214	AF130079	Homo sapiens	PRO2852	121	59
8215	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	109	50
8216	AF090930	Homo sapiens	PRO0478	153	79
8217	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	105	60
8218	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	135	56
8219	M11901	Rattus norvegicus	proline-rich salivary protein	102	42
8220	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	95	32
8221	X52235	Homo sapiens	ORFII	174	39
8222	AF130089	Homo sapiens	PRO2550	159	67
8223	AF068294	Homo sapiens	HDCMB45P	161	58
8224	M62387	Oryctolagus cuniculus	ubiquitin conjugating-protein	219	90
8225	AF113685	Homo sapiens	PRO0974	136	65
8226	D38112	Homo sapiens	NADH dehydrogenase subunit 3	430	85
8227	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	115	58
8228	Y36156	Homo sapiens	Human secreted protein #28.	117	50
8229	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	130	44
8230	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	145	50
8231	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	105	46
8232	S62928	Homo sapiens	PRB1M protein precursor	113	37
8233	AB047600	Macaca fascicularis	hypothetical protein	142	62
8234	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	104	48
8235	U12695	Pan paniscus	cytochrome oxidase subunit II	259	84
8236	K01664	Drosophila melanogaster	Bkm-like protein	116	61
8237	AF116661	Homo sapiens	PRO1438	135	56
8238	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	107	53
8239	U93572	Homo sapiens	p40	168	49
8240	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	100	72
8241	Z70292	Homo sapiens	chemokine CC-1	231	83
8242	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	119	82
8243	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	97	83
8244	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	114	78
8245	G00338	Homo sapiens	Human secreted protein, SEQ ID NO: 4419.	81	65
8246	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	74	60
8247	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	115	58
8248	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	127	58
8249	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	107	84
8250	AF118082	Homo sapiens	PRO1902	136	50

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8251	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	196	59
8252	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	106	81
8253	AF130089	Homo sapiens	PRO2550	143	53
8254	AK024455	Homo sapiens	FLJ00047 protein	151	68
8255	AK022821	Homo sapiens	unnamed protein product	140	68
8256	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	143	53
8257	M24509	Mus musculus	ferritin heavy chain	347	69
8258	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	142	57
8259	U93570	Homo sapiens	p40	254	57
8260	AF218028	Homo sapiens	unknown	129	71
8261	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	77	68
8262	D38112	Homo sapiens	cytochrome c oxidase subunit 3	604	90
8263	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	132	60
8264	AL139298	Streptomyces coelicolor A3(2)	putative membrane protein	92	34
8265	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	138	70
8266	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	100	64
8267	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	113	38
8268	X92485	Plasmodium vivax	pval	102	63
8269	X61048	Hydra sp.	mini-collagen	110	46
8270	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	88	82
8271	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	121	75
8272	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	107	48
8273	AF090944	Homo sapiens	PRO0663	122	42
8274	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	81	85
8275	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	140	54
8276	AF130089	Homo sapiens	PRO2550	275	56
8277	L27428	Homo sapiens	reverse transcriptase	105	27
8278	S79410	Mus musculus	nuclear localization signal binding protein	112	54
8279	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	159	73
8280	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	109	71
8281	AF104921	Homo sapiens	succinyl-CoA synthetase alpha subunit	188	42
8282	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	39
8283	X55683	Lycopersicon esculentum	extensin (class I)	96	36
8284	AF225910	Mus musculus	DAZ-associated protein 1	117	33
8285	AF130089	Homo sapiens	PRO2550	347	75
8286	AB046100	Macaca fascicularis	unnamed protein product	140	45
8287	X55684	Lycopersicon	extensin (class I)	67	45

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		esculentum			
8288	AF029670	Homo sapiens	Rad51C truncated protein	186	69
8289	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	149	50
8290	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	119	67
8291	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	152	50
8292	D89999	Gallus gallus	muscle derived protein	1134	66
8293	L11566	Homo sapiens	ribosomal protein L18	335	69
8294	W61170	Homo sapiens	Partial polypeptide sequence from CP140 partial cDNA.	441	95
8295	S62077	Homo sapiens	HP1Hs alpha=25 kda chromosomal autoantigen	175	94
8296	AF119882	Homo sapiens	PRO2492	125	48
8297	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	156	54
8298	AK025116	Homo sapiens	unnamed protein product	259	82
8300	X92485	Plasmodium vivax	pval	162	47
8301	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	157	76
8302	AF092176	Homo sapiens	MHC class II antigen	280	84
8303	AF118082	Homo sapiens	PRO1902	174	52
8304	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	105	50
8305	AK023563	Homo sapiens	unnamed protein product	244	60
8306	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	136	66
8307	U15647	Mus musculus	reverse transcriptase	107	38
8308	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	110	40
8309	AB005540	Rattus rattus	PCTAIRE2	166	59
8310	M37679	Mus musculus	Ig heavy chain precursor	95	64
8311	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	137	82
8312	W29643	Homo sapiens	Human secreted protein CW383_1.	312	100
8313	AF113685	Homo sapiens	PRO0974	116	39
8314	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	128	69
8315	Z28407	Homo sapiens	ribosomal protein L8	497	78
8316	AE003536	Drosophila melanogaster	CG6451 gene product	237	51
8317	M19419	Mus musculus	proline-rich salivary protein	115	39
8318	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	92	53
8319	Y29862	Homo sapiens	Human secreted protein clone du515_21.	399	81
8320	Z34278	Homo sapiens	mucin	103	25
8321	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	142	91
8322	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	82	62
8323	Z46791	Caenorhabditis elegans	contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=67.1, E-value=1.2e-16, N=3; PF01484 (Nematode cuticle collagen N-terminal domain), Score=82.0, E-value=3.9e-21, N=1	122	37
8324	AF021232	Homo sapiens	TRAIL-R4-A	113	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8325	AB046085	Macaca fascicularis	unnamed protein product	292	75
8326	AF113944	Muntiacus muntjak	prion protein	96	39
8327	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	125	63
8328	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	123	62
8329	AJ005897	Homo sapiens	JM5	275	73
8330	AF119900	Homo sapiens	PRO2822	138	76
8331	AF163573	Homo sapiens	CARKL	359	84
8332	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	103	37
8333	AF026246	Homo sapiens	HERV-E integrase	354	78
8334	J03756	Homo sapiens	hGH-V2	362	82
8335	AB001517	Homo sapiens	KNP-I alpha protein	126	76
8336	X97490	Mus musculus	PNG protein	469	98
8337	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	159	74
8338	V18354_cd1	Homo sapiens	17-NOV-1992 Human R20 seven transmembrane (7TM) receptor genomic DNA.	379	92
8339	V18354_cd1	Homo sapiens	17-NOV-1992 Human R20 seven transmembrane (7TM) receptor genomic DNA.	402	93
8340	Z11502	Homo sapiens	intestine-specific annexin.	385	89
8341	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	110	54
8342	AC003113	Arabidopsis thaliana	F24O1.6	68	50
8343	X12517	Homo sapiens	C protein (AA 1-159)	321	82
8344	D86549	Homo sapiens	p97 homologous protein	279	96
8345	Y73384	Homo sapiens	HTRM clone 2284580 protein sequence.	1513	100
8346	AP001745	Homo sapiens	human cDNA DKFZp586F0422, Accession No. AL050173	118	40
8347	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	121	49
8348	AF091090	Homo sapiens	unknown	125	44
8349	AF106542	Homo sapiens	pregnancy-specific beta-1 glycoprotein 1	145	100
8350	AF090942	Homo sapiens	PRO0657	252	65
8351	L23116	Homo sapiens	galactocerebrosidase	185	85
8352	AJ243803	Streptomyces coelicolor A3(2)	hypothetical protein	97	36
8353	Y11339	Homo sapiens	GalNAc alpha-2,6-sialyltransferase I	306	100
8354	U09477	Homo sapiens	p53-binding protein	388	100
8355	L27584	Homo sapiens	Ca channel B3 subunit	197	100
8356	AF071569	Homo sapiens	multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform	574	100
8357	W54282	Homo sapiens	Protein sequence of the di-alpha haemoglobin gene contained in pSS1.	321	81
8358	Y12916	Homo sapiens	Amino acid sequence of a human secreted peptide.	759	100
8359	AF038961	Homo sapiens	SL15 protein	166	100
8360	W75093	Homo sapiens	Human secreted protein encoded by gene 37 clone HFVGS85.	328	90
8361	R95326	Homo sapiens	Tumor necrosis factor receptor I death domain ligand (clone 2DD).	386	97

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8362	AF026954	Bos taurus	pyruvate dehydrogenase phosphatase regulatory subunit precursor; PDP α	269	88
8363	X07855	Homo sapiens	G-Protein	289	98
8364	AL110247	Homo sapiens	hypothetical protein	265	97
8365	AB046774	Homo sapiens	KIAA1554 protein	3619	99
8366	M10050	Homo sapiens	fatty acid binding protein	97	100
8367	M20882	Homo sapiens	pregnancy-specific beta-glycoprotein e	1097	99
8368	AB051901	Homo sapiens	VDUP1	662	98
8369	U72678	Mus musculus	EF-9	176	65
8370	AL117237	Homo sapiens	hypothetical protein	478	60
8371	M10617	Homo sapiens	L-FABP	104	84
8372	AJ249980	Homo sapiens	hypothetical protein	1527	97
8373	AF003136	Caenorhabditis elegans	contains weak similarity to an AMP-binding motif	242	55
8374	X91638	Gallus gallus	BRM protein	225	90
8375	W75093	Homo sapiens	Human secreted protein encoded by gene 37 clone HFVGS85.	369	100
8376	Z36714	Homo sapiens	cyclin F	519	95
8377	X86401	Homo sapiens	L-arginine: glycine amidinotransferase	200	97
8378	M12413	Homo sapiens	apolipoprotein B100	1278	99
8379	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	159	66
8380	AF151860	Homo sapiens	CGI-102 protein	202	77
8381	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	255	92
8382	AF017807	Homo sapiens	Arp2/3 complex 16kDa subunit	418	87
8383	U28727	Homo sapiens	pregnancy-associated plasma protein-A preproform	196	97
8384	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	128	85
8385	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	203	69
8386	AF090931	Homo sapiens	PRO0483	145	77
8387	S63758	Mus sp.	metallothionein-I gene transcription activator	324	98
8388	W89030	Homo sapiens	Polypeptide fragment encoded by gene 165.	174	66
8389	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	93	70
8390	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	157	46
8391	V29245_cd1	Homo sapiens	15-NOV-1996 Nucleotide sequence of the human selenium-binding protein.	421	82
8392	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	184	77
8393	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	99	77
8394	AK023563	Homo sapiens	unnamed protein product	285	75
8395	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	161	75
8396	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	121	61
8397	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	108	70
8398	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	150	57
8399	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	108	63
8400	W88607	Homo sapiens	Secreted protein encoded by gene 74 clone HHSEG23.	146	55

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8401	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	90	69
8402	AF119851	Homo sapiens	PRO1722	133	65
8403	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	67	76
8404	L06498	Homo sapiens	ribosomal protein S20	170	94
8405	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	58
8406	AF118086	Homo sapiens	PRO1992	142	80
8407	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	153	81
8408	AF090919	Homo sapiens	PRO0327	96	74
8409	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	127	62
8410	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	150	100
8411	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	103	75
8412	AF116715	Homo sapiens	PRO2829	158	76
8413	AF229067	Homo sapiens	PADI-H protein	137	56
8414	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	131	77
8415	AF068294	Homo sapiens	HDCMB45P	132	54
8416	W34499	Homo sapiens	Obesity receptor C protein.	251	77
8417	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	272	57
8418	S79410	Mus musculus	nuclear localization signal binding protein	113	54
8419	AK025047	Homo sapiens	unnamed protein product	128	58
8420	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	130	46
8421	AL132841	Caenorhabditis elegans	Y15E3A.3	135	56
8422	AF130051	Homo sapiens	PRO0898	164	72
8423	G00092	Homo sapiens	Human secreted protein, SEQ ID NO: 4173.	161	96
8424	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	108	100
8425	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	134	75
8426	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	91	48
8427	AF194641	Homo sapiens	immunoglobulin lambda light chain variable region	174	69
8428	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	146	68
8429	M64322	Homo sapiens	protein tyrosine phosphatase	201	100
8430	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	135	55
8431	AF090931	Homo sapiens	PRO0483	158	87
8432	J04495	Macaca mulatta	alpha-globin	150	100
8433	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	150	78
8434	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	137	48
8435	AJ272324	Homo sapiens	adaptor molecule-1	333	100
8436	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	91	48
8437	M18085	Homo sapiens	glycoprotein IIb	154	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8438	X92485	Plasmodium vivax	pval	138	64
8439	G03136	Homo sapiens	Human secreted protein, SEQ ID NO: 7217.	126	56
8440	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	105	72
8441	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhala.	122	55
8442	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	139	69
8443	Y36203	Homo sapiens	Human secreted protein #75.	103	70
8444	AB034633	Mus musculus	deubiquitinating enzyme	129	100
8445	U01849	Trypanosoma brucei	ORF2	95	41
8446	J05497	Rattus norvegicus	snRNP-associated polypeptide N	115	37
8447	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	137	50
8448	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	222	100
8449	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	168	94
8450	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	152	63
8451	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	162	91
8452	W78226	Homo sapiens	Fragment of human secreted protein encoded by gene 1.	804	97
8453	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	109	100
8454	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	138	88
8455	AF099505	Homo sapiens	colon carcinoma related protein	100	63
8456	AF217511	Homo sapiens	uncharacterized bone marrow protein BM034	130	96
8457	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	70
8458	L17007	Didelphis marsupialis	protamine 1	101	80
8459	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	145	62
8460	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	121	75
8461	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	110	81
8462	AF016371	Homo sapiens	U-snRNP-associated cyclophilin	108	70
8463	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	80	93
8464	AF130089	Homo sapiens	PRO2550	190	65
8465	AF197913	Helicoverpa armigera nuclear polyhedrosis virus	basic DNA-binding protein BDBP	159	55
8466	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	183	70
8467	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	97	60
8468	AF118082	Homo sapiens	PRO1902	72	42
8469	AF217449	Schistosoma mekongi	NADH dehydrogenase subunit 6	107	40
8470	G03258	Homo sapiens	Human secreted protein, SEQ ID NO:	88	75

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7339.		
8471	AF090931	Homo sapiens	PRO0483	161	79
8472	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	127	56
8473	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	50
8474	AF022789	Homo sapiens	ubiquitin hydrolyzing enzyme I	140	100
8475	X03145	Homo sapiens	pot. ORF VI	349	81
8476	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	65
8477	R59842	Homo sapiens	ApoE4L1 protease.	115	69
8478	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	112	56
8479	K01664	Drosophila melanogaster	Bkm-like protein	140	44
8480	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	95	70
8481	AF090931	Homo sapiens	PRO0483	111	67
8482	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	122	92
8483	M69297	Homo sapiens	ORF 3	102	39
8484	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	148	72
8485	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	136	65
8486	AF032906	Homo sapiens	cathepsin Z precursor; CTSZ	299	100
8487	X15917	Paramecium aurelia	ND2 protein (AA 1-193) (unusual start codon)	94	35
8488	U93574	Homo sapiens	putative p150	109	35
8489	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	142	72
8490	X92485	Plasmodium vivax	pval	120	85
8491	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	109	42
8492	M15530	Homo sapiens	B-cell growth factor	126	64
8493	AF090895	Homo sapiens	PRO0117	123	60
8494	G02403	Homo sapiens	Human secreted protein, SEQ ID NO: 6484.	166	100
8495	AF116661	Homo sapiens	PRO1438	126	63
8496	AF130089	Homo sapiens	PRO2550	298	70
8497	AF090895	Homo sapiens	PRO0117	113	75
8498	AF090930	Homo sapiens	PRO0478	142	68
8499	AF126163	Homo sapiens	HHLA3 protein	139	72
8500	G02360	Homo sapiens	Human secreted protein, SEQ ID NO: 6441.	109	75
8501	S79410	Mus musculus	nuclear localization signal binding protein	98	48
8502	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	132	63
8503	AF119851	Homo sapiens	PRO1722	107	53
8504	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	158	67
8505	AF090931	Homo sapiens	PRO0483	128	50
8506	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	126	56
8507	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	154	82
8508	X92485	Plasmodium	pval	83	70

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
8509	AL390114	Leishmania major	extremely cysteine/valine rich protein	144	50
8510	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	124	86
8511	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	141	51
8512	AF229067	Homo sapiens	PADI-H protein	155	76
8513	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	170	68
8514	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	157	66
8515	AF090930	Homo sapiens	PRO0478	88	80
8516	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	134	59
8517	K01664	Drosophila melanogaster	Bkm-like protein	102	92
8518	M31145	Homo sapiens	insulin-like growth factor binding protein precursor	460	96
8519	M18193	Homo sapiens	inter-alpha-trypsin inhibitor heavy chain old gene name 'ITI'	118	41
8520	AF116689	Homo sapiens	PRO2168	127	92
8521	AF130051	Homo sapiens	PRO0898	133	85
8522	L27428	Homo sapiens	reverse transcriptase	201	72
8523	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	108	74
8524	AF161356	Homo sapiens	HSPC093	127	60
8525	Y02926	Homo sapiens	Fragment of human secreted protein encoded by gene 101.	95	83
8526	AF118086	Homo sapiens	PRO1992	95	64
8527	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	108	50
8528	AB046048	Macaca fascicularis	unnamed portein product	154	62
8529	AF130089	Homo sapiens	PRO2550	150	70
8530	Y03000	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	111	55
8531	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	108	65
8532	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	172	59
8533	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	395	91
8534	S79410	Mus musculus	nuclear localization signal binding protein	100	45
8535	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	107	95
8536	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	128	89
8537	Z28407	Homo sapiens	ribosomal protein L8	242	79
8538	AF130089	Homo sapiens	PRO2550	139	71
8539	Q55625_cd1	Homo sapiens	22-JUN-1992 Human beta globin 5'-UTR-CDS-3'-UTR.	274	76
8540	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	154	61
8541	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	69
8542	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	64
8543	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	240	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6953.		
8544	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	117	85
8545	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	110	95
8546	AF119851	Homo sapiens	PRO1722	146	80
8547	U49973	Homo sapiens	ORF2: function unknown	105	86
8548	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	71
8549	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	152	53
8550	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	80	40
8551	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	140	74
8552	V00672	Pan troglodytes	reading frame protein 4	142	92
8553	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	164	63
8554	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	148	71
8555	AB046100	Macaca fascicularis	unnamed protein product	144	58
8556	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	322	73
8557	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	140	62
8558	U30888	Homo sapiens	tRNA-Guanine Transglycosylase	276	86
8559	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	114	71
8560	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	108	72
8561	G03136	Homo sapiens	Human secreted protein, SEQ ID NO: 7217.	110	57
8562	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	140	83
8563	W34499	Homo sapiens	Obesity receptor C protein.	188	92
8564	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	124	56
8565	L07946	Volvox carteri	histone H1-I	108	38
8566	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	132	77
8567	M13941	Human herpesvirus 4	nuclear antigen 1	100	43
8568	Y36156	Homo sapiens	Human secreted protein #28.	136	67
8569	X70343	Nicotiana sylvestris	extensin	92	34
8570	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	381	87
8571	V00672	Pan troglodytes	reading frame protein 4	146	93
8572	D38116	Pan paniscus	ATPase subunit 6	116	96
8573	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	132	52
8574	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	217	100
8575	M58009	Pan troglodytes	cytochrome c oxidase subunit II	271	84
8576	D38112	Homo sapiens	ATPase subunit 6	117	96
8577	D38112	Homo sapiens	ATPase subunit 6	180	93
8578	D38112	Homo sapiens	NADH dehydrogenase subunit 1	179	91
8579	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	88

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8580	M15530	Homo sapiens	B-cell growth factor	109	71
8581	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	127	77
8582	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	109	47
8583	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	131	71
8584	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	241	97
8585	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	185	80
8586	M28016	Homo sapiens	cytochrome b	129	92
8587	M58009	Pan troglodytes	cytochrome c oxidase subunit II	153	96
8588	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	90
8589	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	109	51
8590	L00016	Homo sapiens	urf4	176	94
8591	AF150105	Homo sapiens	small zinc finger-like protein	523	100
8592	U15306	Homo sapiens	NFX1	123	95
8594	R44519	Homo sapiens	Adult human alpha-globin V107S.	222	78
8595	Y03000	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	128	70
8596	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	151	90
8597	X67688	Homo sapiens	transketolase	123	84
8598	L00016	Homo sapiens	urf4	130	85
8599	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	109	54
8600	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	159	89
8601	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	151	54
8602	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	115	43
8603	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	95
8604	S79980	Bos taurus	ribosomal protein L37	109	84
8605	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	127	48
8606	D38112	Homo sapiens	ATPase subunit 6	202	100
8607	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	150	42
8608	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	127	58
8609	AF229067	Homo sapiens	PADI-H protein	112	78
8610	AF130089	Homo sapiens	PRO2550	125	86
8611	J03071	Homo sapiens	chorionic somatomammotropin CS-5	710	97
8612	AL390114	Leishmania major	extremely cysteine/valine rich protein	104	41
8613	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	84
8614	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	116	70
8615	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	91
8616	M28016	Homo sapiens	cytochrome b	148	93
8617	AF118082	Homo sapiens	PRO1902	94	66
8618	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	182	82
8619	X02585	Xenopus laevis	unidentified open reading frame 1 (166	170	72

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			aa)		
8620	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	125	57
8621	AC004450	Arabidopsis thaliana	putative extensin	140	48
8622	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	195	79
8623	AF130089	Homo sapiens	PRO2550	150	78
8624	L00016	Homo sapiens	urf4	280	92
8625	AF130051	Homo sapiens	PRO0898	161	76
8626	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	123	49
8627	L00016	Homo sapiens	urf4	201	95
8628	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	169	82
8629	AF119851	Homo sapiens	PRO1722	171	65
8630	X55654	Homo sapiens	cytochrome C oxidase II subunit	120	92
8631	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	108	56
8632	X55654	Homo sapiens	cytochrome C oxidase II subunit	107	95
8633	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	132	86
8634	AJ224997	Rattus norvegicus	huntingtin	73	59
8635	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	80
8636	M19061	Ateles geoffroyi	delta-globin	100	40
8637	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	102	65
8638	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	104	50
8639	AF116715	Homo sapiens	PRO2829	158	76
8640	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	142	62
8641	Y09010	Mus musculus	Ser/Thr kinase	193	95
8642	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	227	79
8643	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	116	95
8644	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	88
8645	V46311_cd1	Homo sapiens	12-JAN-1998 Human secreted protein cDNA from clone D157.	197	100
8646	Y17379	Homo sapiens	NADH:ubiquinone oxidoreductase 51-kD subunit	240	97
8647	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	142	68
8648	AJ388520	Canis familiaris	Ribosomal protein	134	100
8649	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	136	56
8650	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	116	80
8651	S79410	Mus musculus	nuclear localization signal binding protein	99	36
8652	G00492	Homo sapiens	Human secreted protein, SEQ ID NO: 4573.	136	64
8653	AF229067	Homo sapiens	PADI-H protein	134	69
8654	AF090942	Homo sapiens	PRO0657	103	42
8655	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	184	84

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8656	U37359	Homo sapiens	MRE11 homologue hMre11	238	97
8657	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	113	60
8658	G00262	Homo sapiens	Human secreted protein, SEQ ID NO: 4343.	124	83
8659	AF161356	Homo sapiens	HSPC093	149	64
8660	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	121	44
8661	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	107	37
8662	U19098	Lycopersicon chilense	proline-rich protein	72	48
8663	AF118082	Homo sapiens	PRO1902	95	75
8664	AF130089	Homo sapiens	PRO2550	307	79
8665	AL390114	Leishmania major	extremely cysteine/valine rich protein	115	40
8666	X55683	Lycopersicon esculentum	extensin (class I)	102	32
8667	AK026841	Homo sapiens	unnamed protein product	276	100
8668	AL109963	Homo sapiens	dJ1188J21.1 (FSH primary response (LRPR1, rat) homolog 1)	597	100
8669	Y01181	Homo sapiens	Polypeptide fragment encoded by gene 12.	123	58
8670	W48352	Homo sapiens	Human breast cancer related protein BCFLT1.	103	65
8671	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	121	61
8672	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	184	82
8673	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	211	93
8674	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	126	61
8675	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	114	66
8676	X55691	Lycopersicon esculentum	glycine-rich protein	85	38
8677	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	188	80
8678	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	183	75
8679	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	71
8680	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	96	82
8681	U80761	Homo sapiens	CTG26 alternate open reading frame	136	88
8682	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	137	93
8683	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	107	45
8684	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	141	90
8685	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	127	55
8686	W64486	Homo sapiens	Human DR3 protein.	139	100
8687	M18093	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	134	33
8688	K03202	Homo sapiens	salivary proline-rich protein precursor	119	35
8689	U36448	Homo sapiens	Ca2+-dependent activator protein for	107	91

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			secretion		
8690	G02409	Homo sapiens	Human secreted protein, SEQ ID NO: 6490.	80	43
8691	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	147	74
8692	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	126	95
8693	AF130089	Homo sapiens	PRO2550	126	35
8694	M58009	Pan troglodytes	cytochrome c oxidase subunit II	233	97
8695	M11902	Mus musculus	proline-rich salivary protein	98	35
8696	W34499	Homo sapiens	Obesity receptor C protein.	263	83
8697	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	181	73
8698	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	48
8699	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	88
8700	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	51
8701	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	73
8702	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	133	62
8703	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	184	92
8704	D38112	Homo sapiens	ATPase subunit 6	117	96
8705	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	97	58
8706	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	115	79
8707	AF118086	Homo sapiens	PRO1992	167	81
8708	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	114	51
8709	L10908	Mus musculus	Gcap1 gene product	179	38
8710	S79410	Mus musculus	nuclear localization signal binding protein.	135	69
8711	AF130089	Homo sapiens	PRO2550	399	78
8712	X55654	Homo sapiens	cytochrome C oxidase II subunit	107	95
8713	AF118082	Homo sapiens	PRO1902	123	58
8714	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	173	81
8715	V35554_cdl	Homo sapiens	21-NOV-1996 Human tumour antigen protein (clone 3) encoding cDNA.	258	83
8716	AF130089	Homo sapiens	PRO2550	143	51
8717	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rhala.	92	52
8718	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	147	71
8719	AF153208	Homo sapiens	GC-rich sequence DNA-binding factor candidate	115	70
8720	AF090931	Homo sapiens	PRO0483	145	87
8721	X92485	Plasmodium vivax	pval	125	79
8722	U72543	Sus scrofa	ubiquitin-like/S30 ribosomal fusion protein	201	97
8723	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	223	85
8724	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	121	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8725	AF130051	Homo sapiens	PRO0898	102	72
8726	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	185	78
8727	R24750	Homo sapiens	hGH variant #38-- 174S-176Y 10F 14S 18F 21L 167S 171D 175T 179T.	116	82
8728	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	92	72
8729	X53375	Helianthus annuus	anther-specific protein SF18	114	39
8730	S74221	Homo sapiens	IK factor=cytokine down-regulating HLA class II	159	42
8731	AC003058	Arabidopsis thaliana	unknown protein	166	89
8732	AB027508	Homo sapiens	hVPS11	194	50
8733	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	144	93
8734	AF266479	Homo sapiens	rectachrome 1	116	74
8735	AL132841	Caenorhabditis elegans	Y15E3A.3	125	60
8736	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	152	65
8737	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	79	56
8738	U93565	Homo sapiens	putative p150	190	52
8739	AF026689	Homo sapiens	prostate-specific transglutaminase	117	57
8740	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	109	70
8741	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	165	61
8742	M58009	Pan troglodytes	cytochrome c oxidase subunit II	213	97
8743	M17887	Homo sapiens	acidic ribosomal phosphoprotein (P2)	106	74
8744	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	116	49
8745	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	134	68
8746	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	135	71
8747	M76546	Helianthus annuus	hydroxyproline-rich protein	94	40
8748	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	173	76
8749	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	166	67
8750	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	272	57
8751	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	131	71
8752	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	123	37
8753	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	180	55
8754	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	105	44
8755	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	103	78
8756	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	284	87
8757	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	190	89

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8758	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	103	40
8759	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	120	61
8760	AF132984	Homo sapiens	nuclear pore complex interacting protein NPIP	196	94
8761	AF130079	Homo sapiens	PRO2852	125	65
8762	AF155232	Pisum sativum	extensin	177	42
8763	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	95
8764	X75438	Sus scrofa	homologue of proline/arginine rich antibacterial peptides	96	38
8765	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	157	96
8766	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	137	75
8767	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	207	95
8768	AL161543	Arabidopsis thaliana	extensin like protein	100	38
8769	K03202	Homo sapiens	salivary proline-rich protein precursor	110	47
8770	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	178	78
8771	D83407	Homo sapiens	a thyroid hormone responsive gene in human skin fibroblasts	133	100
8772	V00662	Homo sapiens	URF A6L (NADH dehydrogenase subunit)	172	73
8773	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	107	66
8774	AL390114	Leishmania major	extremely cysteine/valine rich protein	117	100
8775	AF090931	Homo sapiens	PRO0483	175	88
8776	S79410	Mus musculus	nuclear localization signal binding protein	125	58
8777	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	126	73
8778	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	154	70
8779	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome..	149	50
8780	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	170	91
8781	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	103	65
8782	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	184	70
8783	AC003058	Arabidopsis thaliana	unknown protein	169	97
8784	U55376	Caenorhabditis elegans	F16H11.2 gene product	141	90
8785	U55376	Caenorhabditis elegans	F16H11.2 gene product	150	100
8786	AL132841	Caenorhabditis elegans	Y15E3A.3	127	96
8787	AF266479	Homo sapiens	rectachrome 1	148	61
8788	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	106	95
8789	AL132841	Caenorhabditis elegans	Y15E3A.3	162	96
8790	AC006693	Caenorhabditis	Hypothetical protein W02H5.c	180	94

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		<i>elegans</i>			
8791	U28971	<i>Caenorhabditis elegans</i>	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	159	80
8792	AF150105	<i>Homo sapiens</i>	small zinc finger-like protein	505	98
8793	AL390935	<i>Leishmania major</i>	probable pro0195	85	31
8794	Y19767	<i>Homo sapiens</i>	SEQ ID NO 485 from WO9922243.	115	55
8795	AF118082	<i>Homo sapiens</i>	PRO1902	123	75
8796	D38112	<i>Homo sapiens</i>	ATPase subunit 6	438	82
8797	AF118086	<i>Homo sapiens</i>	PRO1992	156	81
8798	Y53037	<i>Homo sapiens</i>	Human secreted protein clone dx219_13 protein sequence SEQ ID NO:80.	196	100
8799	X92485	<i>Plasmodium vivax</i>	pva1	132	63
8800	G02532	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 6613.	170	65
8801	G00397	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 4478.	123	58
8802	AF116909	<i>Homo sapiens</i>	unknown	116	63
8803	X92485	<i>Plasmodium vivax</i>	pva1	127	82
8804	G03438	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7519.	140	67
8805	Z95114	<i>Homo sapiens</i>	bK212A2.2 (apolipoprotein L, 2)	294	100
8806	AF143369	<i>Mus musculus</i>	msg1-related protein 2	348	83
8807	G00500	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 4581.	110	76
8808	AP000616	<i>Oryza sativa</i>	similar to RING-H2 finger protein RHA1a (AF078683)	129	91
8809	AF230279	<i>Caenorhabditis elegans</i>	SWI3-like protein; PSA-1	126	37
8810	D38112	<i>Homo sapiens</i>	NADH dehydrogenase subunit 4L	168	82
8811	Y86248	<i>Homo sapiens</i>	Human secreted protein HCHPF68, SEQ ID NO:163.	122	54
8812	D38112	<i>Homo sapiens</i>	ATPase subunit 6	207	100
8813	W99376	<i>Homo sapiens</i>	Human fibroblast growth factor 2 24 kD isoform N-terminus.	93	41
8814	G03043	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7124.	157	57
8815	X54978	<i>Bos taurus</i>	17,000 dalton myosin light chain	133	96
8816	M58459	<i>Homo sapiens</i>	ribosomal protein S4Y isoform	260	100
8817	D38112	<i>Homo sapiens</i>	NADH dehydrogenase subunit 1	256	90
8818	U23947	<i>Mycoplasma pulmonis</i>	VsaD1	132	31
8819	G03172	<i>Homo sapiens</i>	Human secreted protein, SEQ ID NO: 7253.	140	69
8820	L00016	<i>Homo sapiens</i>	urf4	205	90
8821	X55683	<i>Lycopersicon esculentum</i>	extensin (class I)	111	43
8822	AL160493	<i>Leishmania major</i>	probable (hhv-6) u1102, variant a DNA, complete virion genome	94	43
8823	X66285	<i>Mus musculus</i>	HC1 ORF	94	53
8824	AF061340	<i>Artibeus jamaicensis</i>	F1 ATPase subunit 6	97	90
8825	M18093	<i>Phaseolus vulgaris</i>	hydroxyproline-rich glycoprotein	123	36
8826	AF119855	<i>Homo sapiens</i>	PRO1847	113	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8827	M28016	Homo sapiens	cytochrome b	140	93
8828	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	142	56
8829	AK024455	Homo sapiens	FLJ00047 protein	145	59
8830	D38112	Homo sapiens	ATPase subunit 6	194	95
8831	D38112	Homo sapiens	ATPase subunit 6	184	90
8832	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	60
8833	AF130079	Homo sapiens	PRO2852	115	88
8834	AB003784	Drosophila simulans	Histone H3	135	100
8835	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	173	82
8836	X70343	Nicotiana glauca	extensin	112	37
8837	L17318	Rattus norvegicus	proline-rich proteoglycan	142	38
8838	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	148	74
8839	W34625	Homo sapiens	Human C3 protein mutant FT-3.	277	100
8840	AF116638	Homo sapiens	PRO1546	78	41
8841	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	138	61
8842	AF130087	Homo sapiens	PRO2411	131	67
8843	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	150	72
8844	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	155	60
8845	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	108	66
8846	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	68
8847	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	146	70
8848	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	131	68
8849	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	273	79
8850	K02120	Bovine leukemia virus	gag	201	54
8851	AF229067	Homo sapiens	PADI-H protein	162	57
8852	AF090931	Homo sapiens	PRO0483	125	82
8853	R14584	Homo sapiens	TGF beta 1 binding protein encoded by clone BPA 13.	189	100
8854	U52197	Mus musculus	poly(A) polymerase III	183	85
8855	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	193	72
8856	G00549	Homo sapiens	Human secreted protein, SEQ ID NO: 4630.	104	66
8857	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	93	64
8858	Q55625_cd1	Homo sapiens	22-JUN-1992 Human beta globin 5'-UTR-CDS-3'-UTR.	412	98
8859	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	152	67
8860	G02828	Homo sapiens	Human secreted protein, SEQ ID NO: 6909.	112	72
8861	AF130079	Homo sapiens	PRO2852	160	64
8862	G00407	Homo sapiens	Human secreted protein, SEQ ID NO:	101	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4488.		
8863	X64707	Homo sapiens	BBC1	216	100
8864	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	127	65
8865	G00092	Homo sapiens	Human secreted protein, SEQ ID NO: 4173.	210	100
8866	AL137351	Homo sapiens	hypothetical protein	327	100
8867	AF090942	Homo sapiens	PRO0657	105	38
8868	AK023050	Homo sapiens	unnamed protein product	137	60
8869	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	101	65
8870	AF216751	Homo sapiens	CDA14	282	96
8871	AL133262	Homo sapiens	dJ319D22.1 (CDC5-like protein)	158	90
8872	V32779_cd1	Homo sapiens	11-MAR-1997 Novel human F0 ATP synthase subunit encoding DNA sequence.	267	81
8873	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	118	58
8874	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	89	43
8875	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	154	63
8876	AK001873	Homo sapiens	unnamed protein product	373	100
8877	X52138	Homo sapiens	L7a protein	259	82
8878	X52138	Homo sapiens	L7a protein	273	87
8879	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	147	57
8880	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	128	57
8881	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	159	71
8882	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	153	67
8883	AF130089	Homo sapiens	PRO2550	134	79
8884	U36898	Rattus norvegicus	pheromone receptor VN6	143	53
8885	S79410	Mus musculus	nuclear localization signal binding protein	143	64
8886	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	138	92
8887	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	124	72
8888	R48296	Homo sapiens	Human PGF-2/NT-3.	118	66
8889	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	81	77
8890	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	120	50
8891	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	121	77
8892	X53375	Helianthus annuus	anther-specific protein SF18	109	64
8893	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	119	54
8894	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	136	68
8895	AF090894	Homo sapiens	PRO0113	114	60
8896	AF161356	Homo sapiens	HSPC093	148	51
8897	AF116638	Homo sapiens	PRO1546	91	45
8898	U22231	Felis catus	ribosomal protein S3a	201	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8899	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	114	75
8900	AF090894	Homo sapiens	PRO0113	114	61
8901	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	63
8902	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	126	95
8903	R90288	Homo sapiens	Modified pigment epithelium-derived factor (rPEDF).	258	88
8904	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	86
8905	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	118	66
8906	X70343	Nicotiana glauca	extensin	122	37
8907	G02386	Homo sapiens	Human secreted protein, SEQ ID NO: 6467.	162	70
8908	AF130089	Homo sapiens	PRO2550	125	85
8909	AF220264	Homo sapiens	MOST-1	113	47
8910	Y25769	Homo sapiens	Human secreted protein encoded from gene 59.	119	77
8911	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	77	52
8912	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	162	83
8913	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	104	77
8914	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	138	64
8915	AF090944	Homo sapiens	PRO0663	73	58
8916	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	151	76
8917	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	84	47
8918	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	64
8919	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	254	82
8920	AJ245416	Homo sapiens	G7b protein	360	86
8921	D90228	Homo sapiens	mitochondrial acetoacetyl-CoA thiolase precursor	190	100
8922	AF229067	Homo sapiens	PADI-H protein	157	65
8923	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	132	65
8924	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	62	68
8925	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	116	63
8926	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	140	65
8927	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	184	59
8928	AF287892	Homo sapiens	sialic acid binding immunoglobulin-like lectin 8 long splice variant	994	76
8929	AF030131	Mus musculus	Plenty of SH3s; POSH	181	77
8930	J02459	bacteriophage lambda	E (capsid component;341)	814	98
8931	U13866	unidentified cloning vector	non-functional lacZ alpha peptide	112	59

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8932	U67540	Methanococcus jannaschii	conserved hypothetical protein	98	56
8933	Z74472	Caenorhabditis elegans	<p>predicted using Genefinder—contains similarity to Pfam domain: PF01391 (Collagen triple helix repeat (20 copies)), Score=84.3, E-value=8.1e-22, N=2; PF01484 (Nematode cuticle collagen N-terminal domain), Score=34.2, E-value=9.9e-07, N=1—cDNA EST yk100d10.3 comes from this gene; cDNA EST EMBL:D65979 comes from this gene—cDNA EST yk100d4.3 comes from this gene; cDNA EST yk123g7.3 comes from this gene—cDNA EST yk58e6.3 comes from this gene; cDNA EST yk67a5.3 comes from this gene—cDNA EST EMBL:T01590 comes from this gene; cDNA EST yk60c11.3 comes from this gene—cDNA EST yk89c10.3 comes from this gene; cDNA EST yk85g9.3 comes from this gene—cDNA EST yk83e2.5 comes from this gene; cDNA EST yk75f2.3 comes from this gene—cDNA EST CEESK90F comes from this gene; cDNA EST yk79f5.5 comes from this gene—cDNA EST yk64b12.3 comes from this gene; cDNA EST yk64h9.3 comes from this gene—cDNA EST yk74d1.3 comes from this gene; cDNA EST yk75e4.3 comes from this gene—cDNA EST yk83e2.3 comes from this gene; cDNA EST yk91c12.3 comes from this gene—cDNA EST yk98f2.3 comes from this gene; cDNA EST yk60h4.5 comes from this gene—cDNA EST yk60c11.5 comes from this gene; cDNA EST yk64h9.5 comes from this gene—cDNA EST yk64a9.5 comes from this gene; cDNA EST yk64b12.5 comes from this gene—cDNA EST yk67a5.5 comes from this gene; cDNA EST yk74d1.5 comes from this gene—cDNA EST yk75e4.5 comes from this gene; cDNA EST yk75f2.5 comes from this gene—cDNA EST yk79e6.5 comes from this gene; cDNA EST yk80d2.5 comes from this gene—cDNA EST yk85g9.5 comes from this gene; cDNA EST yk89c10.5 comes from this gene—cDNA EST yk89c4.5 comes from this gene; cDNA EST yk90e11.5 comes from this gene—cDNA EST yk91c12.5 comes from this gene; cDNA EST yk96e2.5 comes from this gene—cDNA EST yk98c2.5 comes from this gene; cDNA EST yk98f2.5 comes from this gene—cDNA EST yk98h11.5 comes</p>	101	38

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			from this gene; cDNA EST yk107e7.5 comes from this gene~cDNA EST yk313g9.3 comes from this gene; cDNA EST yk313g9.5 comes from this gene~cDNA EST yk312g1.3 comes from this gene; cDNA EST yk312g1.5 comes from this gene~cDNA EST yk293c4.3 comes from this gene; cDNA EST yk293c4.5 comes from this gene		
8934	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	127	63
8935	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	48
8936	X03741	Homo sapiens	myosin heavy chain (635 AA)	1343	99
8937	M29295	Rattus norvegicus	small nuclear ribonucleoparticle-associated protein	106	52
8938	D00097	Homo sapiens	serum amyloid P component	188	100
8939	W34499	Homo sapiens	Obesity receptor C protein.	255	83
8940	L00016	Homo sapiens	urf4	293	83
8941	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	164	94
8942	AB007148	Homo sapiens	ribosomal protein S3a	153	73
8943	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	213	95
8944	M10119	Homo sapiens	ferritin light subunit	129	100
8945	M74718	Homo sapiens	SEF2-1A protein	118	84
8946	AL355178	Homo sapiens	dJ947L8.1.6 (novel CUB and Sushi (SCR repeat) domain protein)	366	51
8947	Y56033	Homo sapiens	Polyproline-rich domain from dynamin.	70	51
8948	X06547	Homo sapiens	glutathione S-transferase (GST-Pi) (AA 1 - 210)	172	97
8949	AF119851	Homo sapiens	PRO1722	154	78
8950	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	123	88
8951	X54802	Homo sapiens	cytochrome-c oxidase subunit IV	116	95
8952	AJ011580	bacteriophage PS34	gp23	338	98
8953	Y59441	Homo sapiens	Human delta3 fragment #5.	271	96
8954	J02459	bacteriophage lambda	B (capsid component;533)	807	99
8955	AL132841	Caenorhabditis elegans	Y15E3A.3	172	94
8956	W34499	Homo sapiens	Obesity receptor C protein.	166	89
8957	X92485	Plasmodium vivax	pva1	135	71
8958	AB010340	Mus musculus	mszf81	122	60
8959	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	103	51
8960	X14898	Cricetulus sp.	ORF (AA 1-286) (1 is 2nd base in codon)	108	54
8961	AF090931	Homo sapiens	PRO0483	119	82
8962	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	130	72
8963	AF170724	Homo sapiens	cell cycle checkpoint protein CHFR	1364	99
8964	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	151	43
8965	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	250	74

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
8966	Y87233	Homo sapiens	Human signal peptide containing protein HSPP-10 SEQ ID NO:10.	445	100
8967	AF127085	Mus musculus	semaphorin cytoplasmic domain-associated protein 3B	112	80
8968	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	109	46
8969	AF090894	Homo sapiens	PRO0113	153	61
8970	Y19730	Homo sapiens	SEQ ID NO 448 from WO9922243.	158	49
8971	U38544	Mus musculus	alpha-1 type 1 collagen	102	52
8972	X92485	Plasmodium vivax	pva1	113	50
8973	AF241228	Xenopus laevis	Friend of GATA	143	100
8974	AF090930	Homo sapiens	PRO0478	79	41
8975	AF238374	Homo sapiens	mutant fibroblast growth factor receptor 3; FGFR3	115	50
8976	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	99	43
8977	AB001838	Homo sapiens	recoverin	179	80
8978	AF118082	Homo sapiens	PRO1902	73	70
8979	AF116715	Homo sapiens	PRO2829	102	76
8980	AF090942	Homo sapiens	PRO0657	132	61
8981	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	158	65
8982	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	108	84
8983	A00127	Homo sapiens	melanoma associated antigen P97	366	94
8984	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	158	88
8985	Y59778	Homo sapiens	Human normal ovarian tissue derived protein 55.	71	61
8986	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	42
8987	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	98	50
8988	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	80	51
8989	Y24025	Homo sapiens	Amino acid sequence of the human MMSC1 protein.	160	100
8990	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	130	67
8991	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	165	82
8992	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	111	62
8993	M28016	Homo sapiens	cytochrome b	130	100
8994	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	133	90
8995	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	298	89
8996	Y16430	Mus musculus	ribosomal protein L35a	101	65
8997	Y45318	Homo sapiens	Human secreted protein fragment encoded from gene 18.	96	76
8998	AL049659	Arabidopsis thaliana	putative protein	126	42
8999	AE003500	Drosophila melanogaster	CG12379 gene product	285	67
9000	R37991	Homo sapiens	Sequence of a new cytokine which inhibites induction by gammainterferon of expression of Class II histocompatibility antigens.	124	48

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9001	AF090930	Homo sapiens	PRO0478	193	89
9002	AP000381	Arabidopsis thaliana	gb AAF57656.1~gene_id:K17E12.13~similar to unknown protein	193	29
9003	M17885	Homo sapiens	acidic ribosomal phosphoprotein (P0)	364	66
9004	D63424	Homo sapiens	glycogen synthase kinase 3alpha	126	81
9005	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	75
9006	AL117637	Homo sapiens	hypothetical protein	257	92
9007	AE001381	Plasmodium falciparum	hypothetical protein	141	26
9008	W34499	Homo sapiens	Obesity receptor C protein.	152	86
9009	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	199	80
9010	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	202	94
9011	AF090931	Homo sapiens	PRO0483	135	68
9012	M11717	Homo sapiens	heat shock protein	696	100
9013	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	123	75
9014	R59842	Homo sapiens	ApoE4L1 protease.	86	85
9015	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	96	65
9016	AF229067	Homo sapiens	PADI-H protein	119	54
9017	AF090944	Homo sapiens	PRO0663	138	54
9018	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	103	50
9019	X92485	Plasmodium vivax	pval	101	73
9020	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	82	72
9021	AF073519	Homo sapiens	small EDRK-rich factor 1, long isoform	116	66
9022	AF229067	Homo sapiens	PADI-H protein	127	45
9023	M33112	Homo sapiens	amyloid-beta protein	105	67
9024	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	79	68
9025	AF161361	Homo sapiens	HSPC098	130	55
9026	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	169	72
9027	AF130051	Homo sapiens	PRO0898	138	77
9028	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	132	49
9029	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	117	58
9030	AC002310	Homo sapiens	Unknown gene product	155	85
9031	X92485	Plasmodium vivax	pval	112	42
9032	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	130	52
9033	G00487	Homo sapiens	Human secreted protein, SEQ ID NO: 4568.	123	69
9034	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	138	61
9035	AL390114	Leishmania major	extremely cysteine/valine rich protein	111	66
9036	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	173	59
9037	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	100	54
9038	AF220264	Homo sapiens	MOST-1	96	80

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9039	AF130051	Homo sapiens	PRO0898	119	68
9040	AF116715	Homo sapiens	PRO2829	121	63
9041	L76200	Homo sapiens	guanylate kinase	193	83
9042	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	125	55
9043	AF152513	Homo sapiens	protocadherin gamma A6 short form protein	334	100
9044	AF130079	Homo sapiens	PRO2852	125	33
9045	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	128	64
9046	AF090942	Homo sapiens	PRO0657	126	65
9047	AF284223	Homo sapiens	terra-like protein	228	100
9048	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	68
9049	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	132	92
9050	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	123	75
9051	AL034344	Homo sapiens	dJ118B18.1 (forkhead box C1)	323	100
9052	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	106	62
9053	AF225910	Mus musculus	DAZ-associated protein 1	100	45
9054	AF130087	Homo sapiens	PRO2411	147	70
9055	W80400	Homo sapiens	A secreted protein encoded by clone dd71_2.	858	97
9056	X70343	Nicotiana glauca	extensin	113	33
9057	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	57
9058	R95913	Homo sapiens	Neural thread protein.	142	38
9059	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	131	56
9060	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	131	50
9061	X70343	Nicotiana glauca	extensin	103	42
9062	AJ271872	Nicotiana glauca	extensin	129	33
9063	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	151	73
9064	AF266164	Rattus norvegicus	densin-180 variant D	144	96
9065	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	135	68
9066	M28016	Homo sapiens	cytochrome b	178	87
9067	M28016	Homo sapiens	cytochrome b	193	95
9068	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	60
9069	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	111	100
9070	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	141	72
9071	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	147	64
9072	AL390114	Leishmania major	extremely cysteine/valine rich protein	109	69
9073	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	171	85
9074	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	88	88
9075	Y14482	Homo sapiens	Fragment of human secreted protein	137	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			encoded by gene 17.		
9076	L38941	Homo sapiens	ribosomal protein L34	139	88
9077	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065....	164	86
9078	X55684	Lycopersicon esculentum	extensin (class I)	72	35
9079	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	176	82
9080	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	229	59
9081	AF130089	Homo sapiens	PRO2550	118	71
9082	X92485	Plasmodium vivax	pval	125	71
9083	AF216650	Homo sapiens	MTAP	154	73
9084	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	124	78
9085	J02459	bacteriophage lambda	E (capsid component;341)	191	73
9086	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	138	61
9087	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	130	75
9088	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	144	61
9089	AK024455	Homo sapiens	FLJ00047 protein	145	82
9090	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	181	60
9091	AF090895	Homo sapiens	PRO0117	87	66
9092	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	211	86
9093	AF130079	Homo sapiens	PRO2852	157	74
9094	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	180	82
9095	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	97	42
9096	X65551	Homo sapiens	antigen of the monoclonal antibody Ki-67	106	65
9097	W34499	Homo sapiens	Obesity receptor C protein.	231	80
9098	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	127	63
9099	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	129	78
9100	AF229067	Homo sapiens	PADI-H protein	162	59
9101	G00673	Homo sapiens	Human secreted protein, SEQ ID NO: 4754.	157	65
9102	Y60010	Homo sapiens	Human endometrium tumour EST encoded protein 70.	69	63
9103	R95913	Homo sapiens	Neural thread protein.	124	72
9104	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	104	68
9105	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	156	88
9106	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	170	57
9107	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	163	89
9108	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	123	41
9109	L41944	Homo sapiens	interferon receptor	162	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9110	AK000496	Homo sapiens	unnamed protein product	138	78
9111	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	81	62
9112	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	142	52
9113	M26361	Mus musculus	LINE/Ig H-chain fusion protein	105	50
9114	AF073519	Homo sapiens	small EDRK-rich factor 1, long isoform	119	56
9115	AF119900	Homo sapiens	PRO2822	140	58
9116	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	158	60
9117	L00016	Homo sapiens	urf5	171	97
9118	AC006276	Homo sapiens	R28379_3	138	100
9119	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	131	72
9120	AF119855	Homo sapiens	PRO1847	155	81
9121	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	105	84
9122	Y87103	Homo sapiens	Human secreted protein sequence SEQ ID NO:142.	115	78
9123	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	134	53
9124	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	103	40
9125	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	96	63
9126	AF130089	Homo sapiens	PRO2550	125	78
9127	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	98	56
9128	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	107	75
9129	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	131	49
9130	AK024455	Homo sapiens	FLJ00047 protein	130	78
9131	W88435	Homo sapiens	Disease associated protein kinase DAPK-4.	336	100
9132	U63332	Homo sapiens	super cysteine rich protein; SCRP	144	59
9133	Y94922	Homo sapiens	Human secreted protein clone pv6_1 protein sequence SEQ ID NO:50.	154	90
9134	AF317425	Homo sapiens	GAC-1	182	70
9135	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	174	54
9136	AF116715	Homo sapiens	PRO2829	116	71
9137	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	122	65
9138	AF130089	Homo sapiens	PRO2550	140	62
9139	AF161221	Homo sapiens	kallikrein-like protein 6	204	90
9140	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	110	48
9141	U27486	Pseudorabies virus	EP0	84	44
9142	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	150	96
9143	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	220	80
9144	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	163	84
9145	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	180	77
9146	U52077	Homo sapiens	mariner transposase	365	78
9147	W88627	Homo sapiens	Secreted protein encoded by gene 94	143	67

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			clone HPMBQ32.		
9148	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	100	81
9149	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	118	66
9150	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	105	54
9151	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	101	70
9152	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	163	66
9153	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	160	72
9154	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	106	63
9155	Y02926	Homo sapiens	Fragment of human secreted protein encoded by gene 101.	95	80
9156	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	133	67
9157	G03924	Homo sapiens	Human secreted protein, SEQ ID NO: 8005.	265	80
9158	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	131	72
9159	AF130089	Homo sapiens	PRO2550	180	61
9160	AF116715	Homo sapiens	PRO2829	184	82
9161	K01664	Drosophila melanogaster	Bkm-like protein	200	69
9162	D88146	Homo sapiens	UDP-galactose transporter 2	101	100
9163	AF107406	Homo sapiens	GW128	155	60
9164	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	97	51
9165	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	146	60
9166	AF210651	Homo sapiens	NAG18	83	65
9167	V00672	Pan troglodytes	reading frame protein 4	119	95
9168	Y01155	Homo sapiens	Secreted protein encoded by gene 4 clone HIBCW32.	225	74
9169	AF161356	Homo sapiens	HSPC093	100	75
9170	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	174	66
9171	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	115	86
9172	AF119855	Homo sapiens	PRO1847	178	59
9173	AF130087	Homo sapiens	PRO2411	129	48
9174	AF130079	Homo sapiens	PRO2852	149	59
9175	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	101	90
9176	AF090894	Homo sapiens	PRO0113	118	65
9177	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	105	46
9178	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	100	52
9179	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	161	70
9180	AF116715	Homo sapiens	PRO2829	127	64
9181	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	144	71
9182	AF229067	Homo sapiens	PADI-H protein	164	64
9183	G02532	Homo sapiens	Human secreted protein, SEQ ID NO:	134	80

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6613.		
9184	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	106	64
9185	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	132	57
9186	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	113	65
9187	AF090931	Homo sapiens	PRO0483	117	68
9188	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	136	67
9189	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	130	47
9190	D38112	Homo sapiens	cytochrome c oxidase subunit I	269	85
9191	M18094	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	150	40
9192	G00552	Homo sapiens	Human secreted protein, SEQ ID NO: 4633.	153	73
9193	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	62
9194	M18093	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	103	31
9195	X77816	Rattus norvegicus	PR-Vbeta1	98	47
9196	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	107	48
9197	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	111	68
9198	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	164	83
9199	J02459	bacteriophage lambda	E (capsid component;341)	235	85
9200	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	117	65
9201	X67640	Homo sapiens	HS24/P52	222	75
9202	X67640	Homo sapiens	HS24/P52	231	81
9203	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	128	66
9204	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	107	74
9206	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	186	66
9207	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	136	56
9208	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	160	67
9209	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	131	68
9210	AF116715	Homo sapiens	PRO2829	123	81
9211	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	70
9212	AF118086	Homo sapiens	PRO1992	84	57
9213	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	115	62
9214	J02459	bacteriophage lambda	E (capsid component;341)	247	92
9215	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	74	76
9216	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	134	74

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9217	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	137	53
9218	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	130	44
9219	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	68
9220	L41944	Homo sapiens	interferon receptor	141	50
9221	AF130079	Homo sapiens	PRO2852	170	70
9222	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	100	85
9223	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	142	56
9224	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	104	63
9225	U80761	Homo sapiens	CTG26 alternate open reading frame	92	84
9226	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	157	65
9227	AK027208	Homo sapiens	unnamed protein product	138	68
9228	B25722	Homo sapiens	Human secreted protein sequence encoded by gene 9 SEQ ID NO:111.	125	87
9229	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	127	88
9230	AK025047	Homo sapiens	unnamed protein product	179	64
9231	AF090894	Homo sapiens	PRO0113	195	57
9232	AB046048	Macaca fascicularis	unnamed protein product	176	54
9233	AB008227	Adiantum capillus-veneris	Extensin	93	34
9234	AF130089	Homo sapiens	PRO2550	98	73
9235	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	135	52
9236	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	162	62
9237	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	126	59
9238	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	126	52
9239	AE003499	Drosophila melanogaster	CG12706 gene product	166	37
9240	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	161	64
9241	X92485	Plasmodium vivax	pva1	112	61
9242	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	69	42
9243	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	140	80
9244	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	187	92
9245	M22332	Homo sapiens	unknown protein	117	40
9246	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	109	66
9247	AL136173	Homo sapiens	dJ914B9.1 (novel protein (HSPC162) similar to Rattus norvegicus bithoraxoid-like protein)	305	76
9248	AF116661	Homo sapiens	PRO1438	141	53
9249	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	144	76

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9250	J02459	bacteriophage lambda	E (capsid component;341)	245	89
9251	J02459	bacteriophage lambda	E (capsid component;341)	245	92
9252	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	128	63
9253	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	124	72
9254	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	90
9255	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	132	65
9256	X52164	Mus musculus	Q300 protein (AA 1-77)	106	62
9257	AF217374	Acanthaster planci	cytochrome oxidase subunit I	259	98
9258	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	94	64
9259	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	107	54
9260	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	66
9261	M28016	Homo sapiens	cytochrome b	148	93
9262	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	112	68
9263	R55749	Homo sapiens	Extracellular domain of human high affinity IFN-gamma receptor.	116	83
9264	K02403	Homo sapiens	complement component C4A	9025	99
9265	X92485	Plasmodium vivax	pval	161	55
9266	AK024455	Homo sapiens	FLJ00047 protein	98	83
9267	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	103	51
9268	AF130089	Homo sapiens	PRO2550	124	77
9269	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	94	54
9270	Y19684	Homo sapiens	SEQ ID NO 402 from WO9922243.	96	81
9271	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	132	53
9272	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	155	72
9273	AF229067	Homo sapiens	PADI-H protein	127	54
9274	Y36203	Homo sapiens	Human secreted protein #75.	154	77
9275	X92485	Plasmodium vivax	pval	157	72
9276	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	132	60
9277	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	156	84
9278	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	138	84
9279	Y20772	Homo sapiens	Human neurofilament-M mutant protein fragment 54.	112	70
9280	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	146	59
9281	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	103	63
9282	K01664	Drosophila melanogaster	Bkm-like protein	89	60
9283	X92485	Plasmodium	pval	124	79

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		vivax			
9284	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	95	75
9285	AF130087	Homo sapiens	PRO2411	138	78
9286	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	140	54
9287	AF004340	Homo sapiens	ATPase 6/8	98	100
9288	S79410	Mus musculus	nuclear localization signal binding protein	102	68
9289	J02459	bacteriophage lambda	I (tail component;223)	457	97
9290	AC003058	Arabidopsis thaliana	unknown protein	177	84
9291	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	107	87
9292	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	311	91
9293	S79410	Mus musculus	nuclear localization signal binding protein	139	61
9294	R28916	Homo sapiens	Type III procollagen (prior art).	117	33
9295	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	126	77
9296	AF130089	Homo sapiens	PRO2550	137	52
9297	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	93	79
9298	U22376	Homo sapiens	alternatively spliced product using exon 13A	239	77
9299	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	134	69
9300	AL390114	Leishmania major	extremely cysteine/valine rich protein	105	24
9301	D90282	Homo sapiens	carbamyl phosphate synthetase I (EC 6.3.4.16)	276	96
9302	J02459	bacteriophage lambda	E (capsid component;341)	231	93
9303	M15077	Photinus pyralis	Luciferase	557	100
9304	L00016	Homo sapiens	urf4	303	93
9305	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	141	69
9306	L46721	Homo sapiens	mucin	204	80
9307	S79410	Mus musculus	nuclear localization signal binding protein	110	84
9308	J02459	bacteriophage lambda	E (capsid component;341)	218	93
9309	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	78	66
9310	AF130075	Homo sapiens	PRO2532	92	69
9311	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	97	51
9312	J02459	bacteriophage lambda	E (capsid component;341)	201	79
9313	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	133	95
9314	AK024455	Homo sapiens	FLJ00047 protein	128	68
9315	D38112	Homo sapiens	ATPase subunit 6	223	81
9316	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	113	85
9317	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	117	88
9318	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	257	72

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9319	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	101	61
9320	AK001116	Homo sapiens	unnamed protein product	96	40
9321	G02535	Homo sapiens	Human secreted protein, SEQ ID NO: 6616.	174	60
9322	AF037081	Pan troglodytes	ribonuclease k6 precursor	109	100
9323	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	149	63
9324	AF153056	Fasciola hepatica	tegumental antigen	60	44
9325	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	200	69
9326	G02755	Homo sapiens	Human secreted protein, SEQ ID NO: 6836.	80	57
9327	AF118086	Homo sapiens	PRO1992	139	60
9328	G02360	Homo sapiens	Human secreted protein, SEQ ID NO: 6441.	110	73
9329	AF107406	Homo sapiens	GW128	142	56
9330	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	156	75
9331	X92485	Plasmodium vivax	pval	121	56
9332	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	179	52
9333	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	113	67
9334	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	108	46
9335	M22332	Homo sapiens	unknown protein	158	60
9336	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	95	46
9337	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	160	76
9338	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	150	68
9339	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	169	59
9340	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	154	64
9341	AK024455	Homo sapiens	FLJ00047 protein	117	79
9342	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	191	76
9343	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	133	82
9344	AF032457	Homo sapiens	BimEL	123	100
9345	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	117	46
9346	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	153	75
9347	X53020	Plasmodium falciparum	erythrocyte membrane-associated antigen	68	75
9348	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	120	70
9349	AF130089	Homo sapiens	PRO2550	116	69
9350	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	165	72
9351	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	94	82
9352	AL080242	Homo sapiens	bA554C12.1 (RBX1 or ROC1 (ring-box or ring finger protein 1))	184	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9353	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	125	64
9354	X71442	Rattus norvegicus	ORF 1; putative	96	40
9355	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	98	46
9356	AF090931	Homo sapiens	PRO0483	148	76
9357	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	144	56
9358	AC005175	Homo sapiens	TA2R, HUMAN, BETA ISOFORM; TXA2-R; PROSTANOID TP RECEPTOR	153	63
9359	AF116715	Homo sapiens	PRO2829	125	66
9360	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	143	72
9361	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	178	75
9362	Y14437	Homo sapiens	Human secreted protein encoded by gene 27 clone HSAWA27.	90	57
9363	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	86	76
9364	AF229067	Homo sapiens	PADI-H protein	116	51
9365	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	248	64
9366	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	104	76
9367	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	95	76
9368	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	105	74
9369	R86406	Homo sapiens	Human matrix metalloprotease MMPm1a.	108	83
9370	AF181977	Hepatitis GB virus C	E2 protein	95	38
9371	AF090931	Homo sapiens	PRO0483	151	62
9372	AF090894	Homo sapiens	PRO0113	133	57
9373	AK002154	Homo sapiens	unnamed protein product	226	55
9374	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	140	71
9375	U77494	Homo sapiens	RANBP8	166	100
9376	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	155	52
9377	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	126	63
9378	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	151	78
9379	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	97	68
9380	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	117	62
9381	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	104	47
9382	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	57
9384	AB047936	Macaca fascicularis	hypothetical protein	95	41
9385	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	57	64
9386	U04810	Homo sapiens	tastin	151	100
9387	U79260	Homo sapiens	unknown	97	79

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9388	U18339	Variola virus	D4L	103	65
9389	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	134	75
9390	AL390935	Leishmania major	possible dopap	99	88
9391	AB015633	Homo sapiens	type II membrane protein	108	100
9392	AF113685	Homo sapiens	PRO0974	98	62
9393	AF064819	Homo sapiens	serine protease DESC1	227	69
9394	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	219	68
9395	G01400	Homo sapiens	Human secreted protein, SEQ ID NO: 5481.	104	100
9396	AK024455	Homo sapiens	FLJ00047 protein	153	68
9397	AF033260	porcine endogenous type C retrovirus	reverse transcriptase	155	53
9398	X12517	Homo sapiens	C protein (AA 1-159)	147	55
9399	AB029948	Homo sapiens	mitochondrial seryl-tRNA synthetase	1203	100
9400	Y87075	Homo sapiens	Human secreted protein sequence SEQ ID NO:114.	234	93
9401	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	150	58
9402	M15530	Homo sapiens	B-cell growth factor	113	74
9403	X56932	Homo sapiens	23 kD highly basic protein	114	85
9404	AC018748	Arabidopsis thaliana	Contains similarity to P11 protein from Drosophila melanogaster gb X59691.	75	65
9405	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	114	88
9406	AF220264	Homo sapiens	MOST-1	124	70
9407	AF119851	Homo sapiens	PRO1722	157	65
9408	X92485	Plasmodium vivax	pval	163	78
9409	X92485	Plasmodium vivax	pval	165	77
9410	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	97	55
9411	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	104	64
9412	AF130089	Homo sapiens	PRO2550	147	55
9413	AF130089	Homo sapiens	PRO2550	175	65
9414	L14848	Homo sapiens	MHC class I-related protein	225	97
9415	R95913	Homo sapiens	Neural thread protein.	107	74
9416	AB001684	Chlorella vulgaris	ORF49b	68	53
9417	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	111	50
9418	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	107	73
9419	AL050285	Homo sapiens	hypothetical protein	194	100
9420	AF090944	Homo sapiens	PRO0663	132	59
9421	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	153	61
9422	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	140	70
9423	M20030	Homo sapiens	small proline rich protein	62	41
9424	AF116718	Homo sapiens	PRO2900	396	100
9425	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	102	35
9426	X61047	Hydra sp.	mini-collagen	92	45

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9427	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	105	71
9428	L10908	Mus musculus	Gcap1 gene product	107	44
9429	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	79	87
9430	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	123	61
9431	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	111	80
9432	X12580	Medicago sativa	put. nodulin (soybean N-75 homolog.)	87	33
9433	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	106	48
9434	AC003028	Arabidopsis thaliana	30S ribosomal protein S31	79	42
9435	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	106	75
9436	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	207	75
9437	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	163	85
9438	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	84	57
9439	AF118086	Homo sapiens	PRO1992	145	75
9440	AF229067	Homo sapiens	PADI-H protein	140	64
9441	M36913	Zea mays	cell wall protein (put.); putative	107	38
9442	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	161	59
9443	AF229067	Homo sapiens	PADI-H protein	147	85
9444	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	171	79
9445	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	155	57
9446	X92485	Plasmodium vivax	pval	97	55
9447	AF119851	Homo sapiens	PRO1722	123	55
9448	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	88
9449	AL391688	Homo sapiens	bA524D16A.2.1 (novel protein similar to mouse granuphilin-a)	258	97
9450	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	91
9451	X92485	Plasmodium vivax	pval	123	88
9452	X83000	Myocastor coypus	lipase related protein 2	168	43
9453	M35603	Mus musculus	Hox-3.1 protein	447	78
9454	M35520	Canis familiaris	GTP-binding protein (rab5)	271	98
9455	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	362	86
9456	A13595	synthetic construct	immunosuppressive protein PP15	111	100
9457	X67788	Rattus norvegicus	ezrin, p81	185	97
9458	U28068	Mus musculus	neurogenic differentiation factor	132	89
9459	AF155140	Homo sapiens	gonadotropin-regulated testicular RNA helicase; GRTH	556	88
9460	AF155140	Homo sapiens	gonadotropin-regulated testicular RNA helicase; GRTH	379	94
9461	AF169689	Homo sapiens	protocadherin alpha 10 alternate isoform	208	95
9462	U73193	Homo sapiens	inward rectifier potassium channel	236	96

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			Kir1.2		
9463	U83278	Bos taurus	neural specific protein CRMP-2	157	61
9464	W48352	Homo sapiens	Human breast cancer related protein BCFLT1.	74	57
9465	AL031673	Homo sapiens	dJ694B14.3 (PUTATIVE novel haloacid dehalogenase-like hydrolase family protein similar to (archaea) bacterial proteins)	444	100
9466	X67247	Homo sapiens	ribosomal protein S8	519	90
9467	S79410	Mus musculus	nuclear localization signal binding protein	115	51
9468	U80761	Homo sapiens	CTG26 alternate open reading frame	95	84
9469	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	145	71
9470	AF130056	Homo sapiens	PRO1367	98	76
9471	X71354	Homo sapiens	vesicular monoamine transporter	102	95
9472	U66372	Bos taurus	ribosomal protein S29	120	95
9473	D32002	Homo sapiens	nuclear cap binding protein	583	96
9474	W54282	Homo sapiens	Protein sequence of the di-alpha haemoglobin gene contained in pSS1.	469	91
9475	V49572_cd1	Homo sapiens	13-NOV-1996 Human stomach cancer clone HP10122 cDNA #1.	562	100
9476	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	247	88
9477	AB043820	Homo sapiens	platelet glycoprotein VI-2	95	47
9478	AB020236	Homo sapiens	ribosomal protein L27A	437	86
9479	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	149	52
9480	AF205633	Homo sapiens	ninjurin2	364	100
9481	D14886	Homo sapiens	TFIIA-37	196	100
9482	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	166	76
9483	AF178842	Homo sapiens	Rhesus blood group-associated glycoprotein	128	75
9484	AF134895	Homo sapiens	glyoxylate reductase	838	95
9485	AC004832	Homo sapiens	similar to 45 kDa secretory protein ; similar to CAA10644.1 (PID:g4164418)	562	98
9486	Z35761	Homo sapiens	TEL/ABL	230	71
9487	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	149	72
9488	AL032631	Caenorhabditis elegans	predicted using Genefinder	159	31
9489	AJ271079	Oenothera elata subsp. hookeri	Ycf2 protein	113	36
9490	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	135	40
9491	Y53005	Homo sapiens	Human secreted protein clone pm749_8 protein sequence SEQ ID NO:16.	124	61
9492	Y21091	Homo sapiens	Human p53 cellular tumour antigen mutant protein fragment 28.	85	41
9493	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	153	76
9494	AF119851	Homo sapiens	PRO1722	94	54
9495	R04932	Homo sapiens	Interferon-gamma receptor segment from clone 39 responsible for binding the target.	142	100
9496	U40952	Caenorhabditis elegans	C03B1.10 gene product	103	75
9497	M63838	Homo sapiens	interferon-gamma induced protein	128	92

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9498	AL451017	Neurospora crassa	related to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C	147	44
9499	AF108831	Homo sapiens	K:Cl cotransporter 3	244	77
9500	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene preoduct.	154	68
9501	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	139	63
9502	AE003499	Drosophila melanogaster	CG12706 gene product	180	36
9503	X02344	Homo sapiens	beta-tubulin	363	94
9504	D78014	Homo sapiens	dihydropyrimidinase related protein-3	189	84
9505	U59446	Brassica napus	myrosinase-binding protein related protein	116	40
9506	AB010437	Rattus rattus	cadherin-8	239	50
9507	AF229067	Homo sapiens	PADI-H protein	178	74
9508	AJ224819	Homo sapiens	tumor suppressor	291	85
9509	AF017275	Mus musculus	growth factor independence-1B	242	40
9510	AF177203	Homo sapiens	cerebral cell adhesion molecule	388	52
9511	AY007160	Homo sapiens	similar to Homo sapiens CGI-57 protein mRNA with GenBank Accession Number AF151815.1	1533	99
9512	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	104	66
9513	X52164	Mus musculus	Q300 protein (AA 1-77)	92	59
9514	X80035	Oryctolagus cuniculus	cysteine rich hair keratin associated protein	96	40
9515	D86491	Xenopus laevis	Nfil	1777	76
9516	Y70761	Homo sapiens	Human beta-amyloid peptide (BAP) binding protein, BBP3.	168	80
9517	AK024500	Homo sapiens	FLJ00109 protein	1714	100
9518	AF008220	Bacillus subtilis	YtaG	104	41
9519	AF099977	Mus musculus	schlafen4	163	35
9520	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	162	72
9521	AL035068	Homo sapiens	dJ116G19.1 (novel protein)	102	76
9522	B24527	Homo sapiens	Human secreted protein sequence encoded by gene 15 SEQ ID NO:153.	729	90
9523	AF129756	Homo sapiens	MSH5	182	100
9524	AJ238706	Drosophila melanogaster	monocarboxylate transporter 1 homologue	126	32
9525	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	250	97
9526	D86604	Mus musculus	Bach2	200	92
9527	AB032918	Hylobates moloch	dopamine receptor D4	91	36
9528	AB007830	Homo sapiens	CSR2	995	99
9529	AC004472	Homo sapiens	P1.11659_4	449	98
9530	AF273047	Homo sapiens	CTCL tumor antigen se20-7	104	29
9531	AF130079	Homo sapiens	PRO2852	153	67
9532	X07881	Homo sapiens	proline-rich protein G1	105	43
9533	AK001845	Homo sapiens	unnamed protein product	1368	63
9534	S79410	Mus musculus	nuclear localization signal binding protein	94	41
9535	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	185	86
9536	X99583	Homo sapiens	CHL1 protein	635	98
9537	AL022170	Homo sapiens	dJ501N12.1	111	37
9538	X66179	Xenopus laevis	p70 S6 kinase	120	75

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9539	U68380	Gallus gallus	csdp	289	98
9540	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	97	90
9541	AB013918	Homo sapiens	CAD	369	78
9542	U29380	Caenorhabditis elegans	similar to adenylate cyclase	501	42
9543	AF020312	Mus musculus	proline-rich protein 9-1	95	51
9544	G03435	Homo sapiens	Human secreted protein, SEQ ID NO: 7516.	142	96
9545	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	142	66
9546	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	110	47
9547	AB044546	Homo sapiens	mitogen-activated protein kinase kinase kinase	407	60
9548	U52111	Homo sapiens	Ca ²⁺ /Calmodulin-dependent protein kinase I	660	100
9549	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	129	68
9550	Y87852	Homo sapiens	Human FGF-5 protein fragment.	146	100
9551	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	109	50
9552	D45131	Homo sapiens	basigin	311	66
9553	A14656	synthetic construct	protein antigen	450	89
9554	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	133	52
9555	X73458	Homo sapiens	protein kinase	568	85
9556	AJ131890	Homo sapiens	DNA polymerase lambda	1549	100
9557	S56555	Homo sapiens	paraoxonase/arylesterase	224	85
9558	M22332	Homo sapiens	unknown protein	90	38
9559	B24598	Homo sapiens	Human secreted protein sequence encoded by gene 47 SEQ ID NO:224.	66	44
9560	G03203	Homo sapiens	Human secreted protein, SEQ ID NO: 7284.	95	51
9561	Y08061	Homo sapiens	Human c-myc protein fragment.	77	76
9562	X55687	Lycopersicon esculentum	extensin (class II)	69	60
9563	AC002333	Arabidopsis thaliana	putative SF16 protein {Helianthus annuus}	111	31
9564	AF118082	Homo sapiens	PRO1902	106	61
9565	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	85	52
9566	U10323	Homo sapiens	NF45 protein	480	82
9567	AF100757	Homo sapiens	COP9 complex subunit 4	686	90
9568	AL035608	Homo sapiens	dJ479J7.2 (transmembrane 4 superfamily member 6)	293	90
9569	G00413	Homo sapiens	Human secreted protein, SEQ ID NO: 4494.	118	63
9570	U47856	Araneus diadematus	fibroin-4	98	44
9571	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	83	54
9572	AJ006239	Homo sapiens	dihydropteridine reductase	461	84
9573	G00821	Homo sapiens	Human secreted protein, SEQ ID NO: 4902.	248	75
9574	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	90	36
9575	V00488	Homo sapiens	alpha globin	508	84
9576	AF116719	Homo sapiens	PRO2987	483	91

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9577	L77967	Ovis aries	small proline-rich protein with paired repeat	62	38
9578	D38112	Homo sapiens	NADH dehydrogenase subunit 4	474	92
9579	P90387	Homo sapiens (Human)	N-terminal of human serum albumin polypeptide.	274	67
9580	U22961	Homo sapiens	similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	271	88
9581	U15779	Homo sapiens	p70	101	57
9582	M19419	Mus musculus	proline-rich salivary protein	102	36
9583	L22030	Glycine max	hydroxyproline-rich glycoprotein	114	40
9584	AF041330	Bodo saltans	NADH dehydrogenase subunit 5	105	32
9585	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	141	61
9586	U93569	Homo sapiens	putative p150	232	51
9587	AF144054	Homo sapiens	apoptosis related protein APR-4	120	52
9588	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	128	58
9589	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	90	61
9590	L27428	Homo sapiens	reverse transcriptase	120	46
9591	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	85	62
9592	AJ133489	Canis familiaris	albumin	204	60
9593	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	294	68
9594	M15386	Homo sapiens	gamma-globin	316	77
9595	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	134	68
9596	AF116719	Homo sapiens	PRO2987	309	89
9597	AF116719	Homo sapiens	PRO2987	485	94
9598	AF068294	Homo sapiens	HDCMB45P	131	34
9599	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	152	70
9600	AF118082	Homo sapiens	PRO1902	151	59
9601	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	186	68
9602	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	176	65
9603	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	261	80
9604	AF194537	Homo sapiens	NAG13	154	61
9605	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	96	67
9606	K02576	Homo sapiens	salivary proline-rich protein 1	100	33
9607	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	134	48
9608	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	129	67
9609	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	101	32
9610	AF118080	Homo sapiens	PRO1880	237	100
9611	AF119851	Homo sapiens	PRO1722	138	81
9612	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	178	55
9613	AF090930	Homo sapiens	PRO0478	88	71
9614	AF068294	Homo sapiens	HDCMB45P	121	49
9615	G01657	Homo sapiens	Human secreted protein, SEQ ID NO:	118	79

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			5738.		
9616	AF090931	Homo sapiens	PRO0483	143	63
9617	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	92	44
9618	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	121	56
9619	AB046061	Macaca fascicularis	unnamed protein product	93	44
9620	Y87116	Homo sapiens	Human secreted protein sequence SEQ ID NO:155.	122	71
9621	AF113685	Homo sapiens	PRO0974	156	65
9622	AF097178	Equus caballus	glyceraldehyde-3-phosphate dehydrogenase	119	75
9623	U83303	Homo sapiens	line-1 reverse transcriptase	134	62
9624	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	112	53
9625	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	123	77
9626	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	164	73
9627	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	236	71
9628	AF130079	Homo sapiens	PRO2852	138	50
9629	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	130	60
9630	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	167	61
9631	G03102	Homo sapiens	Human secreted protein, SEQ ID NO: 7183.	87	50
9632	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	128	41
9633	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	134	81
9634	AF118082	Homo sapiens	PRO1902	114	57
9635	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	133	54
9636	L07543	Leishmania tarentolae	MURF4	85	42
9637	U49973	Homo sapiens	ORF2: function unknown	163	44
9638	AF090895	Homo sapiens	PRO0117	77	41
9639	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	108	71
9640	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	90	46
9641	AF118078	Homo sapiens	PRO1848	114	66
9642	AK024455	Homo sapiens	FLJ00047 protein	131	79
9643	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	130	62
9644	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	141	42
9645	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	69	62
9646	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	69	35
9647	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	478	90
9648	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	155	50
9649	G02538	Homo sapiens	Human secreted protein, SEQ ID NO:	104	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6619.		
9650	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	173	38
9651	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	118	36
9652	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	162	64
9653	D00570	Mus musculus	open reading frame (196 AA)	182	51
9654	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	138	54
9655	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	105	74
9656	W88947	Homo sapiens	Polypeptide fragment encoded by gene 118.	82	70
9657	W88947	Homo sapiens	Polypeptide fragment encoded by gene 118.	79	39
9658	M24732	Homo sapiens	lamin-like protein	76	31
9659	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	161	73
9660	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene preduct.	149	48
9661	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	135	62
9662	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	126	71
9663	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	141	63
9664	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	153	66
9665	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	142	93
9666	AF113685	Homo sapiens	PRO0974	112	73
9667	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	133	62
9668	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	102	47
9669	B12310	Homo sapiens	Human secreted protein encoded by gene 10 clone HDPGP94.	80	41
9670	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	106	58
9671	AF090942	Homo sapiens	PRO0657	118	66
9672	AF161356	Homo sapiens	HSPC093	94	63
9673	AF090930	Homo sapiens	PRO0478	167	64
9674	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	98	50
9675	G02640	Homo sapiens	Human secreted protein, SEQ ID NO: 6721.	87	70
9676	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	119	60
9677	X13412	Rattus rattus	flk protein	614	69
9678	AJ006770	Cicer arietinum	extensin	163	48
9679	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	120	67
9680	G00494	Homo sapiens	Human secreted protein, SEQ ID NO: 4575.	106	58
9681	U63542	Homo sapiens	FAP protein	120	68
9682	M15530	Homo sapiens	B-cell growth factor	146	76
9683	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	180	62
9684	AF321379	Callicebus moloch	gamma2-globin	108	86

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9685	L27428	Homo sapiens	reverse transcriptase	122	39
9686	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	77	51
9687	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	104	58
9688	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	123	58
9689	X81713	Homo sapiens	smallest subunit of TFIIA	210	91
9690	AF193330	Human respiratory syncytial virus	G protein	100	25
9691	AF150100	Homo sapiens	small zinc finger-like protein	205	83
9692	AF068294	Homo sapiens	HDCMB45P	122	54
9693	AF189307	Homo sapiens	unknown	96	50
9694	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	165	50
9695	AF130089	Homo sapiens	PRO2550	198	68
9696	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	170	80
9697	AK024455	Homo sapiens	FLJ00047 protein	137	63
9698	M24732	Homo sapiens	lamin-like protein	92	42
9699	AF116715	Homo sapiens	PRO2829	119	75
9700	AF130089	Homo sapiens	PRO2550	234	57
9701	V00662	Homo sapiens	ATPase 6	255	77
9702	L10908	Mus musculus	Gcap1 gene product	93	35
9703	AF130089	Homo sapiens	PRO2550	208	78
9704	AF194537	Homo sapiens	NAG13	89	51
9705	U79260	Homo sapiens	unknown	98	77
9706	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	78	43
9707	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	70	92
9708	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	136	60
9709	AF194537	Homo sapiens	NAG13	99	48
9710	AF130089	Homo sapiens	PRO2550	87	58
9711	X03145	Homo sapiens	pot. ORF III	135	41
9712	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	97	35
9713	AF116695	Homo sapiens	PRO2221	185	50
9714	AF130051	Homo sapiens	PRO0898	108	68
9715	AF130089	Homo sapiens	PRO2550	143	50
9716	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	124	49
9717	L27428	Homo sapiens	reverse transcriptase	133	50
9718	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	88	43
9719	L27428	Homo sapiens	reverse transcriptase	127	56
9720	M74009	Theropithecus gelada	cytochrome c oxidase subunit II	283	67
9721	M10546	Homo sapiens	cytochrome oxidase I	292	84
9722	AF130051	Homo sapiens	PRO0898	96	57
9723	U93564	Homo sapiens	putative p150	144	49
9724	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	373	76
9725	AK000496	Homo sapiens	unnamed protein product	155	55
9726	G02640	Homo sapiens	Human secreted protein, SEQ ID NO: 6721.	94	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9727	AF130089	Homo sapiens	PRO2550	154	40
9728	AF130089	Homo sapiens	PRO2550	127	61
9729	M19419	Mus musculus	proline-rich salivary protein	98	39
9730	D90053	Sus scrofa	destrin	119	43
9731	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	138	50
9732	AF090942	Homo sapiens	PRO0657	72	45
9733	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	110	44
9734	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	159	94
9735	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	150	85
9736	L27428	Homo sapiens	reverse transcriptase	217	33
9737	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	89	65
9738	AF007064	Saccharomyces cerevisiae	basic protein	108	31
9739	B01372	Homo sapiens	Neuron-associated protein.	128	60
9740	G03140	Homo sapiens	Human secreted protein, SEQ ID NO: 7221.	109	50
9741	AF194537	Homo sapiens	NAG13	123	54
9742	Y69166	Homo sapiens	A mature human N-acetylglycosaminyl transferase protein.	101	77
9743	X92485	Plasmodium vivax	pval	106	41
9744	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	122	76
9745	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	128	50
9746	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	87	64
9747	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	163	69
9748	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	124	74
9749	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	97	66
9750	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	156	71
9751	G03925	Homo sapiens	Human secreted protein, SEQ ID NO: 8006.	157	71
9752	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	97	51
9753	X92485	Plasmodium vivax	pval	91	39
9754	Y07786	Vibrio cholerae	Rfc-like protein	92	32
9755	AF068294	Homo sapiens	HDCMB45P	125	63
9756	L27428	Homo sapiens	reverse transcriptase	91	34
9757	AK024455	Homo sapiens	FLJ00047 protein	143	59
9758	S79410	Mus musculus	nuclear localization signal binding protein	103	41
9759	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	96	67
9760	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	179	58
9761	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	154	65
9762	G03807	Homo sapiens	Human secreted protein, SEQ ID NO:	91	78

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7888.		
9763	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	119	60
9764	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	111	85
9765	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	116	36
9766	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	165	74
9767	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	162	74
9768	G04091	Homo sapiens	Human secreted protein, SEQ ID NO: 8172.	117	52
9769	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	92	50
9770	AF130089	Homo sapiens	PRO2550	104	31
9771	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	154	62
9772	U52077	Homo sapiens	mariner transposase	194	56
9773	Y87297	Homo sapiens	Human signal peptide containing protein HSPP-74 SEQ ID NO:74.	345	100
9774	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	73	36
9775	M11901	Rattus norvegicus	proline-rich salivary protein	96	32
9776	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	124	53
9777	L27428	Homo sapiens	reverse transcriptase	251	53
9778	K02576	Homo sapiens	salivary proline-rich protein 1	141	40
9779	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	111	58
9780	AJ224997	Rattus norvegicus	huntingtin	64	64
9781	AF283769	Homo sapiens	similar to GenBank Accession Number AC021163	119	53
9782	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	81	50
9783	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	68
9784	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	85	65
9785	AF144054	Homo sapiens	apoptosis related protein APR-4	83	53
9786	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	75	41
9787	M64792	Rattus norvegicus	salivary proline-rich protein	122	45
9788	D90053	Sus scrofa	destrin	146	43
9789	A18812	Brassica napus	extensin	104	34
9790	AF130089	Homo sapiens	PRO2550	102	66
9791	AF130089	Homo sapiens	PRO2550	326	70
9792	D38112	Homo sapiens	cytochrome c oxidase subunit 1	495	79
9793	M10546	Homo sapiens	cytochrome oxidase I	343	75
9794	Y85062	Homo sapiens	Interleukin 1 converting enzyme homologue (ICEL) protein sequence.	106	58
9795	X92485	Plasmodium vivax	pva1	108	48
9796	M15530	Homo sapiens	B-cell growth factor	119	70
9797	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	148	65
9798	X61046	Hydra sp.	mini-collagen	101	55

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9799	U93571	Homo sapiens	p40	82	36
9800	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	170	52
9801	X92485	Plasmodium vivax	pval	113	45
9802	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	63	44
9803	D38112	Homo sapiens	cytochrome c oxidase subunit 3	583	89
9804	G01736	Homo sapiens	Human secreted protein, SEQ ID NO: 5817.	150	47
9805	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	132	71
9806	X92485	Plasmodium vivax	pval	106	53
9807	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	163	67
9808	AF119851	Homo sapiens	PRO1722	341	68
9809	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	77	57
9810	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	72
9811	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	113	65
9812	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	118	37
9813	G03703	Homo sapiens	Human secreted protein, SEQ ID NO: 7784.	121	72
9814	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	72	92
9815	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	71	71
9816	AF118082	Homo sapiens	PRO1902	93	45
9817	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	207	59
9818	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	99	46
9819	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	130	69
9820	L10908	Mus musculus	Gcap1 gene product	99	37
9821	A00469	Homo sapiens	growth hormone	254	81
9822	U79260	Homo sapiens	unknown	85	39
9823	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	125	62
9824	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	103	74
9825	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	126	51
9826	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	148	44
9827	Y24789	Homo sapiens	Human secreted protein bf377_1.	265	100
9828	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	72	60
9829	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	118	45
9830	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	104	51
9831	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	118	74
9832	AF151866	Homo sapiens	CGI-108 protein	115	31
9833	U93563	Homo sapiens	putative p150	127	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9834	AE003859	Xylella fastidiosa	hypothetical protein	97	30
9835	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	138	65
9836	B01372	Homo sapiens	Neuron-associated protein.	150	88
9837	G03115	Homo sapiens	Human secreted protein, SEQ ID NO: 7196.	115	57
9838	AF068294	Homo sapiens	HDCMB45P	90	65
9839	S77772	Homo sapiens	aspartylglucosaminidase, AGA {C-terminal, alternatively spliced} {EC 3.5.1.26}	71	66
9840	AF090942	Homo sapiens	PRO0657	115	76
9841	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	75	54
9842	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	156	67
9843	AF130089	Homo sapiens	PRO2550	216	75
9844	M15530	Homo sapiens	B-cell growth factor	113	67
9845	U93567	Homo sapiens	p40	248	75
9846	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	151	55
9847	AK024455	Homo sapiens	FLJ00047 protein	151	64
9848	AF118082	Homo sapiens	PRO1902	58	81
9849	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	129	65
9850	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	329	77
9851	AF090944	Homo sapiens	PRO0663	122	80
9852	X71442	Rattus norvegicus	ORF 1; putative	109	48
9853	AF130089	Homo sapiens	PRO2550	126	60
9854	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	98	62
9855	U93563	Homo sapiens	putative p150	136	48
9856	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	276	74
9857	AF017777	Drosophila melanogaster	la costa	99	43
9858	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	99	37
9859	K02576	Homo sapiens	salivary proline-rich protein I	106	37
9860	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	138	71
9861	AF116909	Homo sapiens	unknown	103	43
9862	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	113	38
9863	Y21811	Homo sapiens	CPF polypeptide 36PRO.	131	58
9864	U93567	Homo sapiens	p40	252	70
9865	AF090895	Homo sapiens	PRO0117	164	60
9866	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	109	47
9867	AF090930	Homo sapiens	PRO0478	106	84
9868	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	167	84
9869	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	83	60
9870	AF119900	Homo sapiens	PRO2822	134	48
9871	AF116715	Homo sapiens	PRO2829	111	81
9872	U52077	Homo sapiens	mariner transposase	332	76

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9873	Y69166	Homo sapiens	A mature human N-acetylglucosaminyl transferase protein.	95	85
9874	U93570	Homo sapiens	putative p150	243	44
9875	L27428	Homo sapiens	reverse transcriptase	127	54
9876	S80119	Rattus sp.	reverse transcriptase homolog	163	43
9877	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	113	64
9878	AF187823	Zea mays	transposase DOPA	132	38
9879	W40353	Homo sapiens	Human unspecified protein from US5702907.	101	41
9880	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	133	43
9881	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	101	59
9882	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	148	52
9883	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	57	65
9884	X92485	Plasmodium vivax	pval	129	43
9885	M64792	Rattus norvegicus	salivary proline-rich protein	98	37
9886	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNF1U96.	89	59
9887	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	155	54
9888	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	121	40
9889	D38112	Homo sapiens	NADH dehydrogenase subunit 2	346	68
9890	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	133	38
9891	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	143	66
9892	X53581	Rattus norvegicus	ORF7	81	56
9893	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	109	53
9894	AE003859	Xylella fastidiosa	hypothetical protein	99	27
9895	U83303	Homo sapiens	line-1 reverse transcriptase	157	58
9896	L26953	Homo sapiens	chromosomal protein	107	68
9897	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	95	51
9898	U93569	Homo sapiens	putative p150	106	52
9899	U15647	Mus musculus	reverse transcriptase	118	47
9900	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	118	70
9901	U93563	Homo sapiens	putative p150	116	39
9902	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	153	81
9903	X03145	Homo sapiens	pot. ORF V	148	54
9904	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	84	65
9905	AF066073	Dictyostelium discoideum	SP85; PsB	113	52
9906	AF090895	Homo sapiens	PRO0117	125	58
9907	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	102	57
9908	M24732	Homo sapiens	lamin-like protein	95	35

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
9909	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	96	55
9910	AF118080	Homo sapiens	PRO1880	120	66
9911	AF116719	Homo sapiens	PRO2987	216	72
9912	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	150	75
9913	G03703	Homo sapiens	Human secreted protein, SEQ ID NO: 7784.	129	76
9914	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	72	58
9915	G00233	Homo sapiens	Human secreted protein, SEQ ID NO: 4314.	103	71
9916	S79410	Mus musculus	nuclear localization signal binding protein	114	75
9917	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	75	83
9918	AF116712	Homo sapiens	PRO2738	106	69
9919	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	90	77
9920	AF068294	Homo sapiens	HDCMB45P	296	59
9921	G02996	Homo sapiens	Human secreted protein, SEQ ID NO: 7077.	58	54
9922	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	143	69
9923	U38979	Homo sapiens	hPMSR3	135	46
9924	AB002317	Homo sapiens	KIAA0319	294	75
9925	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	169	42
9926	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	153	59
9927	G00214	Homo sapiens	Human secreted protein, SEQ ID NO: 4295.	261	97
9928	Y14483	Homo sapiens	Fragment of human secreted protein encoded by gene 18.	863	76
9929	AF130051	Homo sapiens	PRO0898	128	60
9930	AF130089	Homo sapiens	PRO2550	123	41
9931	AF064597	Homo sapiens	LINE-1 like protein	101	48
9932	AF027144	Homo sapiens	zinc finger protein	76	42
9933	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	120	44
9934	U93569	Homo sapiens	putative p150	105	68
9935	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	133	51
9936	Y73344	Homo sapiens	HTRM clone 0258181 protein sequence.	145	46
9937	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	123	77
9938	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	159	40
9939	D63643	Homo sapiens	clathrin coat assembly protein-like	232	69
9940	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	75	65
9941	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	176	71
9942	X04588	Homo sapiens	cytoskeletal tropomyosin (AA 1-248)	379	81
9943	G03683	Homo sapiens	Human secreted protein, SEQ ID NO: 7764.	58	52
9944	AF130114	Homo sapiens	PRO2459	117	67
9945	U49973	Homo sapiens	ORF1; MER37; putative transposase	297	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			similar to pogo element		
9946	D00570	Mus musculus	open reading frame (251 AA)	214	63
9947	X03717	Homo sapiens	pot. unidentified reading frame	76	35
9948	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	127	64
9949	J02621	Homo sapiens	high mobility group protein 14	90	50
9950	AF090931	Homo sapiens	PRO0483	114	75
9951	AF164612	Homo sapiens	Gag protein	132	63
9952	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	112	65
9953	Y08061	Homo sapiens	Human c-myb protein fragment.	118	59
9954	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCAC181.	138	74
9955	G00974	Homo sapiens	Human secreted protein, SEQ ID NO: 5055.	94	38
9956	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	124	61
9957	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	177	51
9958	X92485	Plasmodium vivax	pva1	137	44
9959	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	142	53
9960	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	174	68
9961	S79410	Mus musculus	nuclear localization signal binding protein	123	38
9962	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	124	56
9963	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	80	57
9964	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	136	82
9965	Y27908	Homo sapiens	Human secreted protein encoded by gene No. 119.	92	53
9966	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	76	40
9967	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	136	38
9968	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	101	67
9969	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	90	83
9970	Y36156	Homo sapiens	Human secreted protein #28.	170	68
9971	U79260	Homo sapiens	unknown	142	67
9972	L27428	Homo sapiens	reverse transcriptase	108	63
9973	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	119	60
9974	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	78	85
9975	W88947	Homo sapiens	Polypeptide fragment encoded by gene 118.	79	39
9976	AF090944	Homo sapiens	PRO0663	109	73
9977	AF116715	Homo sapiens	PRO2829	120	56
9978	U93563	Homo sapiens	putative p150	132	57
9979	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	97	80
9980	U42580	Paramecium bursaria	A658R	70	40

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		Chlorella virus 1			
9981	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	87	61
9982	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	135	70
9983	X61047	Hydra sp.	mini-collagen	90	36
9984	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	98	40
9985	Y41552	Homo sapiens	Fragment of human secreted protein encoded by gene 80.	90	42
9986	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	132	52
9987	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	115	41
9988	AF042832	Homo sapiens	forkhead-related transcription factor FREAC-9	89	36
9989	X03717	Homo sapiens	pot. unidentified reading frame	105	67
9990	AL390935	Leishmania major	possible dopap	118	74
9991	AF201949	Homo sapiens	60S ribosomal protein L30 isolog	109	58
9992	AF130114	Homo sapiens	PRO2459	115	68
9993	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	83
9994	AF068294	Homo sapiens	HDCMB45P	196	43
9995	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	117	54
9996	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	74	53
9997	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	132	55
9998	AF102771	Homo sapiens	cardiac-specific ras association (RalGDS/AF-6) domain family 1 protein isoform 1D	148	100
9999	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	213	88
10000	D38112	Homo sapiens	ATPase subunit 6	279	69
10001	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	97	39
10002	AK000496	Homo sapiens	unnamed protein product	154	74
10003	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	125	74
10004	B07702	Homo sapiens	Protein encoded by the endogenous fragment of HERV-W.	143	56
10005	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	97	65
10006	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	154	72
10007	AF021231	Mus musculus	acetylcholinesterase-associated collagen	109	41
10008	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	69	78
10009	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	170	78
10010	AF130051	Homo sapiens	PRO0898	134	67
10011	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	100	44
10012	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	95	78
10013	AF073519	Homo sapiens	small EDRK-rich factor 1, long isoform	90	52
10014	AF130052	Homo sapiens	PRO0956	104	50

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10015	X92485	Plasmodium vivax	pval	119	46
10016	AF130089	Homo sapiens	PRO2550	171	56
10017	AF130089	Homo sapiens	PRO2550	172	58
10018	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	146	38
10019	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	109	54
10020	G02584	Homo sapiens	Human secreted protein, SEQ ID NO: 6665.	109	43
10021	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	70	51
10022	AF090942	Homo sapiens	PRO0657	113	67
10023	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	77	33
10024	X55681	Lycopersicon esculentum	extensin (class I)	95	35
10025	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	93	61
10026	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	153	42
10027	Y73377	Homo sapiens	HTRM clone 1645941 protein sequence.	1180	84
10028	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	108	59
10029	G00366	Homo sapiens	Human secreted protein, SEQ ID NO: 4447.	112	65
10030	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	163	82
10031	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	131	66
10032	G02451	Homo sapiens	Human secreted protein, SEQ ID NO: 6532.	74	48
10033	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	104	85
10034	G03093	Homo sapiens	Human secreted protein, SEQ ID NO: 7174.	192	60
10035	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	153	55
10036	Y14479	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	128	76
10037	AF118086	Homo sapiens	PRO1992	148	68
10038	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	125	47
10039	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	137	65
10040	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	139	45
10041	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	128	75
10042	U83303	Homo sapiens	line-1 reverse transcriptase	100	33
10043	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	102	64
10044	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	135	71
10045	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	148	46
10046	X92485	Plasmodium vivax	pval	98	58

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10047	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	102	87
10048	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	63	84
10049	U09202	Homo sapiens	ornithine decarboxylase antizyme	202	67
10050	X92485	Plasmodium vivax	pval	77	34
10051	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	87	40
10052	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	114	57
10053	AC005396	Arabidopsis thaliana	putative proline-rich protein	100	33
10054	G03600	Homo sapiens	Human secreted protein, SEQ ID NO: 7681.	91	94
10055	X73434	Ovis aries	KAP5.4 keratin protein	76	45
10056	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	82	62
10057	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	115	66
10058	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	116	55
10059	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	130	73
10060	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	100	42
10061	L27428	Homo sapiens	reverse transcriptase	107	43
10062	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	92	47
10063	G03112	Homo sapiens	Human secreted protein, SEQ ID NO: 7193.	93	46
10064	AF220264	Homo sapiens	MOST-1	135	48
10065	AF130114	Homo sapiens	PRO2459	87	68
10066	D86853	Catharanthus roseus	extensin	115	35
10067	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	79	71
10068	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	102	54
10069	U16359	Rattus norvegicus	nitric oxide synthase	93	77
10070	AJ233597	Mus famulus	reverse transcriptase	65	36
10071	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	94	67
10072	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	114	51
10073	AK024455	Homo sapiens	FLJ00047 protein	146	66
10074	X92485	Plasmodium vivax	pval	121	36
10075	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	130	64
10076	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	73	43
10077	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	165	75
10078	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	106	72
10079	AF130050	Homo sapiens	PRO0872	102	63
10080	G04072	Homo sapiens	Human secreted protein, SEQ ID NO:	130	44

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			8153.		
10081	Y87156	Homo sapiens	Human secreted protein sequence SEQ ID NO:195.	285	78
10082	AF068294	Homo sapiens	HDCMB45P	144	68
10083	U41038	Caenorhabditis elegans	Similar to cadherin-type repeat	98	48
10084	X92485	Plasmodium vivax	pval	108	53
10085	AF118082	Homo sapiens	PRO1902	117	57
10086	AF090942	Homo sapiens	PRO0657	88	53
10087	AF118086	Homo sapiens	PRO1992	172	71
10088	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	119	68
10089	K02576	Homo sapiens	salivary proline-rich protein I	117	34
10090	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	154	77
10091	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	138	56
10092	G03119	Homo sapiens	Human secreted protein, SEQ ID NO: 7200.	90	56
10093	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	134	66
10094	M15530	Homo sapiens	B-cell growth factor	116	64
10095	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	124	65
10096	M15530	Homo sapiens	B-cell growth factor	87	68
10097	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	84	79
10098	G00369	Homo sapiens	Human secreted protein, SEQ ID NO: 4450.	150	66
10099	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	157	70
10100	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	103	60
10101	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	114	70
10102	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	130	53
10103	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	156	52
10104	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	87	60
10105	L27428	Homo sapiens	reverse transcriptase	220	38
10106	W90834	Homo sapiens	Human lymphocyte targeted peptide #2.	91	43
10107	AF161356	Homo sapiens	HSPC093	227	61
10108	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	123	64
10109	AF130089	Homo sapiens	PRO2550	126	77
10110	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	118	60
10111	M63274	Plasmodium falciparum	malaria antigen	81	54
10112	AF090944	Homo sapiens	PRO0663	133	70
10113	L27428	Homo sapiens	reverse transcriptase	91	32
10114	Y17221	Homo sapiens	Human secreted protein (clone fk317-3).	112	64
10115	W88947	Homo sapiens	Polypeptide fragment encoded by gene 118.	85	44

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10116	L27428	Homo sapiens	reverse transcriptase	112	44
10117	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	115	61
10118	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	79	34
10119	AF194537	Homo sapiens	NAG13	295	51
10120	D00570	Mus musculus	open reading frame (196 AA)	97	40
10121	X77816	Rattus norvegicus	PR-Vbeta1	122	47
10122	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	148	55
10123	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	92	66
10124	AF090942	Homo sapiens	PRO0657	127	78
10125	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	145	68
10126	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	113	49
10127	U93563	Homo sapiens	putative p150	94	35
10128	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	146	79
10129	AF130089	Homo sapiens	PRO2550	208	75
10130	M15530	Homo sapiens	B-cell growth factor	102	73
10131	X55685	Lycopersicon esculentum	extensin (class I)	122	30
10132	L27428	Homo sapiens	reverse transcriptase	197	40
10133	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	99	73
10134	AF194537	Homo sapiens	NAG13	220	48
10135	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	116	75
10136	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	117	61
10137	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	223	59
10138	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	178	75
10139	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	170	52
10140	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	133	64
10141	AF072164	Homo sapiens	HFSE-1	80	60
10142	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	103	74
10143	M15530	Homo sapiens	B-cell growth factor	91	40
10144	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	103	61
10145	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	162	65
10146	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	128	53
10147	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	112	61
10148	X71975	Drosophila melanogaster	put. homologue to S.cerevisiae GAR1 gene	118	39
10149	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	123	49
10150	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	163	81

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10151	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	106	83
10152	AL390114	Leishmania major	extremely cysteine/valine rich protein	117	52
10153	AF113685	Homo sapiens	PRO0974	133	62
10154	U41038	Caenorhabditis elegans	Similar to cadherin-type repeat	129	67
10155	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	89	50
10156	K02576	Homo sapiens	salivary proline-rich protein 1	131	41
10157	AB011099	Homo sapiens	KIAA0527 protein	94	35
10158	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	78	72
10159	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	139	71
10160	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	161	68
10161	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	162	88
10162	M15530	Homo sapiens	B-cell growth factor	137	63
10163	AF090895	Homo sapiens	PRO0117	93	67
10164	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	109	60
10165	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	126	52
10166	AF118082	Homo sapiens	PRO1902	111	55
10167	AF090895	Homo sapiens	PRO0117	112	75
10168	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	135	69
10169	AF090942	Homo sapiens	PRO0657	149	67
10170	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	145	68
10171	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	85	51
10172	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	136	62
10173	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	158	63
10174	AF090942	Homo sapiens	PRO0657	75	44
10175	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	97	47
10176	Y01154	Homo sapiens	Protein sequence Seq Id 54 from WO9901020.	108	75
10177	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	168	80
10178	M22332	Homo sapiens	unknown protein	131	62
10179	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	160	60
10180	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	65	68
10181	AF119900	Homo sapiens	PRO2822	132	72
10182	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	114	56
10183	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	124	59
10184	AF210651	Homo sapiens	NAG18	150	65
10185	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	109	46
10186	X71442	Rattus	ORF 1; putative	91	47

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		norvegicus			
10187	AK024455	Homo sapiens	FLJ00047 protein	122	54
10188	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	82	72
10189	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	78	61
10190	AF220264	Homo sapiens	MOST-1	165	81
10191	Y91617	Homo sapiens	Human secreted protein sequence encoded by gene 19 SEQ ID NO:290.	54	44
10192	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	119	80
10193	X92485	Plasmodium vivax	pval	128	57
10194	X61296	Rattus norvegicus	open reading frame 2	79	72
10195	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	116	62
10196	AF130089	Homo sapiens	PRO2550	144	62
10197	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	124	56
10198	AF090942	Homo sapiens	PRO0657	133	76
10199	S79304	Rattus sp.	cytochrome oxidase subunit I; COX I	280	66
10200	S61070	Homo sapiens	reverse transcriptase homolog-pol {retroviral element}	188	49
10201	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	125	51
10202	AF068294	Homo sapiens	HDCMB45P	174	65
10203	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	174	50
10204	U93572	Homo sapiens	putative p150	77	40
10205	L27428	Homo sapiens	reverse transcriptase	133	50
10206	J02621	Homo sapiens	high mobility group protein 14	94	57
10207	AF130079	Homo sapiens	PRO2852	144	73
10208	R95913	Homo sapiens	Neural thread protein.	134	51
10209	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	154	76
10210	AB046048	Macaca fascicularis	unnamed porotein product	162	60
10211	AF090931	Homo sapiens	PRO0483	128	79
10212	AF130051	Homo sapiens	PRO0898	144	76
10213	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	95	54
10214	AF130089	Homo sapiens	PRO2550	158	70
10215	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	96	55
10216	M15894	Homo sapiens	chorionic somatomammotropin precursor	116	63
10217	AK024372	Homo sapiens	unnamed protein product	85	56
10218	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	118	69
10219	M37679	Mus musculus	Ig heavy chain precursor	64	83
10220	G03806	Homo sapiens	Human secreted protein, SEQ ID NO: 7887.	91	69
10221	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	127	47
10222	Y36505	Homo sapiens	Fragment of human secreted protein encoded by gene 29.	102	48
10223	AF090940	Homo sapiens	PRO0644	105	76
10224	U49974	Homo sapiens	mariner transposase	155	76
10225	K02576	Homo sapiens	salivary proline-rich protein 1	154	42

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10226	AF293639	Homo sapiens	dioxin receptor repressor	819	98
10227	L27428	Homo sapiens	reverse transcriptase	137	44
10228	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	106	70
10229	U93566	Homo sapiens	p40	206	80
10230	Y08061	Homo sapiens	Human c-myb protein fragment.	114	66
10231	AF118082	Homo sapiens	PRO1902	76	52
10232	AF118086	Homo sapiens	PRO1992	99	75
10233	X53375	Helianthus annuus	anther-specific protein SF18	95	64
10234	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	156	72
10235	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	100	35
10236	L27428	Homo sapiens	reverse transcriptase	244	50
10237	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	93	70
10238	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	142	72
10239	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	149	80
10240	S52010	Mus sp.	1st Met is at position 21	98	42
10241	AL110147	Homo sapiens	hypothetical protein	125	35
10242	X98485	Plasmodium vivax	putative	85	51
10243	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	70	65
10244	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	125	49
10245	U49973	Homo sapiens	ORF2: function unknown	150	81
10246	K02576	Homo sapiens	salivary proline-rich protein 1	113	56
10247	AF130089	Homo sapiens	PRO2550	139	73
10248	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	160	59
10249	U93565	Homo sapiens	putative p150	109	43
10250	AF130089	Homo sapiens	PRO2550	104	54
10251	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	78	36
10252	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	110	58
10253	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	123	54
10254	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	95	57
10255	X03145	Homo sapiens	pot. ORF V	76	63
10256	Y01405	Homo sapiens	Secreted protein encoded by gene 23 clone HDPBA48.	116	65
10257	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	113	68
10258	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	138	68
10259	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	135	60
10260	G02528	Homo sapiens	Human secreted protein, SEQ ID NO: 6609.	95	59
10261	M86246	Homo sapiens	EHS-2	96	62
10262	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	180	66
10263	G03790	Homo sapiens	Human secreted protein, SEQ ID NO:	102	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7871.		
10264	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	313	84
10265	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	144	56
10266	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	150	61
10267	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:125.	408	89
10268	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	74	26
10269	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	133	52
10270	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	105	61
10271	X61048	Hydra sp.	mini-collagen	121	40
10272	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	150	66
10273	L24521	Homo sapiens	transformation-related protein	134	51
10274	G03806	Homo sapiens	Human secreted protein, SEQ ID NO: 7887.	96	47
10275	U59446	Brassica napus	myrosinase-binding protein related protein	115	39
10276	G01480	Homo sapiens	Human secreted protein, SEQ ID NO: 5561.	482	98
10277	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	143	81
10278	U93564	Homo sapiens	putative p150	130	46
10279	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	123	44
10280	AF090944	Homo sapiens	PRO0663	156	73
10281	AF130079	Homo sapiens	PRO2852	146	75
10282	X89401	Homo sapiens	ribosomal protein L21	108	48
10283	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	65	66
10284	Y25821	Homo sapiens	Human secreted protein fragment encoded from gene 41.	1602	98
10285	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	308	43
10286	AF090931	Homo sapiens	PRO0483	131	74
10287	Y48480	Homo sapiens	Human breast tumour-associated protein 25.	203	90
10288	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	116	44
10289	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	160	64
10290	X67863	Mus musculus	T2	147	37
10291	AF229067	Homo sapiens	PADI-H protein	123	43
10292	AF078844	Homo sapiens	hqp0376 protein	125	59
10293	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	123	37
10294	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	103	64
10295	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	162	70
10296	V00662	Homo sapiens	ATPase 6	268	88
10297	AB007861	Homo sapiens	KIAA0401	424	92
10298	M24732	Homo sapiens	lamin-like protein	183	40
10299	D90053	Sus scrofa	destrin	123	48
10300	X61047	Hydra sp.	mini-collagen	86	43

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10301	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	180	50
10302	AF118078	Homo sapiens	PRO1848	157	63
10303	X55681	Lycopersicon esculentum	extensin (class 1)	87	36
10304	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	105	62
10305	X70944	Homo sapiens	PTB-associated splicing factor	84	32
10306	AF068294	Homo sapiens	HDCMB45P	220	42
10307	S79410	Mus musculus	nuclear localization signal binding protein	96	41
10308	AJ005559	Mus musculus	SPR2A protein	64	42
10309	AL353995	Arabidopsis thaliana	AtAGP4	98	38
10310	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	213	92
10311	M15386	Homo sapiens	gamma-globin	614	88
10312	V00488	Homo sapiens	alpha globin	574	90
10313	AL049730	Arabidopsis thaliana	pEARL1 1-like protein	117	38
10314	AL356299	Homo sapiens	bK3216D2.1.1 (S-adenosylhomocysteine hydrolase (SAHH), isoform 1)	256	70
10315	AF194537	Homo sapiens	NAG13	113	63
10316	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	99	62
10317	AF090931	Homo sapiens	PRO0483	86	68
10318	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	102	77
10319	L29219	Homo sapiens	clk1; putative	341	100
10320	V00488	Homo sapiens	alpha globin	314	89
10321	AJ223953	Homo sapiens	hPTTG	354	89
10322	X79389	Homo sapiens	glutathione transferase T1	78	75
10323	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	101	66
10324	AF116715	Homo sapiens	PRO2829	128	73
10325	AF116619	Homo sapiens	PRO1051	125	77
10326	Y14318	Homo sapiens	peroxisomal ABC-transporter	249	100
10327	U73844	Homo sapiens	ESE-1a	185	90
10328	AB051901	Homo sapiens	VDUP1	132	83
10329	AL163300	Homo sapiens	human ubiquitin conjugating enzyme G2 EC 6.3.2.19.	720	100
10330	AF117237	Homo sapiens	prefoldin subunit 2	729	100
10331	D42054	Homo sapiens	KIAA0092 gene product is distantly related to smooth muscle myosin.	352	84
10332	AF038965	Homo sapiens	26S proteasome ATPase subunit	431	100
10333	Y94960	Homo sapiens	Human secreted protein clone ml117_1 protein sequence SEQ ID NO:126.	399	96
10334	X60376	Brassica napus	proline-rich protein	114	31
10335	M34427	Homo sapiens	T-plastin	343	91
10336	V00488	Homo sapiens	alpha globin	445	88
10337	M15386	Homo sapiens	gamma-globin	402	85
10338	X61123	Homo sapiens	BTG1	367	90
10339	U22961	Homo sapiens	similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	278	87
10340	A03992	synthetic construct	growth hormone	145	61
10341	G00437	Homo sapiens	Human secreted protein, SEQ ID NO:	126	57

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4518.		
10342	U02680	Homo sapiens	protein tyrosine kinase	140	92
10343	AF180681	Homo sapiens	guanine nucleotide exchange factor	1425	88
10344	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	123	69
10345	V00488	Homo sapiens	alpha globin	318	93
10346	M17885	Homo sapiens	acidic ribosomal phosphoprotein (P0)	329	98
10347	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	100	66
10348	U29953	Homo sapiens	pigment epithelium-derived factor	359	74
10349	G01790	Homo sapiens	Human secreted protein, SEQ ID NO: 5871.	85	66
10350	V00488	Homo sapiens	alpha globin	361	90
10351	U93567	Homo sapiens	p40	203	84
10352	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	253	85
10353	AF194537	Homo sapiens	NAG13	196	41
10354	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	297	81
10355	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	144	65
10356	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	94	54
10357	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	153	68
10358	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	136	53
10359	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	95	77
10360	X61296	Rattus norvegicus	open reading frame 2	87	40
10361	L24521	Homo sapiens	transformation-related protein	103	32
10362	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	101	55
10363	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	89	80
10364	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	101	58
10365	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	322	85
10366	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	59
10367	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFTU96.	125	53
10368	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	120	59
10369	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	60	83
10370	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	169	81
10371	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	80	75
10372	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	60	83
10373	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	89	77
10375	AF130089	Homo sapiens	PRO2550	139	78
10376	G03793	Homo sapiens	Human secreted protein, SEQ ID NO:	146	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7874.		
10377	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	96	51
10378	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	132	58
10379	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	117	71
10380	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	125	54
10381	U93569	Homo sapiens	putative p150	160	60
10382	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	140	77
10383	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	83	71
10384	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	137	63
10385	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	67	50
10386	X62691	Homo sapiens	ribosomal protein homologous to yeast S24	117	58
10387	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	141	45
10388	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	153	70
10389	U93570	Homo sapiens	putative p150	112	58
10390	AF090942	Homo sapiens	PRO0657	126	68
10391	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	123	64
10392	AF130089	Homo sapiens	PRO2550	144	71
10393	U40739	Homo sapiens	cyclin C	464	86
10394	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	151	75
10395	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	137	55
10396	W88947	Homo sapiens	Polypeptide fragment encoded by gene 118.	165	66
10397	AF090930	Homo sapiens	PRO0478	133	80
10398	AK024455	Homo sapiens	FLJ00047 protein	153	62
10399	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	142	69
10400	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	73	51
10401	AB030033	Dictyostelium discoideum	AmiB	82	33
10402	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	113	63
10403	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	148	77
10404	AK024455	Homo sapiens	FLJ00047 protein	138	71
10405	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	128	59
10406	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	143	76
10407	AF090942	Homo sapiens	PRO0657	105	64
10408	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	93	54
10409	J02621	Homo sapiens	high mobility group protein 14	140	64
10410	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	87	46
10411	G03798	Homo sapiens	Human secreted protein, SEQ ID NO:	79	56

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7879.		
10412	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	79	66
10413	AF130079	Homo sapiens	PRO2852	184	90
10414	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	237	77
10415	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	122	64
10416	AF016099	Mus musculus	endonuclease/reverse transcriptase	89	78
10417	S80864	Homo sapiens	cytochrome c-like polypeptide	184	52
10418	Y30681	Homo sapiens	Splice variant ZAP-1B protein of the human tumor suppressor gene ZAP-1.	131	75
10419	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	160	90
10420	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	131	59
10421	AF090942	Homo sapiens	PRO0657	154	57
10423	L78669	Homo sapiens	CoxII/D-loop DNA fusion protein	106	90
10424	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	105	75
10425	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	130	64
10426	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	122	64
10427	AF068294	Homo sapiens	HDCMB45P	256	56
10428	AF194537	Homo sapiens	NAG13	182	54
10429	AF090931	Homo sapiens	PRO0483	108	79
10430	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	93	68
10431	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10432	X67920	Homo sapiens	tryptophanyl-tRNA synthetase	138	84
10433	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	294	78
10434	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10435	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	125	75
10436	S79410	Mus musculus	nuclear localization signal binding protein	117	72
10437	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	120	67
10438	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	140	69
10439	AF130089	Homo sapiens	PRO2550	106	80
10440	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	331	83
10441	W94294	Homo sapiens	Human phosphatidylinositol transfer protein gamma.	143	96
10442	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	121	87
10443	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10444	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	141	67
10445	U93567	Homo sapiens	p40	262	69
10446	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	112	92
10447	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1	120	83

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			protein		
10448	G02597	Homo sapiens	Human secreted protein, SEQ ID NO: 6678.	104	68
10449	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	115	80
10450	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	117	80
10451	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	104	80
10452	AF130089	Homo sapiens	PRO2550	315	68
10453	G02530	Homo sapiens	Human secreted protein, SEQ ID NO: 6611.	110	71
10454	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	86	34
10455	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	113	85
10456	G03556	Homo sapiens	Human secreted protein, SEQ ID NO: 7637.	180	83
10457	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	119	96
10458	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	133	58
10459	Y41710	Homo sapiens	Human PRO618 protein sequence.	894	71
10460	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	84	71
10461	K02401	Homo sapiens	chorionic somatomammotropin	471	88
10462	G02113	Homo sapiens	Human secreted protein, SEQ ID NO: 6194.	241	73
10463	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	93	68
10464	U15647	Mus musculus	reverse transcriptase	110	47
10465	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	97	57
10466	G02754	Homo sapiens	Human secreted protein, SEQ ID NO: 6835.	145	93
10467	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	137	57
10468	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	62	55
10469	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	93	86
10470	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	119	63
10471	AF068294	Homo sapiens	HDCMB45P	117	43
10472	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	335	72
10473	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	121	62
10474	X79238	Homo sapiens	ribosomal protein L30	126	58
10475	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10476	G02640	Homo sapiens	Human secreted protein, SEQ ID NO: 6721.	106	61
10477	AC006693	Caenorhabditis elegans	Hypothetical protein W02H5.e	119	41
10478	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	87	66
10479	AF130079	Homo sapiens	PRO2852	97	54
10480	AK024455	Homo sapiens	FLJ00047 protein	135	69

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10481	K02401	Homo sapiens	chorionic somatomammotropin	463	80
10482	G00398	Homo sapiens	Human secreted protein, SEQ ID NO: 4479.	69	83
10483	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	132	61
10484	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	119	80
10485	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	90	54
10486	U79260	Homo sapiens	unknown	105	90
10487	Y87156	Homo sapiens	Human secreted protein sequence SEQ ID NO:195.	243	53
10488	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	90	78
10489	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	120	64
10490	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	123	60
10491	Y48576	Homo sapiens	Human breast tumour-associated protein 37.	471	84
10492	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	176	77
10493	S79410	Mus musculus	nuclear localization signal binding protein	135	64
10494	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	123	44
10495	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	86	46
10496	Y67470	Homo sapiens	Np70 protein carboxy terminal region.	145	40
10497	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	111	50
10498	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	96	73
10499	AL132841	Caenorhabditis elegans	Y15E3A.3	142	96
10500	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	120	49
10501	AF220264	Homo sapiens	MOST-1	93	83
10502	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	116	57
10503	G03371	Homo sapiens	Human secreted protein, SEQ ID NO: 7452.	100	70
10504	AF090931	Homo sapiens	PRO0483	88	80
10505	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	89	72
10506	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	121	81
10507	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	188	82
10508	AF130050	Homo sapiens	PRO0872	101	74
10509	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	176	68
10510	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	120	96
10511	AK026249	Homo sapiens	unnamed protein product	97	68
10512	X95276	Plasmodium falciparum	ORF91	75	29
10513	X17093	Homo sapiens	leukocyte antigen F	397	91
10514	W48351	Homo sapiens	Human breast cancer related protein	115	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCRB2.		
10515	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	154	68
10516	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	86	47
10517	AF090944	Homo sapiens	PRO0663	118	48
10518	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	131	77
10519	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	230	58
10520	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10521	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	130	40
10522	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10523	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	139	69
10524	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	125	100
10525	J04495	Macaca mulatta	alpha-globin	144	90
10526	G02535	Homo sapiens	Human secreted protein, SEQ ID NO: 6616.	105	61
10527	AF130089	Homo sapiens	PRO2550	132	67
10528	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	90	53
10529	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	112	75
10530	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	157	79
10531	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	59
10532	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	121	63
10533	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	112	43
10534	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	131	65
10535	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	95	60
10536	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	157	79
10537	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	199	90
10538	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	113	75
10539	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	120	65
10540	AF130089	Homo sapiens	PRO2550	195	67
10541	Y60522	Homo sapiens	Human normal bladder tissue EST encoded protein 194.	73	72
10542	G01175	Homo sapiens	Human secreted protein, SEQ ID NO: 5256.	83	100
10543	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	81	54
10544	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	147	75
10545	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	109	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10546	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	123	46
10547	AF130089	Homo sapiens	PRO2550	133	63
10548	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	246	80
10549	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	122	51
10550	J02459	bacteriophage lambda	J (tail:host specificity;1132)	772	97
10551	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	158	80
10552	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	123	50
10553	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	184	71
10554	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	107	60
10555	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	140	69
10556	U49973	Homo sapiens	ORF2: function unknown	91	70
10557	AF151850	Homo sapiens	CGI-92 protein	459	63
10558	X66285	Mus musculus	HC1 ORF	92	30
10559	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	127	67
10560	AF130050	Homo sapiens	PRO0872	100	71
10561	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	335	80
10562	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	126	58
10563	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	127	76
10564	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	158	62
10565	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	118	77
10566	V00488	Homo sapiens	alpha globin	464	89
10567	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	162	81
10568	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	113	72
10569	G03040	Homo sapiens	Human secreted protein, SEQ ID NO: 7121.	127	47
10570	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	125	65
10571	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	79	88
10572	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	158	80
10573	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	138	56
10574	AF119900	Homo sapiens	PRO2822	154	55
10575	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	87	72
10576	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	131	66
10577	G03112	Homo sapiens	Human secreted protein, SEQ ID NO: 7193.	80	47
10578	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	121	53
10579	Y91577	Homo sapiens	Human secreted protein sequence	335	83

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			encoded by gene 2 SEQ ID NO:250.		
10580	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	104	47
10581	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	324	68
10582	G00589	Homo sapiens	Human secreted protein, SEQ ID NO: 4670.	129	66
10583	AF090895	Homo sapiens	PRO0117	137	63
10584	L27428	Homo sapiens	reverse transcriptase	98	50
10585	G00418	Homo sapiens	Human secreted protein, SEQ ID NO: 4499.	101	68
10586	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	108	82
10587	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	166	76
10588	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	100	70
10589	X03145	Homo sapiens	pot. ORF 1	120	43
10590	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	139	70
10591	AF144054	Homo sapiens	apoptosis related protein APR-4	92	50
10592	AK024455	Homo sapiens	FLJ00047 protein	111	75
10593	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	143	58
10594	G03636	Homo sapiens	Human secreted protein, SEQ ID NO: 7717.	116	54
10595	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	196	57
10596	AF130089	Homo sapiens	PRO2550	140	66
10597	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	115	52
10598	G00481	Homo sapiens	Human secreted protein, SEQ ID NO: 4562.	79	71
10599	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	79
10600	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	119	67
10601	AF090895	Homo sapiens	PRO0117	106	68
10602	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	83	72
10603	AF090930	Homo sapiens	PRO0478	119	70
10604	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	120	83
10605	AF132949	Homo sapiens	CGI-15 protein	114	96
10606	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	176	77
10607	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	155	74
10608	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	127	63
10609	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	88	60
10610	AF130089	Homo sapiens	PRO2550	86	90
10611	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	149	72
10612	L27428	Homo sapiens	reverse transcriptase	311	52
10613	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	83	84
10614	D00570	Mus musculus	open reading frame (196 AA)	116	69

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10615	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	290	62
10616	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	125	51
10617	AF116695	Homo sapiens	PRO2221	131	56
10618	M64793	Rattus norvegicus	salivary proline-rich protein	101	48
10619	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	104	65
10620	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	112	58
10621	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	336	85
10622	AF118082	Homo sapiens	PRO1902	80	73
10623	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	136	50
10624	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	109	67
10625	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	92	75
10626	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	121	62
10627	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	104	52
10628	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	137	66
10629	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	129	67
10630	U93569	Homo sapiens	putative p150	104	52
10631	AF090895	Homo sapiens	PRO0117	136	70
10632	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	89	57
10633	AF113685	Homo sapiens	PRO0974	130	64
10634	AK024455	Homo sapiens	FLJ00047 protein	103	63
10635	M24732	Homo sapiens	lamin-like protein	80	65
10636	U49974	Homo sapiens	mariner transposase	116	72
10637	AK024455	Homo sapiens	FLJ00047 protein	158	67
10638	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	121	64
10639	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	137	57
10640	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	123	72
10641	L27428	Homo sapiens	reverse transcriptase	150	54
10642	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	68	81
10643	U93565	Homo sapiens	putative p150	282	57
10644	AF090942	Homo sapiens	PRO0657	153	74
10645	Y48333	Homo sapiens	Human prostate cancer-associated protein 30.	196	90
10646	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	242	73
10647	U79260	Homo sapiens	unknown	95	77
10648	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	149	64
10649	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	158	87
10650	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	339	89

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10651	U15183	Mycobacterium leprae	proline-rich antigen	102	37
10652	AF217536	Homo sapiens	truncated mevalonate kinase	138	70
10653	AF119855	Homo sapiens	PRO1847	74	100
10654	M15530	Homo sapiens	B-cell growth factor	94	52
10655	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	144	54
10656	M15317	Plasmodium falciparum	histidine-rich protein	124	51
10657	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	143	66
10658	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	114	77
10659	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	172	55
10660	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	150	78
10661	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
10662	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	151	71
10663	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
10664	AK000496	Homo sapiens	unnamed protein product	140	77
10665	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	147	75
10666	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
10667	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	149	78
10668	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	303	78
10669	D00526	Rattus norvegicus	L-gulonolactone oxidase	108	73
10670	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	143	65
10671	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	409	84
10672	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	110	65
10673	G00423	Homo sapiens	Human secreted protein, SEQ ID NO: 4504.	123	43
10674	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	85	36
10675	U93565	Homo sapiens	putative p150	115	45
10676	AF109907	Homo sapiens	S164	205	65
10677	G02620	Homo sapiens	Human secreted protein, SEQ ID NO: 6701.	118	73
10678	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	106	62
10679	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	127	87
10680	Y87156	Homo sapiens	Human secreted protein sequence SEQ ID NO:195.	248	54
10681	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	88	52
10682	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	126	77
10683	S58722	Homo sapiens	X-linked retinopathy protein (C-	123	72

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			terminal, clone XEH.8c}		
10684	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	123	72
10685	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	99	40
10686	AF068294	Homo sapiens	HDCMB45P	182	54
10687	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	104	53
10688	Y86305	Homo sapiens	Human secreted protein HLYES38, SEQ ID NO:220.	277	76
10689	G00233	Homo sapiens	Human secreted protein, SEQ ID NO: 4314.	118	65
10690	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	143	71
10691	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	97	81
10692	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	160	68
10693	AF130089	Homo sapiens	PRO2550	133	56
10694	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	129	71
10695	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	123	71
10696	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	161	45
10697	G00648	Homo sapiens	Human secreted protein, SEQ ID NO: 4729.	88	56
10698	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	75	71
10699	G00517	Homo sapiens	Human secreted protein, SEQ ID NO: 4598.	92	38
10700	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	132	55
10701	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	118	54
10702	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	66	73
10703	S79410	Mus musculus	nuclear localization signal binding protein	124	44
10704	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	113	78
10705	S79410	Mus musculus	nuclear localization signal binding protein	119	50
10706	AK025116	Homo sapiens	unnamed protein product	160	84
10707	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
10708	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	160	81
10709	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	230	76
10710	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	96	45
10711	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	174	70
10712	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	127	50
10713	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	148	45
10714	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	151	80

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10715	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	157	67
10716	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	109	68
10717	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	151	52
10718	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	84	80
10719	M19973	Rattus norvegicus	cytochrome PB24	104	45
10720	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	103	72
10721	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	161	52
10722	L27428	Homo sapiens	reverse transcriptase	159	42
10723	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	127	75
10724	Y00311	Homo sapiens	Human secreted protein encoded by gene 54.	84	50
10725	AF090895	Homo sapiens	PRO0117	170	71
10726	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	105	42
10727	K03205	Homo sapiens	salivary proline-rich protein precursor	123	38
10728	U93563	Homo sapiens	putative p150	162	64
10729	X14576	Murine leukemia virus	gag fusion protein	172	41
10730	AF090895	Homo sapiens	PRO0117	151	60
10731	AF119851	Homo sapiens	PRO1722	127	54
10732	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	152	61
10733	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	156	76
10734	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	135	73
10735	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	151	65
10736	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	141	75
10737	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	74
10738	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	124	69
10739	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	91	60
10740	AF130051	Homo sapiens	PRO0898	90	63
10741	AF090895	Homo sapiens	PRO0117	129	55
10742	AF119900	Homo sapiens	PRO2822	164	85
10743	AJ005560	Mus musculus	SPR2B protein	88	35
10744	Z79996	Homo sapiens	cb33f2.1 (PUTATIVE novel protein similar to C-terminal parts of APOL (apolipoprotein L) and TNF-inducible protein CG12-1)	185	100
10745	G03140	Homo sapiens	Human secreted protein, SEQ ID NO: 7221.	94	88
10746	X82208	Homo sapiens	beta-actinin	134	96
10747	D49744	Mus musculus	farnesyltransferase alpha subunit	228	60
10748	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	127	50
10749	G00442	Homo sapiens	Human secreted protein, SEQ ID NO:	153	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4523.		
10750	AF130089	Homo sapiens	PRO2550	147	62
10751	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	108	71
10752	D17652	Homo sapiens	HBp15/L22	416	72
10753	AB002389	Homo sapiens	KIAA0391	486	86
10754	G03093	Homo sapiens	Human secreted protein, SEQ ID NO: 7174.	238	73
10755	S79410	Mus musculus	nuclear localization signal binding protein	103	57
10756	AF130089	Homo sapiens	PRO2550	104	72
10757	X75421	Hypocrea jecorina	actin	197	66
10758	AF298594	Nicotiana glauca	arabinogalactan protein	107	30
10759	U94832	Homo sapiens	KSRP	95	40
10760	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	179	82
10761	Y86573	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:490.	271	80
10762	Z81528	Caenorhabditis elegans	predicted using Genefinder--contains similarity to Pfam domain: PF00939 (Sodium:sulfate symporter transmembrane region), Score=2.8, E-value=1.2, N=1; PF01757 (Domain of unknown function), Score=556.0, E-value=8.1e-164, N=1	103	27
10763	V00662	Homo sapiens	ATPase 6	593	83
10764	A06977	Homo sapiens	albumin	610	81
10765	X67863	Mus musculus	T2	109	46
10766	AF137030	Homo sapiens	transmembrane protein 2	620	96
10767	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	101	66
10768	X15324	Homo sapiens	angiotensinogen	529	89
10769	M64983	Homo sapiens	fibrinogen beta chain	604	87
10770	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	381	83
10771	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	133	73
10772	M64110	Homo sapiens	caldesmon	346	94
10773	AB014566	Homo sapiens	KIAA0666 protein	145	78
10774	AL138810	Homo sapiens	dJ179L10.2 (Similar to CGI-29 protein)	216	90
10775	AJ223953	Homo sapiens	hPTTG	353	82
10776	U92288	Human herpesvirus 6	HN1	113	39
10777	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	143	78
10778	X12796	Bos taurus	HMG1 protein (AA 1 - 215)	435	96
10779	U86782	Homo sapiens	26S proteasome-associated pad1 homolog	477	89
10780	M60047	Homo sapiens	heparin binding protein	514	81
10781	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	99	48
10782	AF130079	Homo sapiens	PRO2852	175	48
10783	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	115	64
10784	M11147	Homo sapiens	ferritin light chain	439	83
10785	AF090931	Homo sapiens	PRO0483	145	55
10786	AF072441	Homo sapiens	calcineurin binding protein cabin 1	498	90
10787	AF116715	Homo sapiens	PRO2829	127	88

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10788	AF201949	Homo sapiens	60S ribosomal protein L30 isolog	631	91
10789	AC005253	Homo sapiens	R26445_1	403	84
10790	M15386	Homo sapiens	gamma-globin	617	82
10791	Y95005	Homo sapiens	Human secreted protein vc57_1, SEQ ID NO:50.	716	95
10792	G01285	Homo sapiens	Human secreted protein, SEQ ID NO: 5366.	165	52
10793	X67863	Mus musculus	T2	128	50
10794	Y82326	Homo sapiens	Human arginase I SEQ ID NO:17.	507	80
10795	Y00755	Homo sapiens	extracellular matrix protein BM-40 (AA 1 - 303)	559	87
10796	AF119851	Homo sapiens	PRO1722	117	71
10797	AF090930	Homo sapiens	PRO0478	146	63
10798	V00488	Homo sapiens	alpha globin	509	84
10799	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	131	42
10800	X83618	Homo sapiens	hydroxymethylglutaryl-CoA synthase	422	78
10801	AF132952	Homo sapiens	CGI-18 protein	341	88
10802	M17375	Gallus gallus	type XII collagen	88	42
10803	K02401	Homo sapiens	chorionic somatomammotropin	436	85
10804	K02401	Homo sapiens	chorionic somatomammotropin	410	86
10805	U61232	Homo sapiens	cofactor E	359	77
10806	D86438	Homo sapiens	Ibal (ionized calcium binding adapter molecule 1)	406	77
10807	AF118082	Homo sapiens	PRO1902	105	38
10808	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	148	60
10809	AF090942	Homo sapiens	PRO0657	163	52
10810	U63332	Homo sapiens	super cysteine rich protein; SCRP	116	86
10811	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	104	45
10812	X61296	Rattus norvegicus	open reading frame 2	156	41
10813	U82303	Homo sapiens	unknown	103	64
10814	G01478	Homo sapiens	Human secreted protein, SEQ ID NO: 5559.	75	77
10815	U52077	Homo sapiens	mariner transposase	131	85
10816	D38112	Homo sapiens	ATPase subunit 6	251	74
10817	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	103	80
10818	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	102	52
10819	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	94	66
10820	Y21811	Homo sapiens	CPF polypeptide 36PRO.	200	62
10821	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	161	60
10822	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	163	70
10823	U22961	Homo sapiens	similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	337	63
10824	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	122	61
10825	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	122	68
10826	J03634	Homo sapiens	erythroid differentiation protein precursor	222	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10827	D38112	Homo sapiens	NADH dehydrogenase subunit 5	452	78
10828	V00488	Homo sapiens	alpha globin	132	86
10829	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	131	70
10830	AF090942	Homo sapiens	PRO0657	122	43
10831	AF090931	Homo sapiens	PRO0483	141	72
10832	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	138	63
10833	G03806	Homo sapiens	Human secreted protein, SEQ ID NO: 7887.	88	57
10834	AF118082	Homo sapiens	PRO1902	109	62
10835	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	135	44
10836	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	152	86
10837	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	143	47
10838	U52077	Homo sapiens	mariner transposase	259	67
10839	M10546	Homo sapiens	cytochrome oxidase I	341	83
10840	Y44361	Homo sapiens	Human cell cycle regulation protein-2.	144	60
10841	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	96	56
10842	D38112	Homo sapiens	cytochrome c oxidase subunit 3	565	80
10843	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	118	100
10844	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	157	81
10845	AF014889	Homo sapiens	NADH dehydrogenase subunit 2	416	85
10846	AF194537	Homo sapiens	NAG13	177	70
10847	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	108	40
10848	M15530	Homo sapiens	B-cell growth factor	92	67
10849	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	98	52
10850	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	121	76
10851	AF116712	Homo sapiens	PRO2738	84	57
10852	V00662	Homo sapiens	ATPase 6	278	84
10853	U01849	Trypanosoma brucei	ORF1	93	37
10854	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	93	61
10855	AF130089	Homo sapiens	PRO2550	126	72
10856	AF130079	Homo sapiens	PRO2852	154	75
10857	AK025116	Homo sapiens	unnamed protein product	113	70
10858	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	114	71
10859	G03703	Homo sapiens	Human secreted protein, SEQ ID NO: 7784.	97	56
10860	M36647	Homo sapiens	mitochondrial hinge protein precursor	207	78
10861	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	83	50
10862	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	126	46
10863	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	148	63
10864	B01372	Homo sapiens	Neuron-associated protein.	106	38
10865	U38964	Homo sapiens	hPMSR2	152	68
10866	AF119855	Homo sapiens	PRO1847	142	67

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10867	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	99	75
10868	U79260	Homo sapiens	unknown	94	47
10869	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene preduct.	151	52
10870	AJ010025	Homo sapiens	unr-interacting protein	100	64
10871	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	110	44
10872	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	136	71
10873	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFTU96.	126	61
10874	AF130089	Homo sapiens	PRO2550	115	88
10875	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	114	59
10876	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	83	48
10877	AF118086	Homo sapiens	PRO1992	145	82
10878	AF116712	Homo sapiens	PRO2738	110	55
10879	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	123	77
10880	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	111	61
10881	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	106	51
10882	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	107	67
10883	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	101	65
10884	U79260	Homo sapiens	unknown	111	56
10885	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	153	60
10886	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	107	57
10887	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	148	80
10888	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	142	58
10889	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	156	67
10890	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	105	52
10891	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	187	65
10892	A67510	Mus musculus	MUS MUSCULUS GENOMIC DNA CONTAINING N ALLELE OF FV1 GENE.	120	37
10893	AJ223410	Homo sapiens	EBI1-ligand chemokine	174	77
10894	D38112	Homo sapiens	cytochrome c oxidase subunit 1	475	83
10895	V00662	Homo sapiens	ATPase 6	316	95
10896	V00662	Homo sapiens	ATPase 6	427	82
10897	U09500	Homo sapiens	cytochrome b	403	92
10898	U93564	Homo sapiens	p40	215	91
10899	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	69	77
10900	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	159	60
10901	AC003058	Arabidopsis thaliana	unknown protein	93	43

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10902	M10546	Homo sapiens	cytochrome oxidase I	302	66
10903	G00447	Homo sapiens	Human secreted protein, SEQ ID NO: 4528.	102	58
10904	AK024455	Homo sapiens	FLJ00047 protein	118	74
10905	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	108	64
10906	AF090942	Homo sapiens	PRO0657	149	74
10907	J01415	Homo sapiens	cytochrome oxidase subunit 3	167	91
10908	D38112	Homo sapiens	ATPase subunit 6	355	68
10909	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	145	72
10910	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	114	72
10911	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	144	53
10912	V00662	Homo sapiens	ATPase 6	289	69
10913	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	93	51
10914	V00662	Homo sapiens	cytochrome oxidase III	509	86
10915	J03071	Homo sapiens	chorionic somatomammotropin CS-2	459	80
10916	Z28029	Saccharomyces cerevisiae	ORF YKL030w	96	32
10917	G03102	Homo sapiens	Human secreted protein, SEQ ID NO: 7183.	94	56
10918	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	114	36
10919	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	88
10920	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	103	39
10921	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	99	95
10922	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	75	63
10923	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	125	85
10924	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	140	73
10925	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	77	38
10926	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	111	58
10927	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	139	75
10928	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	78
10929	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	77	57
10930	K02576	Homo sapiens	salivary proline-rich protein I	93	53
10931	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	83	54
10932	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	262	84
10933	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	113	72
10934	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	120	62
10935	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	116	69

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
10936	J02963	Homo sapiens	platelet glycoprotein IIb precursor	120	56
10937	AB028893	Homo sapiens	ribosomal protein S11	279	53
10939	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	127	55
10940	AF119900	Homo sapiens	PRO2822	154	53
10941	G03556	Homo sapiens	Human secreted protein, SEQ ID NO: 7637.	127	62
10942	K02576	Homo sapiens	salivary proline-rich protein I	109	41
10943	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	164	61
10944	AF116715	Homo sapiens	PRO2829	119	69
10945	M10546	Homo sapiens	cytochrome oxidase I	303	95
10946	L27428	Homo sapiens	reverse transcriptase	112	51
10947	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	118	90
10948	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	121	83
10949	AF116715	Homo sapiens	PRO2829	134	67
10950	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	139	83
10952	AF130079	Homo sapiens	PRO2852	119	79
10953	Z38128	Mus musculus	histone H1	126	35
10954	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	135	53
10955	L22029	Glycine max	hydroxyproline-rich glycoprotein	126	37
10956	G00500	Homo sapiens	Human secreted protein, SEQ ID NO: 4581.	81	69
10957	AF118082	Homo sapiens	PRO1902	90	51
10958	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	116	53
10959	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	82	51
10960	U79260	Homo sapiens	unknown	97	52
10961	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	194	66
10962	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	124	48
10963	G03084	Homo sapiens	Human secreted protein, SEQ ID NO: 7165.	66	73
10964	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	87
10965	Z28029	Saccharomyces cerevisiae	ORF YKL030w	99	70
10966	V00672	Pan troglodytes	reading frame protein 5	107	70
10967	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	138	58
10968	K02401	Homo sapiens	chorionic somatomammotropin	478	77
10969	D38112	Homo sapiens	cytochrome c oxidase subunit 3	642	86
10970	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	156	57
10971	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	126	56
10972	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	103	51
10973	K02401	Homo sapiens	chorionic somatomammotropin	491	82
10974	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	146	93
10975	D38112	Homo sapiens	NADH dehydrogenase subunit 4	236	85
10976	Y02785	Homo sapiens	Human secreted protein encoded by	108	50

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gene 51 clone HUKEX85.		
10977	J03071	Homo sapiens	chorionic somatomammotropin CS-2	435	73
10978	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	119	74
10979	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	137	73
10980	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	133	63
10981	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	90	65
10982	X92485	Plasmodium vivax	pval	119	47
10983	Y15913	Homo sapiens	COL1A1 and PDGFB fusion transcript	64	47
10984	D38112	Homo sapiens	cytochrome c oxidase subunit 1	463	77
10985	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	309	65
10986	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	145	87
10987	AF130089	Homo sapiens	PRO2550	88	31
10988	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	127	65
10989	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	137	75
10990	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	145	76
10991	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	118	72
10992	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	138	69
10993	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	120	92
10994	AJ277092	Oryctolagus cuniculus	translationally controlled tumor protein 3	172	49
10995	AF052831	Trypanosoma cruzi	unknown	92	37
10996	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	119	53
10997	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	123	43
10998	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	165	52
10999	S52010	Mus sp.	orf1 5' of EpoR	93	39
11000	AF130079	Homo sapiens	PRO2852	131	81
11001	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	111	75
11002	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	132	83
11003	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	151	60
11004	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	159	58
11005	K02401	Homo sapiens	chorionic somatomammotropin	579	89
11006	K02401	Homo sapiens	chorionic somatomammotropin	464	87
11007	M15894	Homo sapiens	chorionic somatomammotropin precursor	370	74
11008	K02401	Homo sapiens	chorionic somatomammotropin	467	88
11009	K02401	Homo sapiens	chorionic somatomammotropin	537	91
11010	K02401	Homo sapiens	chorionic somatomammotropin	475	87
11011	K02401	Homo sapiens	chorionic somatomammotropin	460	88

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11012	G03639	Homo sapiens	Human secreted protein, SEQ ID NO: 7720.	101	61
11013	AF266166	Gillichthys mirabilis	ribosomal protein S13	223	54
11014	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	176	61
11015	AF116715	Homo sapiens	PRO2829	121	69
11016	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	92	75
11017	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	113	78
11018	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	114	40
11019	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	48
11020	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	151	51
11021	X14963	Homo sapiens	collagen-like protein (447 AA)	107	47
11022	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	72
11023	AF116715	Homo sapiens	PRO2829	140	75
11024	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	70
11025	AP000001	Pyrococcus horikoshii	58aa long hypothetical protein	99	52
11026	D38112	Homo sapiens	cytochrome c oxidase subunit 3	601	81
11027	D38112	Homo sapiens	cytochrome c oxidase subunit 3	434	74
11028	Z97333	Homo sapiens	RHCE protein	149	51
11029	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	113	48
11030	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	120	77
11031	U61234	Homo sapiens	cofactor C	226	63
11032	M10546	Homo sapiens	cytochrome oxidase I	116	88
11033	B03148	Homo sapiens	Human neuronal differentiation factor-1 (NDF-1).	584	93
11034	L10910	Homo sapiens	splicing factor	108	58
11035	M26361	Mus musculus	LINE/Ig H-chain fusion protein	140	48
11036	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}.	101	79
11037	AK024455	Homo sapiens	FLJ00047 protein	122	48
11038	AF126163	Homo sapiens	HHLA3 protein	96	68
11039	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	144	79
11040	AK024455	Homo sapiens	FLJ00047 protein	151	62
11041	L06498	Homo sapiens	ribosomal protein S20	321	73
11042	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	84
11043	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	125	68
11044	V00662	Homo sapiens	URF 2 (NADH dehydrogenase subunit)	208	91
11045	G00552	Homo sapiens	Human secreted protein, SEQ ID NO: 4633.	79	62
11046	D38112	Homo sapiens	ATPase subunit 6	297	90
11047	D38112	Homo sapiens	cytochrome c oxidase subunit 3	416	73
11048	G00491	Homo sapiens	Human secreted protein, SEQ ID NO: 4572.	73	80
11049	AF090944	Homo sapiens	PRO0663	96	70
11050	AF130089	Homo sapiens	PRO2550	152	71
11051	Y02671	Homo sapiens	Human secreted protein encoded by	108	81

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gene 22 clone HMSJW18.		
11052	W89031	Homo sapiens	Polypeptide fragment encoded by gene 167.	254	95
11053	AF109907	Homo sapiens	S164	136	45
11054	AF217536	Homo sapiens	truncated mevalonate kinase	117	58
11055	X72004	Halichoerus grypus	ATP synthase subunit 6	160	78
11056	V00662	Homo sapiens	ATPase 6	300	71
11057	AF228021	Bos taurus	cyclophilin I	209	73
11058	L27428	Homo sapiens	reverse transcriptase	303	65
11059	U09116	Homo sapiens	ORF1, encodes a 40 kDa product	464	80
11060	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	145	68
11061	D38112	Homo sapiens	cytochrome c oxidase subunit 3	301	85
11062	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	119	64
11063	Y08061	Homo sapiens	Human c-myc protein fragment.	128	76
11064	U50188	Cavia porcellus	CGRP-receptor component protein	152	88
11065	G03107	Homo sapiens	Human secreted protein, SEQ ID NO: 7188.	104	44
11066	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	112	64
11067	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	71
11068	AE003499	Drosophila melanogaster	CG12706 gene product	145	43
11069	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	160	65
11070	D38112	Homo sapiens	cytochrome c oxidase subunit 1	416	67
11071	D38112	Homo sapiens	cytochrome c oxidase subunit 3	220	86
11072	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	144	63
11073	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	115	60
11074	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	117	65
11075	D38112	Homo sapiens	cytochrome c oxidase subunit 1	589	87
11076	D38112	Homo sapiens	cytochrome c oxidase subunit 1	588	83
11077	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	106	86
11078	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	90	50
11079	AF132200	Homo sapiens	PRO1751	97	89
11080	AF116661	Homo sapiens	PRO1438	109	51
11081	AK024455	Homo sapiens	FLJ00047 protein	93	48
11082	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	84	73
11083	J02963	Homo sapiens	platelet glycoprotein IIb precursor	108	80
11084	AF068294	Homo sapiens	HDCMB45P	229	59
11085	M10546	Homo sapiens	cytochrome oxidase I	137	73
11086	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	105	49
11087	L26953	Homo sapiens	chromosomal protein	122	75
11088	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	103	46
11089	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	112	56
11090	AF130089	Homo sapiens	PRO2550	172	60
11091	K02576	Homo sapiens	salivary proline-rich protein 1	107	35

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11092	AF090930	Homo sapiens	PRO0478	146	75
11093	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	163	82
11094	V00662	Homo sapiens	ATPase 6	130	87
11095	B01372	Homo sapiens	Neuron-associated protein.	122	82
11096	D38112	Homo sapiens	ATPase subunit 6	152	62
11097	U18339	Variola virus	D4L	96	60
11098	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	60
11099	AF130089	Homo sapiens	PRO2550	128	75
11100	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	218	62
11101	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	232	79
11102	AF090930	Homo sapiens	PRO0478	154	73
11103	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	133	65
11104	K03036	Mus musculus	alpha-1 type I procollagen	105	43
11105	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	142	59
11106	L13129	Mus musculus	synexin	119	35
11107	AF280111	Homo sapiens	cytochrome P450 subfamily IIIA polypeptide 43	122	52
11108	J00314	Homo sapiens	beta-tubulin	606	94
11109	X05196	Homo sapiens	aldolase C	412	89
11110	D00570	Mus musculus	open reading frame (196 AA)	127	85
11111	D50532	Homo sapiens	macrophage lectin 2	165	65
11112	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	125	74
11113	M15530	Homo sapiens	B-cell growth factor	163	82
11114	V00662	Homo sapiens	ATPase 6	217	91
11115	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	100
11116	K02576	Homo sapiens	salivary proline-rich protein 1	119	36
11117	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	132	59
11118	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	103	67
11119	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	94	42
11120	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	127	75
11121	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	104	64
11122	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	90	59
11123	AF161356	Homo sapiens	HSPC093	119	64
11124	J02963	Homo sapiens	platelet glycoprotein IIb precursor	102	70
11125	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	149	60
11126	AF068294	Homo sapiens	HDCMB45P	272	59
11127	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	120	79
11128	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	101	78
11129	AF130089	Homo sapiens	PRO2550	124	80
11130	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	109	51
11131	U40265	Trypanosoma cruzi	ATPase subunit 6	102	31

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11132	X01677	Homo sapiens	glyceraldehyde-3-phosphate dehydrogenase	555	88
11133	K02576	Homo sapiens	salivary proline-rich protein 1	108	37
11134	M81757	Homo sapiens	S19 ribosomal protein	232	76
11135	U93565	Homo sapiens	putative p150	173	51
11136	AF061944	Homo sapiens	kinase deficient protein KDP	369	100
11137	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	145	61
11138	AB030255	Homo sapiens	serine/threonine phosphatase 1 gamma	404	83
11139	AL049610	Homo sapiens	dJ1055C14.2 (KIAA0026 (transcription factor-like protein MRGX))	248	77
11140	Y36421	Homo sapiens	Fragment of human secreted protein encoded by gene 8.	81	53
11141	M13692	Homo sapiens	alpha-1 acid glycoprotein precursor	112	41
11142	M16961	Homo sapiens	alpha-2-HS-glycoprotein	543	89
11143	D38112	Homo sapiens	cytochrome c oxidase subunit 3	605	88
11144	AF090944	Homo sapiens	PRO0663	137	67
11145	X92485	Plasmodium vivax	pval	102	57
11146	AF130089	Homo sapiens	PRO2550	113	58
11147	U63542	Homo sapiens	FAP protein	154	57
11148	W03988	Homo sapiens	SH2 domain from human SH-PTP2 (amino acids 1-106).	162	73
11149	AF116695	Homo sapiens	PRO2221	173	44
11150	M15530	Homo sapiens	B-cell growth factor	105	45
11151	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	160	64
11152	M15530	Homo sapiens	B-cell growth factor	124	75
11153	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	117	67
11154	AF118082	Homo sapiens	PRO1902	79	52
11155	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	123	72
11156	Y27893	Homo sapiens	Human secreted protein encoded by gene No. 116.	266	96
11157	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	148	84
11158	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	154	72
11159	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	105	58
11160	X60376	Brassica napus	proline-rich protein	111	39
11161	S79410	Mus musculus	nuclear localization signal binding protein	111	37
11162	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	53
11163	AF090930	Homo sapiens	PRO0478	146	73
11164	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	90	60
11165	AF242772	Homo sapiens	mesenchymal stem cell protein DSCD28	141	51
11166	X82629	Homo sapiens	Mox-2	307	83
11167	D38112	Homo sapiens	NADH dehydrogenase subunit 4	168	91
11168	X55684	Lycopersicon esculentum	extensin (class I)	71	66
11169	AC079041	Arabidopsis thaliana	hypothetical protein	98	45
11170	AF090930	Homo sapiens	PRO0478	156	50

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11171	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	99	70
11172	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	124	54
11173	D38112	Homo sapiens	cytochrome c oxidase subunit 1	587	82
11174	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	127	66
11175	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	157	68
11176	AF090931	Homo sapiens	PRO0483	146	87
11177	M15530	Homo sapiens	B-cell growth factor	153	75
11178	AF090930	Homo sapiens	PRO0478	129	52
11179	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	98	77
11180	AF194537	Homo sapiens	NAG13	165	48
11181	AF068294	Homo sapiens	HDCMB45P	146	53
11182	AF090931	Homo sapiens	PRO0483	153	78
11183	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	141	65
11184	Y13396	Homo sapiens	Amino acid sequence of protein PRO332.	452	92
11185	AF090930	Homo sapiens	PRO0478	132	51
11186	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	178	79
11187	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	237	70
11188	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	117	83
11189	AL080206	Homo sapiens	hypothetical protein	103	71
11190	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	77
11191	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	112	65
11192	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	127	54
11193	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	150	65
11194	M92046	Trypanosoma cruzi	surface antigen	160	26
11195	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	126	72
11196	G03224	Homo sapiens	Human secreted protein, SEQ ID NO: 7305.	98	75
11197	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	117	50
11198	D88548	Homo sapiens	24-kDa subunit of complex I	160	47
11199	AF090852	Antilocapra americana	prion protein	115	38
11200	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	136	62
11201	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	139	75
11202	U93563	Homo sapiens	putative p150	239	43
11203	U93570	Homo sapiens	putative p150	173	45
11204	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	166	68
11205	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	68
11206	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	87	56

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11207	W48808	Homo sapiens	Homo sapiens clone CG109_1 protein.	123	89
11208	D38112	Homo sapiens	cytochrome c oxidase subunit 3	619	87
11209	W48808	Homo sapiens	Homo sapiens clone CG109_1 protein.	125	89
11210	D38112	Homo sapiens	cytochrome c oxidase subunit 3	521	83
11211	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	90	76
11212	D38112	Homo sapiens	cytochrome c oxidase subunit 1	547	81
11213	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	92	74
11214	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	126	63
11215	AF162149	Mycoplasma bovis.	variable surface lipoprotein	118	34
11216	AF130089	Homo sapiens	PRO2550	147	96
11217	AF090931	Homo sapiens	PRO0483	112	77
11218	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	163	70
11219	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	111	55
11220	AF130051	Homo sapiens	PRO0898	122	63
11221	AF130079	Homo sapiens	PRO2852	171	64
11222	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	146	55
11223	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	130	71
11224	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	128	69
11225	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	141	85
11226	G02360	Homo sapiens	Human secreted protein, SEQ ID NO: 6441.	103	90
11227	M15530	Homo sapiens	B-cell growth factor	122	55
11228	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	121	67
11229	M15317	Plasmodium falciparum	histidine-rich protein	116	43
11230	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	131	78
11231	W19932	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS55.	74	76
11232	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	134	67
11233	AK023045	Homo sapiens	unnamed protein product	100	69
11234	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	127	82
11235	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	125	65
11236	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	109	53
11237	AF029403	Homo sapiens	oxysterol 7alpha-hydroxylase	144	72
11238	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	112	44
11239	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	96
11240	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	127	43
11241	L36529	Homo sapiens	protein p84	343	90
11242	M15530	Homo sapiens	B-cell growth factor	122	55
11243	Y01158	Homo sapiens	Secreted protein encoded by gene 18	130	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			clone HCACJ81.		
11244	U92698	Rattus norvegicus	ribosomal protein S2	229	74
11245	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	116	41
11246	W75859	Homo sapiens	Human secretory protein of clone DM340-1.	123	37
11247	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	132	73
11248	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	93	56
11249	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	132	56
11250	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	128	72
11251	S79410	Mus musculus	nuclear localization signal binding protein	115	46
11252	AK021455	Homo sapiens	unnamed protein product	146	81
11253	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	88.	56
11254	S80916	Homo sapiens	parotid "o" protein, Po=salivary proline-rich protein {exon 3}	113	43
11255	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	136	45
11256	G02382	Homo sapiens	Human secreted protein, SEQ ID NO: 6463.	107	67
11257	AF194537	Homo sapiens	NAG13	153	76
11258	M15530	Homo sapiens	B-cell growth factor	130	70
11259	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	131	72
11260	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	104	59
11261	G02922	Homo sapiens	Human secreted protein, SEQ ID NO: 7003.	316	92
11262	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	111	81
11263	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	142	71
11264	AF130089	Homo sapiens	PRO2550	111	66
11265	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	118	71
11266	M15530	Homo sapiens	B-cell growth factor	158	76
11267	AF130079	Homo sapiens	PRO2852	124	68
11268	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	104	50
11269	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	125	57
11270	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	107	63
11271	AF118082	Homo sapiens	PRO1902	87	47
11272	M10546	Homo sapiens	cytochrome oxidase I	305	74
11273	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	108	53
11274	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	235	81
11275	U93570	Homo sapiens	putative p150	182	54
11276	X03145	Homo sapiens	pot. ORF V	144	60
11277	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	103	57
11278	AL035681	Homo sapiens	dJ756G23.1 (novel Leucine Rich	269	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			Protein)		
11279	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	103	61
11280	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	115	70
11281	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	87	71
11282	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	162	81
11283	AF116715	Homo sapiens	PRO2829	141	71
11284	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	111	76
11285	U52077	Homo sapiens	mariner transposase	198	78
11286	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	120	62
11287	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	103	45
11288	W50193	Homo sapiens	Amino acid sequence of salivary protein CON-2.	63	60
11289	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	123	72
11290	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	120	70
11291	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	106	46
11292	AF116715	Homo sapiens	PRO2829	130	63
11293	AF090930	Homo sapiens	PRO0478	134	60
11294	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	119	65
11295	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	102	50
11296	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	141	49
11297	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	154	72
11298	B08918	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:75.	126	54
11299	AK025270	Homo sapiens	unnamed protein product	150	54
11300	AF118078	Homo sapiens	PRO1848	121	63
11301	AF090942	Homo sapiens	PRO0657	81	43
11302	AF116715	Homo sapiens	PRO2829	131	60
11303	AF090931	Homo sapiens	PRO0483	121	71
11304	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	108	82
11305	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	122	59
11306	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	93	89
11307	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	108	65
11308	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	114	51
11309	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	67	55
11310	J02963	Homo sapiens	platelet glycoprotein IIb precursor	105	71
11311	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	104	73
11312	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	88	73

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11313	U40265	Trypanosoma cruzi	ATPase subunit 6	94	31
11314	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	157	53
11315	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	113	54
11316	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	165	90
11317	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	149	74
11318	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	144	55
11319	AF161356	Homo sapiens	HSPC093	112	56
11320	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	102	53
11321	AF116661	Homo sapiens	PRO1438	131	74
11322	AK000496	Homo sapiens	unnamed protein product	137	59
11323	G03703	Homo sapiens	Human secreted protein, SEQ ID NO: 7784.	74	57
11324	U63542	Homo sapiens	FAP protein	151	79
11325	M15530	Homo sapiens	B-cell growth factor	192	45
11326	AF116715	Homo sapiens	PRO2829	164	78
11327	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	127	62
11328	AF090895	Homo sapiens	PRO0117	116	69
11329	AF090942	Homo sapiens	PRO0657	132	62
11330	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	190	72
11331	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	112	49
11332	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	119	38
11333	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	131	52
11334	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	145	53
11335	X92485	Plasmodium vivax	pval	105	38
11336	M15530	Homo sapiens	B-cell growth factor	148	73
11337	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	126	100
11338	AF118086	Homo sapiens	PRO1992	123	80
11339	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	79	66
11340	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	162	73
11341	AF130079	Homo sapiens	PRO2852	145	80
11342	M19419	Mus musculus	proline-rich salivary protein	104	44
11343	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	123	62
11344	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	120	91
11345	U94832	Homo sapiens	KSRP	122	51
11346	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	139	56
11347	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	188	87
11348	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	173	59
11349	W48351	Homo sapiens	Human breast cancer related protein	111	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			BCRB2.		
11350	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	149	62
11351	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	267	68
11352	AF161356	Homo sapiens	HSPC093	134	51
11353	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	139	47
11354	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	115	64
11355	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	126	67
11356	G02507	Homo sapiens	Human secreted protein, SEQ ID NO: 6588.	123	59
11357	AF130089	Homo sapiens	PRO2550	114	62
11358	AK000496	Homo sapiens	unnamed protein product	126	41
11359	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	173	81
11360	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	128	64
11361	AF130056	Homo sapiens	PRO1367	74	57
11362	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	116	63
11363	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	104	91
11364	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	137	53
11365	Z30643	Homo sapiens	chloride channel (putative)	409	98
11366	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	107	68
11367	AF068294	Homo sapiens	HDCMB45P	281	57
11368	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	110	71
11369	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	136	89
11370	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	129	79
11371	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	137	57
11372	U18339	Variola virus	D4L	95	61
11373	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	100	52
11374	M15530	Homo sapiens	B-cell growth factor	135	61
11375	X92485	Plasmodium vivax	pval	111	50
11376	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	177	71
11377	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	111	68
11378	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	96	53
11379	G02567	Homo sapiens	Human secreted protein, SEQ ID NO: 6648.	83	54
11380	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	85
11381	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	156	64
11382	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	121	79
11383	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	104	41

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11384	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	86	53
11385	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	40
11386	AF068294	Homo sapiens	HDCMB45P	158	48
11387	B08976	Homo sapiens	Human secreted protein sequence encoded by gene 28 SEQ ID NO:133.	136	46
11388	AF090931	Homo sapiens	PRO0483	123	74
11389	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	156	75
11390	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	102	48
11391	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	117	54
11392	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	134	43
11393	S79410	Mus musculus	nuclear localization signal binding protein	111	46
11394	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	128	49
11395	AF090930	Homo sapiens	PRO0478	148	70
11396	AF210651	Homo sapiens	NAG18	100	62
11397	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	121	56
11398	AF063243	Bos taurus	ribosomal protein L30	165	77
11399	AF162149	Mycoplasma bovis	variable surface lipoprotein	104	37
11400	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	175	71
11401	D38112	Homo sapiens	NADH dehydrogenase subunit 4	341	92
11402	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	137	90
11403	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	115	70
11404	M10126	Leishmania tarentolae	NH2 terminus uncertain	101	41
11405	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	126	69
11406	X82385	Homo sapiens	RNA polymerase II subunit	296	100
11407	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	68
11408	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	141	44
11409	J02963	Homo sapiens	platelet glycoprotein IIb precursor	118	77
11410	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	169	77
11411	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	169	82
11412	AK025116	Homo sapiens	unnamed protein product	133	44
11413	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	113	63
11414	AK024455	Homo sapiens	FLJ00047 protein	127	65
11415	AK024455	Homo sapiens	FLJ00047 protein	87	63
11416	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	94	57
11417	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	123	58
11418	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	148	69

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11419	S79410	Mus musculus	nuclear localization signal binding protein	113	53
11420	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	166	68
11421	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	124	51
11422	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	113	70
11423	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	88	62
11424	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	136	72
11425	AK002154	Homo sapiens	unnamed protein product	292	75
11426	Y02887	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	98	75
11427	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	143	64
11428	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	131	81
11429	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	130	81
11430	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	172	61
11431	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	112	74
11432	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	128	52
11433	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	128	58
11434	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	147	63
11435	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	139	83
11436	X63220	Bos taurus	NADH dehydrogenase	154	57
11437	AF090895	Homo sapiens	PRO0117	122	59
11438	J04655	Ascaris suum	collagen	90	46
11439	AF090942	Homo sapiens	PRO0657	166	52
11440	AK024455	Homo sapiens	FLJ00047 protein	100	55
11441	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	116	49
11442	M15530	Homo sapiens	B-cell growth factor	105	75
11443	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	133	64
11444	Y19730	Homo sapiens	SEQ ID NO 448 from WO9922243.	115	67
11445	AF090895	Homo sapiens	PRO0117	79	61
11446	AF118086	Homo sapiens	PRO1992	109	63
11447	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	160	80
11448	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	97	75
11450	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	136	72
11451	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	89	55
11452	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	144	71
11453	AF090931	Homo sapiens	PRO0483	140	78
11454	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	129	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11455	G00383	Homo sapiens	Human secreted protein, SEQ ID NO: 4464.	104	63
11456	AF118086	Homo sapiens	PRO1992	151	71
11457	U73168	Homo sapiens	partial CDS, human putative tumor suppressor (U23946)	121	95
11458	S79410	Mus musculus	nuclear localization signal binding protein	96	73
11459	AK000496	Homo sapiens	unnamed protein product	233	63
11460	AK024455	Homo sapiens	FLJ00047 protein	90	73
11461	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	132	64
11462	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	103	86
11463	K03207	Homo sapiens	salivary proline-rich protein precursor	135	36
11464	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	127	88
11465	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	104	77
11466	AF115549	Homo sapiens	Wiskott-Aldrich Syndrome protein	141	48
11467	AF090942	Homo sapiens	PRO0657	89	58
11468	AC005698	Arabidopsis thaliana	T3P18.6	128	47
11469	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	101	48
11470	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	136	81
11471	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	91	45
11472	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	102	77
11473	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	145	55
11474	AF210651	Homo sapiens	NAG18	117	57
11475	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	117	62
11476	AF116715	Homo sapiens	PRO2829	124	77
11477	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	136	45
11478	G02828	Homo sapiens	Human secreted protein, SEQ ID NO: 6909.	85	78
11479	X91940	Homo sapiens	WNT-8B protein	204	97
11480	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	131	71
11481	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	117	63
11482	X92485	Plasmodium vivax	pval	98	52
11483	AF217518	Homo sapiens	uncharacterized bone marrow protein BM042	895	100
11484	U79260	Homo sapiens	unknown	104	80
11485	L27428	Homo sapiens	reverse transcriptase	169	52
11486	M15530	Homo sapiens	B-cell growth factor	122	67
11487	U49974	Homo sapiens	mariner transposase	156	62
11488	AF090942	Homo sapiens	PRO0657	110	44
11489	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	156	65
11490	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	115	52
11491	G03133	Homo sapiens	Human secreted protein, SEQ ID NO:	95	51

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7214.		
11492	AF090930	Homo sapiens	PRO0478	145	58
11493	X63726	Phoca vitulina	cytochrome c oxidase subunit I	556	87
11494	AL021897	Mycobacterium tuberculosis	pra	119	56
11495	X98485	Plasmodium vivax	putative	92	35
11496	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	156	73
11497	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	129	72
11498	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	115	66
11499	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	58
11500	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	113	36
11501	AE003568	Drosophila melanogaster	CG12566 gene product	105	32
11502	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	141	78
11503	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	102	51
11504	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	138	60
11505	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	109	85
11506	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	101	59
11507	M81321	Macaca fascicularis	proline-rich protein	128	48
11508	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	110	78
11509	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	98	60
11510	X07882	Homo sapiens	Po protein	118	41
11511	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	133	79
11512	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	112	68
11513	AF000381	Homo sapiens	non-functional folate binding protein	203	93
11514	X92485	Plasmodium vivax	pval	115	44
11515	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	109	51
11516	G00344	Homo sapiens	Human secreted protein, SEQ ID NO: 4425.	141	78
11517	AF090894	Homo sapiens	PRO0113	108	58
11518	M15530	Homo sapiens	B-cell growth factor	93	72
11519	G03084	Homo sapiens	Human secreted protein, SEQ ID NO: 7165.	66	73
11520	AF117065	Homo sapiens	male-specific lethal-3 homolog 1	200	61
11521	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	335	87
11522	M15530	Homo sapiens	B-cell growth factor	104	74
11523	AF116715	Homo sapiens	PRO2829	122	64
11524	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	145	68
11525	Y02671	Homo sapiens	Human secreted protein encoded by	103	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gene 22 clone HMSJW18.		
11526	X92485	Plasmodium vivax	pval	111	42
11527	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	101	80
11528	Y86472	Homo sapiens	Human gene 52-encoded protein fragment, SEQ ID NO:387.	134	58
11529	AF090931	Homo sapiens	PRO0483	163	76
11530	AF119900	Homo sapiens	PRO2822	139	44
11531	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	126	73
11532	U41038	Caenorhabditis elegans	Similar to cadherin-type repeat	126	50
11533	S79410	Mus musculus	nuclear localization signal binding protein	107	46
11534	AF090930	Homo sapiens	PRO0478	120	81
11535	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	105	64
11536	X92485	Plasmodium vivax	pval	123	56
11537	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	122	72
11538	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	108	64
11539	AE003834	Drosophila melanogaster	CG8054 gene product	456	84
11540	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	135	53
11541	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	99	70
11542	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	77	63
11543	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	123	73
11544	G03052	Homo sapiens	Human secreted protein, SEQ ID NO: 7133.	78	58
11545	U79260	Homo sapiens	unknown	128	43
11546	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	122	56
11547	X92485	Plasmodium vivax	pval	116	46
11548	S79410	Mus musculus	nuclear localization signal binding protein	111	55
11549	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	95	75
11550	U67056	Acanthamoeba castellanii	myosin I heavy chain kinase	111	44
11551	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	159	60
11552	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	127	50
11553	Z34975	Homo sapiens	IdiCp	470	86
11554	AF210651	Homo sapiens	NAG18	101	65
11555	X78677	Homo sapiens	ketoheokinase	241	92
11556	G04039	Homo sapiens	Human secreted protein, SEQ ID NO: 8120.	254	72
11557	AB032976	Homo sapiens	KIAA1150 protein	565	75
11558	U93572	Homo sapiens	p40	127	37

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11559	U27488	Pseudorabies virus	glycoprotein gX	88	38
11560	R80095	Homo sapiens	Human superoxide-dismutase-4 polypeptide.	113	63
11561	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	83	65
11562	AF130089	Homo sapiens	PRO2550	111	33
11563	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	146	60
11564	AF090895	Homo sapiens	PRO0117	172	77
11566	V01512	Homo sapiens	c-fos	416	82
11567	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	72	33
11568	X16074	Mus sp.	L-34 protein (AA 1-264)	117	35
11569	Y45381	Homo sapiens	Human secreted protein fragment encoded from gene 28.	131	77
11570	AK025395	Homo sapiens	unnamed protein product	683	98
11571	D78255	Mus musculus	PAP-1	134	80
11572	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	110	70
11573	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	131	78
11574	J01415	Homo sapiens	cytochrome oxidase subunit 3	141	59
11575	S79410	Mus musculus	nuclear localization signal binding protein	102	58
11576	AC007842	Homo sapiens	BC331191_1	409	86
11577	Z22636	Sinorhizobium meliloti	Thi	103	36
11578	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	83	36
11579	G03703	Homo sapiens	Human secreted protein, SEQ ID NO: 7784.	115	60
11580	AF162149	Mycoplasma bovis	variable surface lipoprotein	167	44
11581	AF130079	Homo sapiens	PRO2852	117	77
11582	AF229067	Homo sapiens	PADI-H protein	136	75
11583	R10755	Homo sapiens	Non-A non-B hepatitis specific antigenic protein encoded by phageclone lambda HC2533.	132	72
11584	Z70292	Homo sapiens	chemokine CC-1	386	93
11585	R10755	Homo sapiens	Non-A non-B hepatitis specific antigenic protein encoded by phageclone lambda HC2533.	107	67
11586	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	134	75
11587	X05006	Homo sapiens	S-protein	237	100
11588	Y21850	Homo sapiens	Human signal peptide-containing protein (SIGP) (clone ID 1880830).	365	77
11589	U43959	Homo sapiens	beta 4 adducin	114	54
11590	AF030162	Homo sapiens	inner mitochondrial membrane translocase Tim23	104	95
11591	X03557	Homo sapiens	56-KDa protein (aa 1-478)	491	74
11592	AF151074	Homo sapiens	HSPC240	151	73
11593	AF116719	Homo sapiens	PRO2987	558	89
11594	AF090942	Homo sapiens	PRO0657	120	41
11595	X55039	Homo sapiens	centromere autoantigen B (CENP-B)	160	32
11596	X98475	Mus musculus	vasodilator-stimulated phosphoprotein	101	43
11597	G00589	Homo sapiens	Human secreted protein, SEQ ID NO: 4670.	140	73

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11598	U07151	Homo sapiens	ARL3	113	35
11599	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	123	79
11600	AL050084	Homo sapiens	hypothetical protein	119	100
11601	AF090931	Homo sapiens	PRO0483	124	73
11602	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	132	60
11603	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	156	82
11604	AF224494	Mus musculus	arsenite inducible RNA associated protein	473	79
11605	M60047	Homo sapiens	heparin binding protein	597	95
11606	G00933	Homo sapiens	Human secreted protein, SEQ ID NO: 5014.	721	97
11607	W12091	Homo sapiens	C57S derivative of antigen non-specific human GIF.	573	98
11608	AF229439	Mus musculus	zinc finger protein 289	535	80
11609	M86637	Brugia pahangi	unknown	104	38
11610	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	93	70
11611	G02224	Homo sapiens	Human secreted protein, SEQ ID NO: 6305.	508	94
11612	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	108	51
11613	AK024372	Homo sapiens	unnamed protein product	105	77
11614	Y94918	Homo sapiens	Human secreted protein clone dd504_18 protein sequence SEQ ID NO:42.	310	62
11615	Y48547	Homo sapiens	Human breast tumour-associated protein 8.	641	96
11616	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	108	81
11617	L34081	Homo sapiens	bile acid CoA: Amino acid N-acyltransferase	356	82
11618	G01399	Homo sapiens	Human secreted protein, SEQ ID NO: 5480.	570	98
11619	AF020038	Homo sapiens	NADP-dependent isocitrate dehydrogenase	272	83
11620	AB051901	Homo sapiens	VDUP1	247	98
11621	Y48547	Homo sapiens	Human breast tumour-associated protein 8.	691	92
11622	U22961	Homo sapiens	similar to human albumin, Swiss-Prot Accession Number P02768; Method: conceptual translation supplied by author	382	71
11623	A06977	Homo sapiens	albumin	562	92
11624	X73460	Homo sapiens	ribosomal protein L3	502	84
11625	AL035398	Homo sapiens	dJ796117.1 (PUTATIVE novel protein)	373	98
11626	D50310	Homo sapiens	cyclin I	175	100
11627	AE000950	Archaeoglobus fulgidus	thermosome, subunit alpha (thsA)	131	25
11628	D88315	Mus musculus	tetracycline transporter-like protein	137	81
11629	Y36204	Homo sapiens	Human secreted protein #76.	406	100
11630	AF130089	Homo sapiens	PRO2550	110	63
11631	J02982	Homo sapiens	glycophorin B precursor	95	100
11632	AF116719	Homo sapiens	PRO2987	558	93
11633	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	137	92
11634	U09823	Oryctolagus	elongation factor 1 alpha	483	85

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		cuniculus			
11635	G01922	Homo sapiens	Human secreted protein, SEQ ID NO: 6003.	157	73
11636	AF116719	Homo sapiens	PRO2987	491	90
11637	D14421	Rattus norvegicus	b isotype of B regulatory subunit of protein phosphatase 2A	208	86
11638	AF116719	Homo sapiens	PRO2987	544	93
11639	AF130079	Homo sapiens	PRO2852	127	81
11640	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	150	59
11641	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	100	66
11642	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	119	71
11643	Y86574	Homo sapiens	Human gene 91-encoded protein fragment, SEQ ID NO:491.	64	100
11644	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	82	70
11645	G02360	Homo sapiens	Human secreted protein, SEQ ID NO: 6441.	109	74
11646	AF130089	Homo sapiens	PRO2550	128	52
11647	AK024455	Homo sapiens	FLJ00047 protein	138	61
11648	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	73	84
11649	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	128	60
11650	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	83	78
11651	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	105	64
11652	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	103	62
11653	AF130089	Homo sapiens	PRO2550	116	69
11654	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	176	54
11655	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	129	63
11656	AF130089	Homo sapiens	PRO2550	135	77
11657	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	146	93
11658	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	123	61
11659	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	117	47
11660	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	92	84
11661	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	70	75
11662	U00029	Saccharomyces cerevisiae	Yhr217cp	101	50
11663	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	107	88
11664	G03062	Homo sapiens	Human secreted protein, SEQ ID NO: 7143.	110	90
11665	U63542	Homo sapiens	FAP protein	119	69
11666	AF130114	Homo sapiens	PRO2459	78	38
11667	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	106	64
11668	G00397	Homo sapiens	Human secreted protein, SEQ ID NO:	137	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4478.		
11669	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	77	63
11670	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	116	68
11671	AK021618	Homo sapiens	unnamed protein product	97	43
11672	G02482	Homo sapiens	Human secreted protein, SEQ ID NO: 6563.	108	55
11673	S75997	Rattus sp.	nucleoporin p62 homolog	95	40
11674	AF229163	Homo sapiens	natural resistance-associated macrophage protein 1	104	54
11675	M15530	Homo sapiens	B-cell growth factor	89	81
11676	M92357	Homo sapiens	B94 protein	143	100
11677	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	132	74
11678	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	126	64
11679	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	166	66
11680	U16359	Rattus norvegicus	nitric oxide synthase	108	85
11681	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	145	92
11682	M15530	Homo sapiens	B-cell growth factor	127	64
11683	AF090931	Homo sapiens	PRO0483	152	60
11684	AF130087	Homo sapiens	PRO2411	150	68
11685	U18339	Variola virus	D4L	94	70
11686	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	104	80
11687	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	134	68
11688	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	131	70
11689	AF090944	Homo sapiens	PRO0663	129	73
11690	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	111	67
11691	U79260	Homo sapiens	unknown	98	44
11692	W78226	Homo sapiens	Fragment of human secreted protein encoded by gene 1.	361	64
11693	G00962	Homo sapiens	Human secreted protein, SEQ ID NO: 5043.	269	100
11694	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	132	83
11695	Y94526	Homo sapiens	Human lysine-rich statherin protein.	136	82
11696	AF116637	Homo sapiens	PRO1489	232	95
11697	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	108	50
11698	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	120	81
11699	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	150	80
11700	AK024455	Homo sapiens	FLJ00047 protein	148	68
11701	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	131	72
11702	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	105	45
11703	AC005545	Homo sapiens	delta-adaptin, partial CDS	127	38
11704	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	143	81

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11705	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	67
11706	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	153	67
11707	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	129	88
11708	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	89	69
11709	AB047600	Macaca fascicularis	hypothetical protein	95	63
11710	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	100	76
11711	J02963	Homo sapiens	platelet glycoprotein IIb precursor	112	80
11712	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	117	58
11713	AF008196	Homo sapiens	bax epsilon	140	71
11714	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	113	56
11715	G00397	Homo sapiens	Human secreted protein; SEQ ID NO: 4478.	125	67
11716	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	121	74
11717	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	125	51
11718	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	96	81
11719	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	106	85
11720	AJ243883	Periplaneta americana	putative transcription factor	118	57
11721	AF220264	Homo sapiens	MOST-1	121	74
11722	AF130051	Homo sapiens	PRO0898	169	72
11723	K02401	Homo sapiens	chorionic somatomammotropin	507	95
11724	K02401	Homo sapiens	chorionic somatomammotropin	461	85
11725	U93564	Homo sapiens	p40	340	90
11726	AF130089	Homo sapiens	PRO2550	107	73
11727	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	128	79
11728	J02963	Homo sapiens	platelet glycoprotein IIb precursor	109	90
11729	Y51824	Homo sapiens	Human OSBH protein.	182	89
11730	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	107	80
11731	K02401	Homo sapiens	chorionic somatomammotropin	459	94
11732	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	93	42
11733	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	111	67
11734	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	103	43
11735	S79410	Mus musculus	nuclear localization signal binding protein	98	75
11736	AF090931	Homo sapiens	PRO0483	123	88
11737	K02401	Homo sapiens	chorionic somatomammotropin	340	92
11738	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	73
11739	G02624	Homo sapiens	Human secreted protein, SEQ ID NO: 6705.	131	57
11740	X55695	Lycopersicon esculentum	glycine-rich protein	164	48
11741	AK024455	Homo sapiens	FLJ00047 protein	89	77

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11742	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:125.	415	90
11743	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	105	94
11744	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	116	87
11745	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	131	69
11746	W13831	Homo sapiens	Human cyclin E delta 9 mutant.	140	52
11747	AB001431	Mus musculus	motor domain of KIF14	179	84
11748	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	141	72
11749	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	99	63
11750	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	88	64
11751	AF090931	Homo sapiens	PRO0483	118	68
11752	AF150105	Homo sapiens	small zinc finger-like protein	194	68
11753	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	127	69
11754	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	100	80
11755	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	109	65
11756	K02401	Homo sapiens	chorionic somatomammotropin	427	87
11757	U52077	Homo sapiens	mariner transposase	113	82
11758	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	133	54
11759	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	111	80
11760	AF090944	Homo sapiens	PRO0663	143	76
11761	D38112	Homo sapiens	NADH dehydrogenase subunit 6	529	99
11762	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	171	58
11763	AF132200	Homo sapiens	PRO1751	127	66
11764	AK025116	Homo sapiens	unnamed protein product	141	80
11765	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	75	62
11766	AF090930	Homo sapiens	PRO0478	106	59
11767	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	127	80
11768	AF090931	Homo sapiens	PRO0483	164	60
11769	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	102	81
11770	AF161356	Homo sapiens	HSPC093	131	68
11771	AF130089	Homo sapiens	PRO2550	160	82
11772	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	140	79
11773	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	136	71
11774	AF090942	Homo sapiens	PRO0657	153	78
11775	AJ223410	Homo sapiens	EBI1-ligand chemokine	108	52
11776	K02401	Homo sapiens	chorionic somatomammotropin	395	91
11777	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	107	70
11778	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	99	62
11779	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	84	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11780	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	116	68
11781	AF194537	Homo sapiens	NAG13	201	65
11782	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	139	68
11783	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	149	59
11784	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	112	78
11785	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	99	68
11786	AF130089	Homo sapiens	PRO2550	108	83
11787	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	124	88
11788	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	103	100
11789	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	146	60
11790	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	165	73
11791	AL035494	Homo sapiens	dJ635G19.2.3 (novel protein (PUTATIVE PARTIAL isoform 3))	106	56
11792	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	100	66
11793	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	125	61
11794	A20770	synthetic construct	(Asp1-Thr161)-EPI	95	76
11795	S74221	Homo sapiens	IK factor—cytokine down-regulating HLA class II	108	61
11796	K01664	Drosophila melanogaster	Bkm-like protein	96	77
11797	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	111	65
11798	Y75995	Homo sapiens	Human skin cell protein, SEQ ID NO:173.	324	87
11799	J03071	Homo sapiens	chorionic somatomammotropin CS-5	120	75
11800	L00693	Homo sapiens	carcinoembryonic antigen	96	85
11801	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	80	44
11802	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	125	64
11803	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	142	82
11804	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	107	85
11805	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	152	80
11806	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	122	61
11807	U91985	Homo sapiens	DNA fragmentation factor-45	585	92
11808	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	125	60
11809	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	170	89
11810	Y87156	Homo sapiens	Human secreted protein sequence SEQ ID NO:195.	191	76
11811	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	120	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11812	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	156	55
11813	P92219	Homo sapiens (human)	CR1 protein.	121	84
11814	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	107	75
11815	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	74	78
11816	M15530	Homo sapiens	B-cell growth factor	148	68
11817	AF090942	Homo sapiens	PRO0657	139	60
11818	W90847	Homo sapiens	Human lymphocyte targeted peptide #15.	117	100
11819	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	133	73
11820	Z72853	Saccharomyces cerevisiae	ORF YGR069w	94	42
11821	G03710	Homo sapiens	Human secreted protein, SEQ ID NO: 7791.	176	65
11822	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	60
11823	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	104	68
11824	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	99	51
11825	W90172	Homo sapiens	Human heart muscle specific protein.	256	34
11826	AB017007	Homo sapiens	PMS2L16	248	89
11827	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	127	86
11828	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	135	71
11829	AF119851	Homo sapiens	PRO1722	129	60
11830	AF132200	Homo sapiens	PRO1751	120	77
11831	Y08061	Homo sapiens	Human c-myc protein fragment.	133	83
11832	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	128	64
11833	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	152	100
11834	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	156	73
11835	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	88
11836	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	95
11837	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:125.	411	91
11838	AK000496	Homo sapiens	unnamed protein product	113	78
11839	AF119855	Homo sapiens	PRO1847	84	68
11840	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	128	88
11841	S79410	Mus musculus	nuclear localization signal binding protein	113	69
11842	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	151	55
11843	AF090942	Homo sapiens	PRO0657	139	65
11844	AF220264	Homo sapiens	MOST-1	88	69
11845	AF184612	Drosophila melanogaster	split ends	95	47
11846	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	136	82

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11847	AB017007	Homo sapiens	PMS2L16	310	100
11848	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	100	79
11849	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	111	61
11850	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	110	72
11851	AF090931	Homo sapiens	PRO0483	164	80
11852	AF116661	Homo sapiens	PRO1438	124	67
11853	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	119	72
11854	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	135	59
11855	U63332	Homo sapiens	super cysteine rich protein; SCRP	100	84
11856	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	120	54
11857	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	135	68
11858	AK024455	Homo sapiens	FLJ00047 protein	123	69
11859	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	94	66
11860	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	94	66
11861	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	108	75
11862	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	108	86
11863	AF130050	Homo sapiens	PRO0872	81	58
11864	AF119900	Homo sapiens	PRO2822	152	90
11865	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	78	45
11866	J03071	Homo sapiens	chorionic somatomammotropin CS-2	526	93
11867	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	80
11868	G00591	Homo sapiens	Human secreted protein, SEQ ID NO: 4672.	119	58
11869	Y10830	Homo sapiens	Amino acid sequence of a human secreted protein.	246	100
11870	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	101	59
11871	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	120	59
11872	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	129	84
11873	D28113	Homo sapiens	MOBP	458	80
11874	D28114	Homo sapiens	MOBP	306	68
11875	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	101	85
11876	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	110	64
11877	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	189	57
11878	M15530	Homo sapiens	B-cell growth factor	98	62
11879	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	130	100
11880	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	99	70
11881	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	101	53

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11882	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	219	75
11883	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	131	61
11884	U93563	Homo sapiens	putative p150	139	75
11885	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene preproduct.	154	52
11886	AF090944	Homo sapiens	PRO0663	149	80
11887	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	107	94
11888	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	138	62
11889	L26953	Homo sapiens	chromosomal protein	123	75
11890	U16359	Rattus norvegicus	nitric oxide synthase	105	69
11891	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	129	83
11892	R10755	Homo sapiens	Non-A non-B hepatitis specific antigenic protein encoded by phageclone lambda HC2533.	126	78
11893	G00481	Homo sapiens	Human secreted protein, SEQ ID NO: 4562.	82	70
11894	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	149	90
11895	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	118	75
11896	G02451	Homo sapiens	Human secreted protein, SEQ ID NO: 6532.	167	86
11897	D38112	Homo sapiens	NADH dehydrogenase subunit 6	136	77
11898	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	126	58
11899	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	158	78
11900	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	137	71
11901	G00613	Homo sapiens	Human secreted protein, SEQ ID NO: 4694.	85	62
11902	G02558	Homo sapiens	Human secreted protein, SEQ ID NO: 6639.	242	73
11903	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	127	59
11904	G03472	Homo sapiens	Human secreted protein, SEQ ID NO: 7553.	182	85
11905	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	135	75
11906	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	128	79
11907	U93574	Homo sapiens	putative p150	169	64
11908	AF090944	Homo sapiens	PRO0663	128	75
11909	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	100	84
11910	AF090930	Homo sapiens	PRO0478	159	76
11911	J03071	Homo sapiens	chorionic somatomammotropin CS-2	496	88
11912	J03071	Homo sapiens	chorionic somatomammotropin CS-2	551	92
11913	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	168	76
11914	K02401	Homo sapiens	chorionic somatomammotropin	450	85
11915	K02401	Homo sapiens	chorionic somatomammotropin	478	87
11916	K02401	Homo sapiens	chorionic somatomammotropin	454	82

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11917	G02382	Homo sapiens	Human secreted protein, SEQ ID NO: 6463.	121	73
11918	X65121	Mus musculus	alpha1 (X) collagen	112	35
11919	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	115	62
11920	AK024455	Homo sapiens	FLJ00047 protein	102	76
11921	AF150087	Homo sapiens	small zinc finger-like protein	181	52
11922	U55376	Caenorhabditis elegans	F16H11.2 gene product	122	78
11923	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	256	80
11924	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	127	74
11925	AF090944	Homo sapiens	PRO0663	144	75
11926	AJ223475	Escherichia coli	InsA protein	477	100
11927	M15386	Homo sapiens	gamma-globin	616	92
11928	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	105	72
11929	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	122	92
11930	AF090895	Homo sapiens	PRO0117	80	71
11931	AF130089	Homo sapiens	PRO2550	129	68
11932	AK025116	Homo sapiens	unnamed protein product	113	53
11933	Y91452	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:125.	114	70
11934	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	69	76
11935	AF116695	Homo sapiens	PRO2221	336	70
11936	AF090931	Homo sapiens	PRO0483	133	77
11937	AF130089	Homo sapiens	PRO2550	135	72
11938	L06237	Homo sapiens	microtubule-associated protein 1B	143	36
11939	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	124	72
11940	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	158	76
11941	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	130	53
11942	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	111	65
11943	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	106	59
11944	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	65
11945	D28113	Homo sapiens	MOBP	186	62
11946	D38112	Homo sapiens	NADH dehydrogenase subunit 1	353	76
11947	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	113	72
11948	D38112	Homo sapiens	NADH dehydrogenase subunit 6	139	87
11949	AJ006591	Homo sapiens	cysteine-rich protein	148	76
11950	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	113	88
11951	AF116695	Homo sapiens	PRO2221	205	57
11952	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	158	75
11953	AF113685	Homo sapiens	PRO0974	107	72
11954	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	107	80
11955	AK026107	Homo sapiens	unnamed protein product	129	84
11956	AF109907	Homo sapiens	S164	140	96

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11957	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	99	100
11958	K02576	Homo sapiens	salivary proline-rich protein 1	124	41
11959	K02401	Homo sapiens	chorionic somatomammotropin	497	90
11960	G00368	Homo sapiens	Human secreted protein, SEQ ID NO: 4449.	155	69
11961	J02963	Homo sapiens	platelet glycoprotein IIb precursor	126	85
11962	M15530	Homo sapiens	B-cell growth factor	114	86
11963	K02401	Homo sapiens	chorionic somatomammotropin	472	87
11964	AK024455	Homo sapiens	FLJ00047 protein	95	61
11965	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	145	78
11966	L27428	Homo sapiens	reverse transcriptase	144	50
11967	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	187	76
11968	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	124	81
11969	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	112	64
11970	AK024455	Homo sapiens	FLJ00047 protein	120	70
11971	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	105	61
11972	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	106	70
11973	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	70	75
11974	G00491	Homo sapiens	Human secreted protein, SEQ ID NO: 4572.	86	60
11975	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	161	72
11976	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	105	42
11977	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	121	58
11978	AK024372	Homo sapiens	unnamed protein product	104	80
11979	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	137	77
11980	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	96	90
11981	S79410	Mus musculus	nuclear localization signal binding protein	100	56
11982	R59842	Homo sapiens	ApoE4L1 protease.	129	62
11983	K01664	Drosophila melanogaster	Bkn-like protein	132	53
11984	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	105	90
11985	M15530	Homo sapiens	B-cell growth factor	117	43
11986	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	99	65
11987	R59843	Homo sapiens	ApoE4Lx2 protease.	117	84
11988	L26953	Homo sapiens	chromosomal protein	124	79
11989	U93564	Homo sapiens	p40	523	88
11990	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	82
11991	AF090894	Homo sapiens	PRO0113	126	56
11992	G00361	Homo sapiens	Human secreted protein, SEQ ID NO: 4442.	129	63
11993	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	144	67
11994	U71363	Homo sapiens	zinc finger protein zfp6	213	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
11995	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	82	65
11996	AF130089	Homo sapiens	PRO2550	145	68
11997	R95913	Homo sapiens	Neural thread protein.	114	88
11998	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	122	56
11999	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	147	81
12000	AF090931	Homo sapiens	PRO0483	152	81
12001	AF090931	Homo sapiens	PRO0483	145	81
12002	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	124	64
12003	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	103	78
12004	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	133	51
12005	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	108	63
12006	L19527	Homo sapiens	ribosomal protein L27	547	93
12007	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	127	82
12008	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	127	82
12009	M55409	Homo sapiens	pancreatic tumor-related protein	257	98
12010	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	127	64
12011	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	291	89
12012	X03717	Homo sapiens	pot. unidentified reading frame	126	43
12013	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	131	80
12014	AB011148	Homo sapiens	KIAA0576 protein	135	84
12015	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	114	87
12016	AK024455	Homo sapiens	FLJ00047 protein	102	70
12017	L27428	Homo sapiens	reverse transcriptase	144	87
12018	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	135	87
12019	D38112	Homo sapiens	NADH dehydrogenase subunit 1	137	93
12020	AK001363	Homo sapiens	unnamed protein product	490	100
12021	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	111	79
12022	W00838	Homo sapiens	Tumour necrosis factor-related gene product.	106	87
12023	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	157	58
12024	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	87	66
12025	R95913	Homo sapiens	Neural thread protein.	157	45
12026	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	138	52
12027	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	116	60
12028	V00488	Homo sapiens	alpha globin	191	100
12029	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	102	87
12030	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	114	79
12031	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	142	86
12032	X01703	Homo sapiens	alpha-tubulin	534	93
12033	U09823	Oryctolagus cuniculus	elongation factor 1 alpha	557	90

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12034	X01703	Homo sapiens	alpha-tubulin	619	94
12035	AF255556	Notothenia coriiceps	alpha tubulin	430	85
12036	X53618	Paracentrotus lividus	alpha-tubulin (AA 1-452)	437	87
12037	M62810	Homo sapiens	mitochondrial transcription factor 1	433	95
12038	Y36156	Homo sapiens	Human secreted protein #28.	157	75
12039	X01703	Homo sapiens	alpha-tubulin	604	97
12040	X01703	Homo sapiens	alpha-tubulin	517	90
12041	S70154	Homo sapiens	cytosolic acetoacetyl-coenzyme A thiolase, CT {EC 2.3.1.9}	533	94
12042	X01703	Homo sapiens	alpha-tubulin	472	85
12043	M23613	Homo sapiens	nucleophosmin	428	80
12044	AL031174	Schizosaccharomyces pombe	hypothetical protein	102	52
12045	Y94653	Homo sapiens	Human netrin-like protein (NEL) amino acid sequence.	152	82
12046	AF016507	Homo sapiens	C-terminal binding protein 2	172	100
12047	X05196	Homo sapiens	aldolase C	454	93
12048	X03796	Mus musculus	aldolase C (aa 1-227)	351	74
12049	X05196	Homo sapiens	aldolase C	408	88
12050	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	147	70
12051	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	169	55
12052	AF090944	Homo sapiens	PRO0663	119	59
12053	V01577	Homo sapiens	variable region	223	93
12054	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	144	74
12055	AF090931	Homo sapiens	PRO0483	121	74
12056	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	105	76
12057	U18339	Variola virus	D4L	100	52
12058	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	135	62
12059	AB001684	Chlorella vulgaris	ORF41c	81	75
12060	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	128	74
12061	AK024455	Homo sapiens	FLJ00047 protein	70	46
12062	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	130	69
12063	AF090944	Homo sapiens	PRO0663	110	66
12064	Y14480	Homo sapiens	Fragment of human secreted protein encoded by gene 14.	109	53
12065	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	94	79
12066	AF090931	Homo sapiens	PRO0483	123	70
12067	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	111	75
12068	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	144	77
12069	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	145	76
12070	G03639	Homo sapiens	Human secreted protein, SEQ ID NO: 7720.	114	81
12071	AF116715	Homo sapiens	PRO2829	138	63
12072	J02963	Homo sapiens	platelet glycoprotein IIb precursor	127	82
12073	U79260	Homo sapiens	unknown	98	73
12074	W88627	Homo sapiens	Secreted protein encoded by gene 94	132	80

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			clone HPMBQ32.		
12075	J02459	bacteriophage lambda	T (tail component;144)	555	98
12076	AK024455	Homo sapiens	FLJ00047 protein	127	65
12077	X00911	Rattus norvegicus	pot. MSA-precursor	190	73
12078	AF164797	Homo sapiens	ribosomal protein L17 isolog	538	95
12079	A06977	Homo sapiens	albumin	602	87
12080	AF000198	Caenorhabditis elegans	Similar to cuticular collagen	118	38
12081	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	142	86
12082	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	103	50
12083	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	142	86
12084	G00413	Homo sapiens	Human secreted protein, SEQ ID NO: 4494.	64	54
12085	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	132	53
12086	A14829	Homo sapiens	preproapolipoprotein	619	82
12087	AF119900	Homo sapiens	PRO2822	107	76
12088	U52077	Homo sapiens	mariner transposase	277	74
12089	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	126	100
12090	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	92
12091	W05278	Homo sapiens	Tumour necrosis factor-related gene product CL6.5.40.	115	42
12092	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	112	81
12093	G03343	Homo sapiens	Human secreted protein, SEQ ID NO: 7424.	114	64
12094	AJ237660	Bacteriophage 21	Ren protein	187	94
12095	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	135	80
12096	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	161	49
12097	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	122	92
12098	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	148	59
12099	AF090942	Homo sapiens	PRO0657	115	70
12100	AF090931	Homo sapiens	PRO0483	112	74
12101	AF090944	Homo sapiens	PRO0663	103	37
12102	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	76	58
12103	J02963	Homo sapiens	platelet glycoprotein IIb precursor	130	80
12104	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	106	84
12105	R95913	Homo sapiens	Neural thread protein.	105	75
12106	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	149	75
12107	Y09561	Homo sapiens	ATP receptor	188	85
12108	AF090895	Homo sapiens	PRO0117	107	83
12109	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	117	65
12110	G02211	Homo sapiens	Human secreted protein, SEQ ID NO:	130	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6292.		
12111	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	117	69
12112	Y12478	Homo sapiens	congenital heart disease 5 protein	291	62
12113	AF220264	Homo sapiens	MOST-1	142	76
12114	Y12077	Homo sapiens	Human 5' EST secreted protein SEQ ID NO: 390.	109	95
12115	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	171	63
12116	AF064869	Rattus norvegicus	brain-enriched guanylate kinase-associated protein 2; BEGA2	294	98
12117	S79410	Mus musculus	nuclear localization signal binding protein	128	36
12119	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	102	73
12120	U79260	Homo sapiens	unknown	98	65
12121	AF161356	Homo sapiens	HSPC093	118	67
12122	AF130087	Homo sapiens	PRO2411	115	80
12123	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	280	75
12124	S48406	Mus sp.	alpha 1 (XII) collagen {triple-helical domain COL2}	59	41
12125	AB030816	Homo sapiens	H-REV107 protein-related protein	420	79
12126	R96418	Homo sapiens	Partial human transforming growth factor beta receptor type II.	169	100
12127	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	91	46
12128	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	109	83
12129	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	127	57
12130	AF119900	Homo sapiens	PRO2822	108	79
12131	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	127	70
12132	AF303828	Mus musculus	ubc-like protein MMS2	131	43
12133	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	127	58
12134	U49974	Homo sapiens	mariner transposase	124	80
12135	X52164	Mus musculus	Q300 protein (AA 1-77)	106	94
12136	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	151	69
12137	AF192913	Homo sapiens	zinc finger protein ZNF180	581	94
12138	X58907	Homo sapiens	steroid 21-monooxygenase	128	58
12139	AF090931	Homo sapiens	PRO0483	121	70
12140	AK024455	Homo sapiens	FLJ00047 protein	84	60
12141	AF090931	Homo sapiens	PRO0483	122	71
12142	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	153	60
12143	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	121	100
12144	G02922	Homo sapiens	Human secreted protein, SEQ ID NO: 7003.	191	62
12145	U57092	Homo sapiens	Rab30	257	87
12146	AF130089	Homo sapiens	PRO2550	129	74
12147	AF090931	Homo sapiens	PRO0483	138	80
12148	G02382	Homo sapiens	Human secreted protein, SEQ ID NO: 6463.	135	60
12149	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	138	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12150	U51723	Plasmodium vivax	V-SERA 1	107	37
12151	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	82	68
12152	Y23884	Homo sapiens	Amino acid sequence of FK506 binding protein 65 (FKBP65).	124	69
12153	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	93	70
12154	AF229067	Homo sapiens	PADI-H protein	162	68
12155	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	125	86
12157	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	113	39
12158	U89439	Bos taurus	ubiquitin-like protein	146	76
12159	G03725	Homo sapiens	Human secreted protein, SEQ ID NO: 7806.	677	98
12160	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	124	90
12161	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	109	80
12162	AF090931	Homo sapiens	PRO0483	125	76
12163	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	191	64
12164	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	96	61
12165	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	115	68
12166	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	219	93
12167	AF118086	Homo sapiens	PRO1992	155	78
12168	X12789	Mus musculus	cytokeratin 8 (AA 1 - 489)	174	63
12169	S79410	Mus musculus	nuclear localization signal binding protein	94	48
12170	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	150	57
12171	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	141	78
12172	AF068294	Homo sapiens	HDCMB45P	184	56
12173	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	116	50
12174	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	107	59
12175	X92485	Plasmodium vivax	pval	108	44
12176	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	102	84
12177	X83703	Homo sapiens	nuclear protein	330	68
12178	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	147	50
12179	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	103	73
12180	AF132200	Homo sapiens	PRO1751	131	64
12181	AC005514	Homo sapiens	CTF5	261	90
12182	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	156	75
12183	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	137	75
12184	P92219	Homo sapiens (human)	CR1 protein.	101	74
12185	G02607	Homo sapiens	Human secreted protein, SEQ ID NO: 6688.	156	56

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12186	G02213	Homo sapiens	Human secreted protein, SEQ ID NO: 6294.	626	97
12187	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	96	51
12188	AF118067	Homo sapiens	PRO1578	89	73
12189	M63154	Homo sapiens	intrinsic factor	130	96
12190	AF090942	Homo sapiens	PRO0657	144	72
12191	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	152	76
12192	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	134	63
12193	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	159	76
12194	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	117	76
12195	AF090931	Homo sapiens	PRO0483	134	62
12196	AF130089	Homo sapiens	PRO2550	117	74
12197	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	113	57
12198	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	126	70
12199	J02459	bacteriophage lambda	Fi (DNA packaging;117)	203	95
12200	Y08061	Homo sapiens	Human c-myb protein fragment.	135	58
12201	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	132	86
12202	AF119900	Homo sapiens	PRO2822	148	68
12203	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	59
12204	R59842	Homo sapiens	ApoE4L1 protease.	118	91
12205	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	121	72
12206	S75997	Rattus sp.	nucleoporin p62 homolog	131	65
12207	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	145	65
12208	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	145	86
12209	AJ242956	Homo sapiens	E1 fusion protein	96	88
12210	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	132	78
12211	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	81
12212	K03179	Homo sapiens	pro-alpha-1 type-I collagen	96	37
12213	G01895	Homo sapiens	Human secreted protein, SEQ ID NO: 5976.	310	57
12214	Y91577	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:250.	493	82
12215	R13144	Homo sapiens	Deleted in Colorectal Carcinomas.	700	98
12216	AF132200	Homo sapiens	PRO1751	109	61
12217	AB013897	Homo sapiens	HKR1	324	64
12218	AF071172	Homo sapiens	HERC2	123	86
12219	L38593	Homo sapiens	integral membrane protein	78	62
12220	AF036233	Homo sapiens	cdc25B phosphatase	204	51
12221	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	107	60
12222	AL049795	Homo sapiens	dj622L5.9 (eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD) (TRIP-1, TGF-beta receptor interacting protein 1))	163	86
12223	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	120	76

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12224	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	102	64
12225	AF130079	Homo sapiens	PRO2852	103	80
12226	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	163	86
12227	AF119855	Homo sapiens	PRO1847	96	78
12228	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	195	87
12229	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	103	90
12230	U49957	Homo sapiens	LIM protein	212	100
12231	AK022759	Homo sapiens	unnamed protein product	646	100
12232	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	110	70
12233	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	109	74
12234	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	123	76
12235	AF220264	Homo sapiens	MOST-1	104	85
12236	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	113	87
12237	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	143	84
12238	AF090942	Homo sapiens	PRO0657	103	66
12239	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	129	72
12240	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	135	75
12241	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA 1a (AF078683)	136	95
12242	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	148	72
12243	K02576	Homo sapiens	salivary proline-rich protein 1	118	39
12244	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	78	100
12245	AC005200	Homo sapiens	plasmalemmal porin	131	79
12246	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	150	65
12247	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	90	55
12248	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	77	64
12249	U63542	Homo sapiens	FAP protein	108	56
12250	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	75
12251	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	139	63
12252	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	122	71
12253	AF118086	Homo sapiens	PRO1992	73	70
12254	AF083929	Mus musculus	ES18	108	44
12255	AF130089	Homo sapiens	PRO2550	124	88
12256	AF090931	Homo sapiens	PRO0483	132	80
12257	X95190	Homo sapiens	branched chain acyl-CoA oxidase	166	86
12258	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	131	53
12259	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	124	88
12260	G00328	Homo sapiens	Human secreted protein, SEQ ID NO:	128	85

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4409.		
12261	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	133	72
12262	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	110	70
12263	Y08061	Homo sapiens	Human c-myc protein fragment.	125	85
12264	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	126	65
12265	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	95
12266	AK024455	Homo sapiens	FLJ00047 protein	108	63
12267	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	166	73
12268	AF090931	Homo sapiens	PRO0483	108	82
12269	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	120	68
12270	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	120	66
12271	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	148	74
12272	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	129	60
12273	AF130089	Homo sapiens	PRO2550	134	79
12274	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	118	80
12275	AF194537	Homo sapiens	NAG13	151	52
12276	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	75	68
12277	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	113	60
12278	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	111	70
12279	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	119	92
12280	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	108	90
12281	U66464	Homo sapiens	hematopoietic progenitor kinase	102	83
12282	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	118	65
12283	W00838	Homo sapiens	Tumour necrosis factor-related gene product.	162	82
12284	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	130	77
12285	AF116661	Homo sapiens	PRO1438	104	74
12286	G00379	Homo sapiens	Human secreted protein, SEQ ID NO: 4460.	98	66
12287	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	105	74
12288	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	129	78
12289	X53581	Rattus norvegicus	ORF7	111	47
12290	AF090931	Homo sapiens	PRO0483	147	87
12291	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	106	69
12292	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	137	53
12293	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	142	56

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12294	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	117	60
12295	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	112	66
12296	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	140	62
12297	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	144	70
12298	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	95	51
12299	S79410	Mus musculus	nuclear localization signal binding protein	108	70
12300	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	122	85
12301	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	117	73
12302	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	115	62
12303	AF130051	Homo sapiens	PRO0898	116	65
12304	J02963	Homo sapiens	platelet glycoprotein IIb precursor	119	60
12305	V00662	Homo sapiens	ATPase 6	118	100
12306	AF107406	Homo sapiens	GW128	98	66
12307	A05308	synthetic construct	glioblastoma-derived T-cell suppressor factor	376	93
12308	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	173	71
12309	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	140	74
12310	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	98	47
12311	Y27571	Homo sapiens	Human secreted protein encoded by gene No. 5.	130	42
12312	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	134	76
12313	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	98	82
12314	U79260	Homo sapiens	unknown	97	64
12315	L27428	Homo sapiens	reverse transcriptase	214	44
12316	D00570	Mus musculus	open reading frame (196 AA)	115	83
12317	AF090931	Homo sapiens	PRO0483	104	74
12318	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	123	84
12319	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	107	70
12320	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	97	62
12321	S79410	Mus musculus	nuclear localization signal binding protein	95	58
12322	G00362	Homo sapiens	Human secreted protein, SEQ ID NO: 4443.	104	59
12323	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	115	75
12324	AF286472	Homo sapiens	retinitis pigmentosa GTPase regulator	121	53
12325	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	162	75
12326	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	129	75
12327	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	125	88

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12328	AF090944	Homo sapiens	PRO0663	122	76
12329	AF090931	Homo sapiens	PRO0483	156	81
12330	W00838	Homo sapiens	Tumour necrosis factor-related gene product.	107	80
12331	AF116715	Homo sapiens	PRO2829	127	72
12332	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	145	49
12333	S80862	Western equine encephalomyelitis virus Western equine encephalomyelitis virus, Peptide Partial, 259 aa	nucleocapsid gene C	108	35
12334	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	141	83
12335	AK024455	Homo sapiens	FLJ00047 protein	133	71
12336	AF090944	Homo sapiens	PRO0663	139	84
12337	J02963	Homo sapiens	platelet glycoprotein IIb precursor	124	71
12338	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	102	69
12339	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	121	81
12340	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	149	54
12341	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	134	66
12342	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	102	60
12343	AF118086	Homo sapiens	PRO1992	80	63
12344	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	104	80
12345	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	145	72
12346	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	143	75
12347	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	116	37
12348	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	176	76
12349	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	103	48
12350	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	81
12351	Y02926	Homo sapiens	Fragment of human secreted protein encoded by gene 101.	108	70
12352	W21581	Homo sapiens	Alzheimer's disease protein encoded by DNA from plasmid pGCS11037.	101	84
12353	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	105	42
12354	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	147	66
12355	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	125	65
12356	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	96	68
12357	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	122	43
12358	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	132	38
12359	G00397	Homo sapiens	Human secreted protein, SEQ ID NO:	94	90

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4478.		
12360	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	113	56
12361	AB001684	Chlorella vulgaris	ORF49b	92	44
12362	U93564	Homo sapiens	p40	257	84
12363	U60269	Homo sapiens	putative envelope protein; orf similar to env of Type A and Type B retroviruses and to class II HERVs	427	84
12364	G03064	Homo sapiens	Human secreted protein, SEQ ID NO: 7145.	102	73
12365	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	102	68
12366	AF090944	Homo sapiens	PRO0663	94	45
12367	Y76198	Homo sapiens	Human secreted protein encoded by gene 75.	150	55
12368	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	105	85
12369	AF130089	Homo sapiens	PRO2550	112	78
12370	AF090895	Homo sapiens	PRO0117	125	64
12371	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	121	95
12372	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	145	72
12373	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	144	72
12374	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	133	79
12375	AP000001	Pyrococcus horikoshii	58aa long hypothetical protein	96	51
12376	U16359	Rattus norvegicus	nitric oxide synthase	105	76
12377	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	123	78
12378	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	126	83
12379	Y53643	Homo sapiens	A bone marrow secreted protein designated BMS6.	329	98
12380	U64094	Homo sapiens	soluble type II interleukin-1 receptor	114	100
12381	J02459	bacteriophage lambda	D (head-DNA stabilization;110)	467	100
12382	L10908	Mus musculus	Gcap1 gene product	100	89
12383	AF220264	Homo sapiens	MOST-1	113	68
12384	U79260	Homo sapiens	unknown	94	60
12385	B01372	Homo sapiens	Neuron-associated protein.	148	52
12386	R13556	Homo sapiens	Protein encoded downstream of hhc_M oncoprotein.	116	63
12387	G00952	Homo sapiens	Human secreted protein, SEQ ID NO: 5033.	125	92
12388	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	130	65
12389	S79410	Mus musculus	nuclear localization signal binding protein	150	62
12390	G00454	Homo sapiens	Human secreted protein, SEQ ID NO: 4535.	102	38
12391	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	113	56
12392	G00332	Homo sapiens	Human secreted protein, SEQ ID NO: 4413.	73	92

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12393	M69297	Homo sapiens	ORF 3	167	75
12394	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	142	43
12395	AF220264	Homo sapiens	MOST-1	131	57
12396	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	139	62
12397	AF130089	Homo sapiens	PRO2550	120	62
12398	AK023117	Homo sapiens	unnamed protein product	529	97
12399	AF123652	Homo sapiens	FEZ1	157	96
12400	D38112	Homo sapiens	NADH dehydrogenase subunit 6	139	87
12401	U49973	Homo sapiens	ORF1; MER37; putative transposase similar to pogo element	306	60
12402	AC005031	Homo sapiens	neuronal apoptosis inhibitory protein	143	96
12403	J03071	Homo sapiens	chorionic somatomammotropin CS-2	585	100
12405	AF095770	Homo sapiens	PTH-responsive osteosarcoma D1 protein	125	100
12406	R07057	Homo sapiens	Smaller hepatocellular oncoprotein (hhcm) gene preoduct.	150	63
12407	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	157	85
12408	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	120	75
12409	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	141	50
12410	G03465	Homo sapiens	Human secreted protein, SEQ ID NO: 7546.	103	51
12411	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	147	71
12412	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	159	70
12413	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	129	79
12414	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	156	72
12415	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	74	72
12416	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	102	50
12417	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	171	75
12418	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	137	55
12419	G00365	Homo sapiens	Human secreted protein, SEQ ID NO: 4446.	111	52
12420	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	129	53
12421	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	110	55
12422	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	126	87
12423	U93564	Homo sapiens	p40	350	93
12424	M17885	Homo sapiens	acidic ribosomal phosphoprotein (P0)	484	88
12425	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	130	69
12426	X60376	Brassica napus	proline-rich protein	89	47
12427	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	83	88
12428	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	117	75
12429	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	107	67

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12430	AK027208	Homo sapiens	unnamed protein product	108	64
12431	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	154	68
12432	AF130089	Homo sapiens	PRO2550	118	88
12433	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	90	55
12434	AK024455	Homo sapiens	FLJ00047 protein	113	75
12435	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	107	80
12436	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	114	75
12437	AC005498	Homo sapiens	R31665_2	163	75
12438	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	132	100
12439	G03116	Homo sapiens	Human secreted protein, SEQ ID NO: 7197.	145	84
12440	AK024455	Homo sapiens	FLJ00047 protein	136	73
12441	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	122	69
12442	AF090942	Homo sapiens	PRO0657	120	72
12443	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	159	53
12444	AF130089	Homo sapiens	PRO2550	110	73
12445	AL021395	Homo sapiens	dJ269M15.1 (similar to peptidylprolyl isomerase (cyclophilin))	225	64
12446	AF090931	Homo sapiens	PRO0483	155	79
12447	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	130	81
12448	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	122	74
12449	AF119855	Homo sapiens	PRO1847	88	72
12450	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	147	84
12451	AK024455	Homo sapiens	FLJ00047 protein	78	68
12452	AF116712	Homo sapiens	PRO2738	118	62
12453	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	109	67
12454	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	144	59
12455	AK024455	Homo sapiens	FLJ00047 protein	146	64
12456	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	166	72
12457	AF090944	Homo sapiens	PRO0663	129	79
12458	G02501	Homo sapiens	Human secreted protein, SEQ ID NO: 6582.	119	70
12459	R22278	Homo sapiens	Human gp.-specific component phenotype Gc1.	250	65
12460	G02480	Homo sapiens	Human secreted protein, SEQ ID NO: 6561.	143	58
12461	Y87156	Homo sapiens	Human secreted protein sequence SEQ ID NO:195.	111	61
12462	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	147	84
12463	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	94	38
12464	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	134	74
12465	AF200715	Homo sapiens	PTB domain adaptor protein CED-6	332	95
12466	G03786	Homo sapiens	Human secreted protein, SEQ ID NO:	139	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7867.		
12467	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	117	55
12468	AF199023	Homo sapiens	phospholipid scramblase 4	476	98
12469	AF265575	Homo sapiens	ubiquitous TPR-motif protein Y isoform	104	89
12470	AF108841	Homo sapiens	pol protein	306	87
12471	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	111	79
12472	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	124	78
12473	U18339	Variola virus	D4L	117	60
12474	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	124	63
12475	AF130089	Homo sapiens	PRO2550	105	52
12476	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	80	62
12477	M91242	Rattus norvegicus	calcium channel alpha-1 subunit	156	68
12478	AF130089	Homo sapiens	PRO2550	154	79
12479	M15530	Homo sapiens	B-cell growth factor	154	70
12480	U39904	Mus musculus	citron	718	97
12481	R99364	Homo sapiens	Human REST protein DNA binding domain.	229	37
12482	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	97	54
12483	AF161356	Homo sapiens	HSPC093	94	55
12484	Y69166	Homo sapiens	A mature human N-acetylglycosaminyl transferase protein.	97	75
12485	AF090942	Homo sapiens	PRO0657	103	55
12486	U79260	Homo sapiens	unknown	98	74
12487	AL160493	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	96	53
12488	U37100	Homo sapiens	aldose reductase-like peptide	400	97
12489	U93569	Homo sapiens	putative p150	141	56
12490	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	104	66
12491	R59842	Homo sapiens	ApoE4L1 protease.	86	89
12492	Y00876	Homo sapiens	Human LAPH-1 protein sequence.	219	45
12493	AK024455	Homo sapiens	FLJ00047 protein	85	53
12494	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	95	63
12495	Y36722	Homo sapiens	Fragment of human secreted protein encoded by gene 98.	216	60
12496	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	102	57
12497	Y77551	Homo sapiens	C-terminal domain of beta1c integrin.	132	67
12498	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	122	69
12499	AF161356	Homo sapiens	HSPC093	98	51
12500	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	150	81
12501	G00492	Homo sapiens	Human secreted protein, SEQ ID NO: 4573.	97	52
12502	AF132200	Homo sapiens	PRO1751	94	69
12503	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	76	65
12504	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	99	75

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12505	M19651	Rattus norvegicus	fos-related antigen	132	92
12506	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	113	48
12507	U94832	Homo sapiens	KSRP	117	48
12508	W47029	Homo sapiens	Human N-proteinase (70 kDa short form).	121	62
12509	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	124	66
12510	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	90	80
12511	AF042384	Homo sapiens	BC-2 protein	516	98
12512	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	96	50
12513	G03482	Homo sapiens	Human secreted protein, SEQ ID NO: 7563.	121	45
12514	AL162044	Homo sapiens	hypothetical protein	174	48
12515	AF130079	Homo sapiens	PRO2852	96	73
12516	B03628	Homo sapiens	Human phospholipase 2 HPPL2.	113	77
12517	D32202	Homo sapiens	alpha 1C adrenergic receptor isoform 2	164	86
12518	G02920	Homo sapiens	Human secreted protein, SEQ ID NO: 7001.	99	85
12519	U00694	Gallus gallus	vitamin D3 hydroxylase associated protein	187	45
12520	AB030829	Rattus norvegicus	carbonic anhydrase III	503	63
12521	J04204	Bos taurus	32 kd accessory protein	618	95
12522	M36341	Homo sapiens	ADP-ribosylation factor 4	374	93
12523	AF090931	Homo sapiens	PRO0483	163	82
12524	AB007925	Homo sapiens	KIAA0456 protein	130	62
12525	G02314	Homo sapiens	Human secreted protein, SEQ ID NO: 6395.	162	79
12526	AF178948	Homo sapiens	TALE homeobox protein Meis2a	321	93
12527	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	156	85
12528	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	126	57
12529	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	145	68
12530	AK024372	Homo sapiens	unnamed protein product	112	56
12531	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	76	65
12532	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	132	66
12533	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	146	53
12534	AF090942	Homo sapiens	PRO0657	83	60
12535	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	136	65
12536	R95913	Homo sapiens	Neural thread protein.	106	52
12537	AF130089	Homo sapiens	PRO2550	148	84
12538	AF102826	Homo sapiens	RD114/simian type D retrovirus receptor	605	91
12539	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	143	52
12540	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	87	65
12541	G03600	Homo sapiens	Human secreted protein, SEQ ID NO: 7681.	209	92

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12542	M31964	Saimiriine herpesvirus 2	collagen-like protein	92	52
12543	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	146	76
12544	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	155	72
12545	AC004912	Homo sapiens	similar to CR16, SH3 domain binding protein; similar to 2205340A (PID:g1587070)	442	98
12546	V00662	Homo sapiens	URF A6L (NADH dehydrogenase subunit)	175	91
12547	AF130089	Homo sapiens	PRO2550	112	40
12548	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	48
12549	X55110	Homo sapiens	neurite outgrowth-promoting protein	479	72
12550	X98296	Homo sapiens	ubiquitin hydrolase	500	88
12551	R94317	Homo sapiens	Hepatocyte proliferation substance HP-041V.	390	92
12552	G01623	Homo sapiens	Human secreted protein, SEQ ID NO: 5704.	142	90
12553	D86966	Homo sapiens	similar to human ZFY protein.	161	56
12554	D00570	Mus musculus	open reading frame (196 AA)	122	67
12555	AF130089	Homo sapiens	PRO2550	94	88
12556	AF043184	Homo sapiens	T cell receptor beta chain	607	84
12557	U93564	Homo sapiens	p40	154	100
12558	U42026	Homo sapiens	plasma membrane Ca ²⁺ -ATPase variant 4a PMCA4a	200	97
12559	S79410	Mus musculus	nuclear localization signal binding protein	103	50
12560	U90552	Homo sapiens	butyrophilin	356	98
12561	K02576	Homo sapiens	salivary proline-rich protein 1	156	37
12562	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	138	41
12563	X16454	Homo sapiens	carcinoembryonic antigen subdomain B	353	98
12564	AL031186	Homo sapiens	bK984G1.4 (Ewing sarcoma breakpoint region 1 protein)	119	100
12565	M68941	Homo sapiens	protein-tyrosine phosphatase	223	93
12566	Y14487	Homo sapiens	cytosolic serine hydroxymethyltransferase	145	84
12567	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	149	61
12568	AB005047	Homo sapiens	SH3 binding protein	124	52
12569	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	102	53
12570	X68142	Oryctolagus cuniculus	elongation factor 1 gamma	678	93
12571	L20315	Mus musculus	MPS1 protein	337	77
12572	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	114	50
12573	AF130089	Homo sapiens	PRO2550	124	71
12574	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	146	51
12575	AF005902	Monodelphis domestica	kinesin homolog	534	82
12576	Y56021	Homo sapiens	Human CD40 receptor interacting protein 4C4.	711	96
12577	Y99662	Homo sapiens	Human GTPase associated protein-13.	634	100
12578	Z48008	Saccharomyces cerevisiae	Sok1p	225	100

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12579	AF112207	Homo sapiens	translation initiation factor eIF-2b delta subunit	195	97
12580	M22538	Homo sapiens	NADH-ubiquinone reductase	224	82
12581	AB034730	Mus musculus	This gene is isolated by means of differential display method using twt, an excellent mouse model for ectopic ossification.; similar to megakaryocyte stimulating factor precursor and cartilage superficial zone protein	112	44
12582	U93567	Homo sapiens	p40	364	93
12583	AY007233	Homo sapiens	phosphoinositol 3-phosphate binding protein-1	475	100
12584	L07592	Homo sapiens	peroxisome proliferator activated receptor	113	81
12585	AE003682	Drosophila melanogaster	CG8135 gene product	191	38
12586	AF119851	Homo sapiens	PRO1722	88	64
12587	AF090895	Homo sapiens	PRO0117	144	59
12588	G03564	Homo sapiens	Human secreted protein, SEQ ID NO: 7645.	144	57
12589	U73199	Mus musculus	Rho-guanine nucleotide exchange factor	111	32
12590	J04615	Homo sapiens	small nuclear ribonucleoprotein	383	97
12591	L77967	Ovis aries	small proline-rich protein with paired repeat	60	33
12592	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	118	78
12593	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	123	83
12594	AF090944	Homo sapiens	PRO0663	152	82
12595	Y15243	Homo sapiens	ULBP-3 amino acid sequence.	852	100
12596	X98235	Drosophila melanogaster	type I	159	42
12597	AF191309	Mus musculus	zinc finger protein	407	66
12598	W82841	Homo sapiens	Human cerebral protein-1.	107	91
12599	AF070664	Homo sapiens	HSPC008	128	89
12600	U03688	Homo sapiens	cytochrome P450	257	96
12601	AB015798	Homo sapiens	DnaJ homolog	226	73
12602	AC003058	Arabidopsis thaliana	unknown protein	88	40
12603	G03267	Homo sapiens	Human secreted protein, SEQ ID NO: 7348.	80	35
12604	AF200187	cercopithecine herpesvirus 15	EBNA2-like protein	109	28
12605	AF161532	Homo sapiens	HSPC047	720	100
12606	M21302	Homo sapiens	small proline rich protein	60	59
12607	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	107	47
12608	AJ302650	Rattus norvegicus	RP59 protein	599	54
12609	J05401	Homo sapiens	sarcomeric mitochondrial creatine kinase precursor (EC 2.7.3.2)	763	96
12610	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	216	87
12611	W78175	Homo sapiens	Human secreted protein encoded by gene 50 clone HSTAG52.	337	100
12612	S79410	Mus musculus	nuclear localization signal binding protein	145	66
12613	AF119855	Homo sapiens	PRO1847	157	61

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12614	U82303	Homo sapiens	unknown	107	62
12615	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	146	49
12616	AF130051	Homo sapiens	PRO0898	254	56
12617	AF037350	Rattus norvegicus	NF-E2-related factor 2	807	59
12618	Y02168	Homo sapiens	A facilitative glucose transporter protein GLUT8.	452	100
12619	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	158	84
12620	G03812	Homo sapiens	Human secreted protein, SEQ ID NO: 7893.	246	60
12621	X55683	Lycopersicon esculentum	extensin (class I)	79	43
12622	AF109907	Homo sapiens	S164	93	40
12623	Y36156	Homo sapiens	Human secreted protein #28.	114	61
12624	AF116712	Homo sapiens	PRO2738	104	48
12625	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	81	65
12626	AF113685	Homo sapiens	PRO0974	104	43
12627	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	116	45
12628	AF107406	Homo sapiens	GW128	133	58
12629	G03415	Homo sapiens	Human secreted protein, SEQ ID NO: 7496.	100	57
12630	AB047600	Macaca fascicularis	hypothetical protein	172	66
12631	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	136	63
12632	AF118082	Homo sapiens	PRO1902	138	45
12633	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	151	62
12634	X52164	Mus musculus	Q300 protein (AA 1-77)	95	58
12635	AF064597	Homo sapiens	LINE-1 like protein	108	46
12636	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	116	49
12637	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	110	52
12638	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	79	70
12639	M29622	Mus musculus	open reading frame 2	81	60
12640	M26460	Homo sapiens	retinoblastoma 1	100	45
12641	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	110	63
12642	AB047936	Macaca fascicularis	hypothetical protein	100	52
12643	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	146	41
12644	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	143	48
12645	AF090942	Homo sapiens	PRO0657	157	54
12646	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	130	56
12647	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	267	65
12648	AF130079	Homo sapiens	PRO2852	109	57
12649	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	99	61
12650	X55686	Lycopersicon	extensin (class II)	65	35

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		esculentum			
12651	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	87	84
12652	AF119851	Homo sapiens	PRO1722	150	70
12653	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	133	50
12654	Y45382	Homo sapiens	Human secreted protein fragment encoded from gene 28.	146	70
12655	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	136	63
12656	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	93	52
12657	U93563	Homo sapiens	putative p150	1046	50
12658	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	346	70
12659	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	104	70
12660	AF119851	Homo sapiens	PRO1722	98	56
12661	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	90	65
12662	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	59	64
12663	AF118082	Homo sapiens	PRO1902	91	66
12664	L10908	Mus musculus	Gcap1 gene product	113	50
12665	M18093	Phaseolus vulgaris	hydroxyproline-rich glycoprotein	124	37
12666	AF090895	Homo sapiens	PRO0117	76	57
12667	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	103	43
12668	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	90	61
12669	M15530	Homo sapiens	B-cell growth factor	90	80
12670	AF198447	Aspergillus nidulans	60S ribosomal protein L3	217	69
12671	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	137	51
12672	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	77	68
12673	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	67	40
12674	X79417	Sus scrofa	40S ribosomal protein S12	377	75
12675	AF107406	Homo sapiens	GW128	74	51
12676	Y73966	Homo sapiens	Human prostate tumor EST fragment derived protein #153.	99	62
12677	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	127	65
12678	G00590	Homo sapiens	Human secreted protein, SEQ ID NO: 4671.	99	62
12679	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	128	85
12680	AF194537	Homo sapiens	NAG13	142	59
12681	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	155	77
12682	AF161356	Homo sapiens	HSPC093	104	50
12683	AF107406	Homo sapiens	GW128	84	54
12684	U83303	Homo sapiens	line-1 reverse transcriptase	90	39
12685	V40883_cdl	Homo sapiens	03-DEC-1997 Coding sequence of clone BG366 2.	728	100
12686	M24732	Homo sapiens	lamin-like protein	94	54
12687	X00824	Gallus gallus	collagen	66	42

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12688	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	184	64
12689	AF118086	Homo sapiens	PRO1992	140	61
12690	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	131	54
12691	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	180	72
12692	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	104	72
12693	AF130089	Homo sapiens	PRO2550	204	51
12694	K01664	Drosophila melanogaster	Bkm-like protein	92	52
12695	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	110	52
12696	L39103	Homo sapiens	glycoprotein Ib alpha	61	45
12697	M15530	Homo sapiens	B-cell growth factor	121	64
12698	M36913	Zea mays	cell wall protein (put.); putative	75	40
12699	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	68
12700	M24732	Homo sapiens	lamin-like protein	95	35
12701	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	67	50
12702	AF298594	Nicotiana glauca	arabinogalactan protein	105	30
12703	X92485	Plasmodium vivax	pval	97	38
12704	AF210651	Homo sapiens	NAG18	89	64
12705	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	190	53
12706	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	93	78
12707	U52077	Homo sapiens	mariner transposase	451	51
12708	AC003058	Arabidopsis thaliana	unknown protein	244	77
12709	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	138	65
12710	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	99	82
12711	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	104	34
12712	AF242772	Homo sapiens	mesenchymal stem cell protein DSCD28	106	45
12713	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	116	36
12714	AF116715	Homo sapiens	PRO2829	139	68
12715	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	89	62
12716	X55684	Lycopersicon esculentum	extensin (class I)	86	54
12717	Z93891	Hegeter politus	cytochrome oxidase	72	48
12718	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	105	46
12719	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	74	46
12720	U30221	Crithidia fasciculata	NADH dehydrogenase subunit 5	92	39
12721	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	131	82
12722	AF107406	Homo sapiens	GW128	72	54
12723	G02639	Homo sapiens	Human secreted protein, SEQ ID NO:	131	55

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6720.		
12724	AF116661	Homo sapiens	PRO1438	145	59
12725	Y53871	Homo sapiens	A human brain-derived signalling factor polypeptide.	584	98
12726	L10908	Mus musculus	Gcap1 gene product	95	37
12727	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	124	37
12728	X55686	Lycopersicon esculentum	extensin (class II)	66	36
12729	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	110	55
12730	L23852	Homo sapiens	Putative 3' end of coding region; putative	83	37
12731	Y13141	Bromheadia finlaysoniana	extensin	59	48
12732	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	88	69
12733	AF090895	Homo sapiens	PRO0117	130	55
12734	R95913	Homo sapiens	Neural thread protein.	162	45
12735	U72355	Homo sapiens	Hsp27 ERE-TATA-binding protein	972	57
12736	AF247039	porcine adenovirus 3	163R*	108	35
12737	M22332	Homo sapiens	unknown protein	148	45
12738	AF090895	Homo sapiens	PRO0117	89	72
12739	B08525	Homo sapiens	Protein encoded by a novel gene associated with colon disease.	296	86
12740	X90872	Homo sapiens	associated to Golgi apparatus	116	54
12741	M26460	Homo sapiens	retinoblastoma 1	75	37
12742	S52010	Mus sp.	orf1 5' of EpoR	104	31
12743	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	88	50
12744	AB047600	Macaca fascicularis	hypothetical protein	111	47
12745	AF090944	Homo sapiens	PRO0663	152	65
12746	Y21106	Homo sapiens	Human bcl2 proto-oncogene wild type protein fragment 3.	62	64
12747	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	97	76
12748	X66861	Mus musculus	Hox-1.4	92	34
12749	AF166125	Homo sapiens	selenoprotein N	978	98
12750	W87504	Homo sapiens	Human N-methyl-D-aspartate receptor subunit encoded by clone NMDA24.	98	29
12751	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	91	78
12752	X72963	Nicotiana tabacum	pAP8 product	80	45
12753	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	123	61
12754	AF146191	Homo sapiens	FRG1	208	85
12755	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	154	75
12756	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	72	48
12757	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	111	51
12758	U83280	Leishmania donovani	39 kDa antigen	106	60
12759	AF116661	Homo sapiens	PRO1438	73	48
12760	AF164615	Homo sapiens	envelope protein.	257	83

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12761	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	135	70
12762	AF073519	Homo sapiens	small EDRK-rich factor 1, long isoform	111	50
12763	M29622	Mus musculus	open reading frame 2	73	68
12764	L27428	Homo sapiens	reverse transcriptase	111	60
12765	S79410	Mus musculus	nuclear localization signal binding protein	106	45
12766	AK024455	Homo sapiens	FLJ00047 protein	108	66
12767	M36914	Zea mays	cell wall protein (put.); putative	78	36
12768	L27428	Homo sapiens	reverse transcriptase	159	59
12769	AJ005567	Mus musculus	SPR21 protein	55	39
12770	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	115	82
12771	G04063	Homo sapiens	Human secreted protein, SEQ ID NO: 8144.	76	64
12772	AF217374	Acanthaster planci	cytochrome oxidase subunit I	126	85
12773	AF130114	Homo sapiens	PRO2459	129	50
12774	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	220	71
12775	AF287482	Chlorobium tepidum	Orf122	166	68
12776	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	84	50
12777	AF130079	Homo sapiens	PRO2852	258	58
12778	AF090931	Homo sapiens	PRO0483	65	76
12779	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	152	66
12780	AB047948	Macaca fascicularis	hypothetical protein	59	37
12781	AF119900	Homo sapiens	PRO2822	132	59
12782	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	97	51
12783	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	77	77
12784	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	93	84
12785	L27428	Homo sapiens	reverse transcriptase	183	39
12786	AF119851	Homo sapiens	PRO1722	128	61
12787	AF116715	Homo sapiens	PRO2829	111	72
12788	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	147	77
12789	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	84	66
12790	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	155	71
12791	AF124729	Mus musculus	acinusS'	122	50
12792	AC003058	Arabidopsis thaliana	unknown protein	86	52
12793	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	108	74
12794	M62415	Pseudopleuronectes americanus	HPLC6	82	35
12795	Y36156	Homo sapiens	Human secreted protein #28.	133	48
12796	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	119	74
12797	L22030	Glycine max	hydroxyproline-rich glycoprotein	170	32
12798	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	114	43
12799	Y76184	Homo sapiens	Human secreted protein encoded by	90	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			gene 61.		
12800	X62677	Oryctolagus cuniculus	retrovirus related reverse transcriptase	102	38
12801	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	98	69
12802	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	177	69
12803	AF130089	Homo sapiens	PRO2550	94	74
12804	S77772	Homo sapiens	aspartylglucosaminidase, AGA {C-terminal, alternatively spliced} {EC 3.5.1.26}	83	68
12805	AF063866	Melanoplus sanguinipes entomopoxvirus	ORF MSV233 hypothetical protein	82	28
12806	AF026689	Homo sapiens	prostate-specific transglutaminase	80	60
12807	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	122	47
12808	X03145	Homo sapiens	pot. ORF V	150	34
12809	L10908	Mus musculus	Gcap1 gene product	111	34
12810	Y95028	Homo sapiens	Human clone vp7_1 ORF2, SEQ ID NO:128.	170	55
12811	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	101	62
12812	AJ233591	Mus musculus	reverse transcriptase	287	67
12813	U82303	Homo sapiens	unknown	149	52
12814	AF107406	Homo sapiens	GW128	103	58
12815	U82303	Homo sapiens	unknown	93	83
12816	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	161	54
12817	B01390	Homo sapiens	Neuron-associated protein.	81	38
12818	AF287482	Chlorobium tepidum	Orf122	174	69
12819	AE003499	Drosophila melanogaster	CG12706 gene product	166	28
12820	M15530	Homo sapiens	B-cell growth factor	124	71
12821	U83303	Homo sapiens	line-1 reverse transcriptase	161	53
12822	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	150	77
12823	G00497	Homo sapiens	Human secreted protein, SEQ ID NO: 4578.	103	66
12824	AF064597	Homo sapiens	LINE-1 like protein	64	45
12825	X71442	Rattus norvegicus	ORF 1; putative	113	45
12826	U62039	Elephantulus edwardii	reverse transcriptase	74	46
12827	M15530	Homo sapiens	B-cell growth factor	127	54
12828	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	94	84
12829	U63332	Homo sapiens	super cysteine rich protein; SCRP	59	57
12830	AF229067	Homo sapiens	PADI-H protein	184	61
12831	K02576	Homo sapiens	salivary proline-rich protein 1	69	34
12832	AF144054	Homo sapiens	apoptosis related protein APR-4	83	46
12833	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	168	61
12834	G03133	Homo sapiens	Human secreted protein, SEQ ID NO: 7214.	142	40
12835	U19098	Lycopersicon chilense	proline-rich protein	81	38
12836	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	229	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12837	Y13141	Bromheadia finlaysoniana	extensin	81	60
12838	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	88	71
12839	X72963	Nicotiana tabacum	pAP8 product	94	40
12840	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	315	56
12841	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	94	55
12842	AK025947	Homo sapiens	unnamed protein product	124	57
12843	AF159055	Homo sapiens	leucine zipper-like protein	69	55
12844	AF040257	Homo sapiens	TNF receptor homolog	98	50
12845	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	94	76
12846	X88799	Oryza sativa	DNA binding protein	94	37
12847	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	98	48
12848	G01984	Homo sapiens	Human secreted protein, SEQ ID NO: 6065.	164	56
12849	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	75	59
12850	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	122	54
12851	M31964	Saimiriine herpesvirus 2	collagen-like protein	79	50
12852	AF118082	Homo sapiens	PRO1902	94	77
12853	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	139	54
12854	R59842	Homo sapiens	ApoE4L1 protease.	108	82
12855	G03295	Homo sapiens	Human secreted protein, SEQ ID NO: 7376.	99	66
12856	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	89	56
12857	D29833	Homo sapiens	proline rich peptide P-B	64	52
12858	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	155	80
12859	G02482	Homo sapiens	Human secreted protein, SEQ ID NO: 6563.	88	61
12860	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	66	33
12861	Y13141	Bromheadia finlaysoniana	extensin	75	47
12862	M29622	Mus musculus	open reading frame 2	74	62
12863	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	141	70
12864	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	117	54
12865	AF090894	Homo sapiens	PRO0113	108	63
12866	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	121	54
12867	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	103	44
12868	S68106	Ascaris suum, Peptide Partial, 100 aa	type IV collagen alpha 2 chain, alpha 2 (IV) {alternatively spliced}	75	35
12869	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	97	56
12870	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	146	62

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12871	G00412	Homo sapiens	Human secreted protein, SEQ ID NO: 4493.	78	76
12872	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	105	56
12873	AB030234	Canis familiaris	D4 dopamine receptor	61	58
12874	M22332	Homo sapiens	unknown protein	128	41
12875	U05313	Trypanosoma brucei	CR3	67	48
12876	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	115	65
12877	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	66	54
12878	X55684	Lycopersicon esculentum	extensin (class I)	78	34
12879	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	122	51
12880	AF130079	Homo sapiens	PRO2852	125	75
12881	AF090895	Homo sapiens	PRO0117	142	59
12882	AF181251	Rattus norvegicus	lung Kruppel-like factor	93	39
12883	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	167	74
12884	M26460	Homo sapiens	retinoblastoma 1	136	41
12885	AJ277557	Homo sapiens	mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2)	280	100
12886	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	119	62
12887	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	145	43
12888	AF119851	Homo sapiens	PRO1722	94	50
12889	K02576	Homo sapiens	salivary proline-rich protein I	121	39
12890	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	95	68
12891	AK024455	Homo sapiens	FLJ00047 protein	77	51
12892	G02827	Homo sapiens	Human secreted protein, SEQ ID NO: 6908.	115	83
12893	L27428	Homo sapiens	reverse transcriptase	89	29
12894	Y01154	Homo sapiens	Protein sequence Seq Id 54 from WO9901020.	112	72
12895	G02597	Homo sapiens	Human secreted protein, SEQ ID NO: 6678.	72	62
12896	AK023563	Homo sapiens	unnamed protein product	260	64
12897	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	76	66
12898	AC002304	Arabidopsis thaliana	F14J16.29	111	36
12899	Y86445	Homo sapiens	Human gene 42-encoded protein fragment, SEQ ID NO:360.	83	53
12900	AF116638	Homo sapiens	PRO1546	123	57
12901	AB010361	Mus musculus	mszf47	64	43
12902	R59842	Homo sapiens	ApoE4L1 protease.	130	86
12903	L06498	Homo sapiens	ribosomal protein S20	249	56
12904	L13635	Rattus norvegicus	growth response protein	176	69
12905	AF156961	Homo sapiens	gag	183	44
12906	AF010144	Homo sapiens	neuronal thread protein AD7c-NTP	207	67
12907	AF107406	Homo sapiens	GW128	99	50
12908	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	93	75

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12909	AF263540	Homo sapiens	MIB006	1809	100
12910	Y48292	Homo sapiens	Human prostate cancer-associated protein 78.	60	50
12911	G03258	Homo sapiens	Human secreted protein, SEQ ID NO: 7339.	179	87
12912	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	108	72
12913	Z72499	Homo sapiens	herpesvirus associated ubiquitin-specific protease (HAUSP)	5242	99
12914	AF092136	Homo sapiens	PTD015	297	100
12915	AF161356	Homo sapiens	HSPC093	123	42
12916	AF044670	Homo sapiens	33 kDa Vamp-associated protein; VAP-33	506	90
12917	W27087	Homo sapiens	Human transforming growth factor alpha HIII.	1243	100
12918	Y59807	Homo sapiens	Human normal ovarian tissue derived protein 84.	111	43
12919	AJ388518	Canis familiaris	non-histone chromosomal protein HMG-17	108	84
12920	AK023392	Homo sapiens	unnamed protein product	119	60
12921	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	104	87
12922	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	124	81
12923	X78444 cd1	Homo sapiens	21-MAY-1997 Human UCSP-2 cDNA.	1090	100
12924	AF116661	Homo sapiens	PRO1438	89	52
12925	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	82	80
12926	AF119855	Homo sapiens	PRO1847	120	63
12927	AF090931	Homo sapiens	PRO0483	92	90
12928	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	119	88
12929	Y91429	Homo sapiens	Human secreted protein sequence encoded by gene 21 SEQ ID NO:150.	108	38
12930	Y12661	Homo sapiens	neuro-endocrine specific protein VGF	2506	99
12931	Y84546	Homo sapiens	Amino acid sequence of a fragment of human collagen type 1 protein.	61	50
12932	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	121	53
12933	G00481	Homo sapiens	Human secreted protein, SEQ ID NO: 4562.	104	52
12934	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	104	60
12935	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	331	77
12936	M15530	Homo sapiens	B-cell growth factor	83	71
12937	G00437	Homo sapiens	Human secreted protein, SEQ ID NO: 4518.	146	64
12938	R59842	Homo sapiens	ApoE4L1 protease.	112	61
12939	AF090895	Homo sapiens	PRO0117	94	80
12940	X73459	Homo sapiens	signal recognition particle subunit 14	549	98
12941	L23545	Homo sapiens	putative	141	45
12942	AF054178	Homo sapiens	CI-B14.5a homolog	238	84
12943	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	110	55
12944	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	143	55
12945	D00570	Mus musculus	open reading frame (251 AA)	166	34
12946	U62039	Elephantulus	reverse transcriptase	63	50

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		edwardii			
12947	AE003499	Drosophila melanogaster	CG12706 gene product	104	31
12948	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	65	100
12949	X70343	Nicotiana glauca	extensin	102	38
12950	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	103	45
12951	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	85	56
12952	AF090895	Homo sapiens	PRO0117	139	68
12953	AF090896	Homo sapiens	PRO0131	93	85
12954	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	101	75
12955	M96982	Homo sapiens	U2 snRNP auxiliary factor small subunit	292	68
12956	X71087	Homo sapiens	monocyte chemoattractant protein (MCP-3)	408	96
12957	S80864	Homo sapiens	cytochrome c-like polypeptide	591	68
12958	AF109907	Homo sapiens	S164	188	63
12959	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	173	50
12960	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	168	62
12961	G03801	Homo sapiens	Human secreted protein, SEQ ID NO: 7882.	98	56
12962	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	106	84
12963	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	125	44
12964	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	107	57
12965	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	71	65
12966	AC009853	Arabidopsis thaliana	hypothetical protein	102	44
12967	AF090942	Homo sapiens	PRO0657	99	62
12968	M15530	Homo sapiens	B-cell growth factor	90	65
12969	AF090895	Homo sapiens	PRO0117	83	54
12970	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	119	54
12971	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	123	57
12972	L32558	Homo sapiens	sequence is expressed in human Tera-2 clone 13 (embryonal carcinoma) cells. The sequence may contain mismatches (one strand sequenced only once). 97% identical in 320 bp overlap with human 54 kDa prot; ORF	426	85
12973	AF008196	Homo sapiens	bax epsilon	78	87
12974	Y20717	Homo sapiens	Human neurofilament-M wild type protein fragment 59.	96	80
12975	AL031848	Homo sapiens	dJ20208.2.2 (novel rodent HES2 (hairly and Enhancer of Split 2) LIKE protein (isoform 2))	176	100
12976	AJ245905	Chlorocebus aethiops	HSBP1-like protein	94	100
12977	AF067519	Homo sapiens	PITSLRE protein kinase beta SV1 isoform	1923	93

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
12978	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	168	73
12979	X52164	Mus musculus	Q300 protein (AA 1-77)	105	39
12980	Y13141	Bromheadia finlaysoniana	extensin	53	36
12981	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	87	77
12982	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	83	89
12983	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	92	46
12984	AF113685	Homo sapiens	PRO0974	111	67
12985	U31086	Gallus gallus	neuron-glia adhesion molecule	52	50
12986	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	132	68
12987	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	91	71
12988	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	135	81
12989	AB029042	Homo sapiens	ATPase inhibitor precursor	364	100
12990	G00442	Homo sapiens	Human secreted protein, SEQ ID NO: 4523.	174	72
12991	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	174	57
12992	G00392	Homo sapiens	Human secreted protein, SEQ ID NO: 4473.	158	57
12993	AF118082	Homo sapiens	PRO1902	77	78
12994	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	76	60
12995	M15530	Homo sapiens	B-cell growth factor	105	76
12996	AJ005562	Mus musculus	SPR2D protein	104	36
12997	Y48346	Homo sapiens	Human prostate cancer-associated protein 43.	184	77
12998	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	82	53
12999	L11645	Homo sapiens	alpha-tubulin	196	68
13000	AF113685	Homo sapiens	PRO0974	123	52
13001	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	78	53
13002	AJ005564	Mus musculus	SPR2F protein	76	44
13003	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	101	76
13004	AL159178	Streptomyces coelicolor A3(2)	putative secreted protein	89	37
13005	L77967	Ovis aries	small proline-rich protein with paired repeat	64	36
13006	G03243	Homo sapiens	Human secreted protein, SEQ ID NO: 7324.	85	70
13007	AF068294	Homo sapiens	HDCMB45P	237	52
13008	G00382	Homo sapiens	Human secreted protein, SEQ ID NO: 4463.	128	50
13009	AF144054	Homo sapiens	apoptosis related protein APR-4	100	75
13010	G03453	Homo sapiens	Human secreted protein, SEQ ID NO: 7534.	148	67
13011	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	152	66
13012	B01390	Homo sapiens	Neuron-associated protein.	99	32
13013	A27282	Homo sapiens	TGR-CL3C	69	42
13014	G00689	Homo sapiens	Human secreted protein, SEQ ID NO:	135	46

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4770.		
13015	AF130089	Homo sapiens	PRO2550	88	60
13016	AF266223	Gillichthys mirabilis	ribosomal protein L27	122	50
13017	S79410	Mus musculus	nuclear localization signal binding protein	116	40
13018	U82303	Homo sapiens	unknown	64	60
13019	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	70	57
13020	G04078	Homo sapiens	Human secreted protein, SEQ ID NO: 8159.	169	91
13021	V00488	Homo sapiens	alpha globin	213	100
13022	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	146	59
13023	G00381	Homo sapiens	Human secreted protein, SEQ ID NO: 4462.	109	86
13024	G03472	Homo sapiens	Human secreted protein, SEQ ID NO: 7553.	151	84
13025	U82303	Homo sapiens	unknown	86	52
13026	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	124	61
13027	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	83	50
13028	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	74	63
13029	Y84546	Homo sapiens	Amino acid sequence of a fragment of human collagen type 1 protein.	59	46
13030	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	96	68
13031	S71494	Mus sp.	SmD homolog {Gly-Arg repeat}	93	55
13032	AF113685	Homo sapiens	PRO0974	100	48
13033	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	242	85
13034	AL390114	Leishmania major	extremely cysteine/valine rich protein	178	41
13035	G01129	Homo sapiens	Human secreted protein, SEQ ID NO: 5210.	228	81
13036	X66285	Mus musculus	HC1 ORF	103	44
13037	AF026689	Homo sapiens	prostate-specific transglutaminase	90	55
13038	U47924	Homo sapiens	RPL13-2	424	63
13039	AF090942	Homo sapiens	PRO0657	111	44
13040	AK025116	Homo sapiens	unnamed protein product	131	52
13041	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	92	72
13042	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	100	69
13043	AF130089	Homo sapiens	PRO2550	109	45
13044	G02879	Homo sapiens	Human secreted protein, SEQ ID NO: 6960.	116	52
13045	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	162	70
13046	L10908	Mus musculus	Gcap1 gene product	162	40
13047	L02321	Homo sapiens	glutathione S-transferase GSTM5-5	1072	93
13048	Y08062	Homo sapiens	Human PRO245 protein fragment derived from DNA35638.	89	60
13049	G02994	Homo sapiens	Human secreted protein, SEQ ID NO: 7075.	153	60
13050	U33547	Homo sapiens	MHC class II antigen	69	85
13051	AC006014	Homo sapiens	similar to mismatch repair proteins; similar to PID:g1304125	652	91

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13052	A27282	Homo sapiens	TGR-CL3C	65	51
13053	Y69166	Homo sapiens	A mature human N-acetylglucosaminyl transferase protein.	106	60
13054	M20030	Homo sapiens	small proline rich protein	57	33
13055	AF022117	Balaena mysticetus	metallothionein	119	62
13056	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	78	43
13057	R20305	Homo sapiens	Val(1) to Met, His(2) deleted, Ala(76) to Lys beta-globin mutant.	274	98
13058	X55686	Lycopersicon esculentum	extensin (class II)	56	39
13059	U10696	Zea mays	Ec metallothionein class II protein	66	26
13060	Y40417	Homo sapiens	A human N-acetylneuraminate lyase (hNANL) protein.	1183	80
13061	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	125	41
13062	AF002210	Homo sapiens	copper chaperone for superoxide dismutase	702	61
13063	AF118086	Homo sapiens	PRO1992	69	84
13064	M24097	Homo sapiens	MHC HLA-C-alpha-2 chain	1550	96
13065	AC003113	Arabidopsis thaliana	F24O1.6	51	40
13066	AF161531	Homo sapiens	HSPC046	488	97
13067	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	141	50
13068	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	116	46
13069	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	145	69
13070	Y87064	Homo sapiens	Human secreted protein sequence SEQ ID NO:103.	224	71
13071	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	153	52
13072	AF216965	Homo sapiens	ancient conserved domain protein 3	876	100
13073	Y15917	Homo sapiens	COL1A1 and PDGFB fusion transcript	108	35
13074	X77664	Homo sapiens	retinoic acid receptor beta isoform 1	53	71
13075	AF156961	Homo sapiens	gag	136	37
13076	R59842	Homo sapiens	ApoE4L1 protease.	117	75
13077	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	121	65
13078	U23183	Caenorhabditis elegans	gene lies in inverted repeat and exon 1 overlaps tRNA; may be pseudogene	100	79
13079	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	125	56
13080	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	138	65
13081	Y12473	Homo sapiens	centrin	359	79
13082	G01518	Homo sapiens	Human secreted protein, SEQ ID NO: 5599.	375	98
13083	Y57891	Homo sapiens	Human transmembrane protein HTPN-15.	1030	99
13084	AB046765	Homo sapiens	KIAA1545 protein	161	93
13085	X55686	Lycopersicon esculentum	extensin (class II)	66	40
13086	AF130079	Homo sapiens	PRO2852	137	45
13087	K01664	Drosophila melanogaster	Bkm-like protein	86	33
13088	G03812	Homo sapiens	Human secreted protein, SEQ ID NO:	105	44

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7893.		
13089	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	114	63
13090	AL121905	Homo sapiens	dJ534B8.3 (novel protein similar to an aspartic protease)	963	100
13091	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	95	47
13092	AB030236	Canis familiaris	D4 dopamine receptor	65	38
13093	AF161356	Homo sapiens	HSPC093	119	48
13094	Z14014	Nicotiana tabacum	Pistil extensin like protein, partial CDS only	67	50
13095	G01249	Homo sapiens	Human secreted protein, SEQ ID NO: 5330.	124	56
13096	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	159	73
13098	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	62
13099	AF130051	Homo sapiens	PRO0898	194	61
13100	Y86445	Homo sapiens	Human gene 42-encoded protein fragment, SEQ ID NO:360.	80	70
13101	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	111	43
13102	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	120	71
13103	G00333	Homo sapiens	Human secreted protein, SEQ ID NO: 4414.	116	63
13104	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	90	64
13105	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	176	56
13106	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	101	75
13107	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	100	65
13108	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	137	77
13109	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	94	88
13110	AF119855	Homo sapiens	PRO1847	103	49
13111	AF119851	Homo sapiens	PRO1722	142	80
13112	Y00311	Homo sapiens	Human secreted protein encoded by gene 54.	107	51
13113	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	104	54
13114	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	144	71
13115	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	138	50
13116	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	110	56
13117	AK025653	Homo sapiens	unnamed protein product	188	100
13118	AF130089	Homo sapiens	PRO2550	129	68
13119	AF161356	Homo sapiens	HSPC093	131	59
13120	G03798	Homo sapiens	Human secreted protein, SEQ ID NO: 7879.	121	45
13121	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	82	55
13122	G00637	Homo sapiens	Human secreted protein, SEQ ID NO:	87	45

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			4718.		
13123	Y38394	Homo sapiens	Human secreted protein encoded by gene No. 9.	213	100
13124	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	108	55
13125	AF119855	Homo sapiens	PRO1847	109	45
13126	R95913	Homo sapiens	Neural thread protein.	137	47
13127	B01390	Homo sapiens	Neuron-associated protein.	101	47
13128	S75895	Homo sapiens	NADH dehydrogenase subunit 2, ND2	122	67
13129	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	105	52
13130	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	170	72
13131	D38112	Homo sapiens	NADH dehydrogenase subunit 3	500	90
13132	AF138957	Bos taurus	type II collagen cyanogen bromide fragment CB8	99	38
13133	AF084256	Homo sapiens	beta glucuronidase isoform d	157	69
13134	U92817	Homo sapiens	unnamed HERV-H protein	113	48
13135	Y19743	Homo sapiens	SEQ ID NO 461 from WO9922243.	967	99
13136	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	155	52
13137	AF090928	Homo sapiens	PRO0470	133	69
13138	AF090931	Homo sapiens	PRO0483	150	60
13139	AF116661	Homo sapiens	PRO1438	146	57
13140	AL022318	Homo sapiens	bK150C2.2 (Phorbol 3)	443	56
13141	S79410	Mus musculus	nuclear localization signal binding protein	114	80
13142	AF055985	Onchocerca volvulus	pyrrolidone-rich antigen	86	43
13143	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	62
13144	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	146	66
13145	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	123	71
13146	AF107406	Homo sapiens	GW128	120	50
13147	L10908	Mus musculus	Gcap1 gene product	91	42
13148	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	66
13149	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	119	67
13150	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	168	86
13151	G00418	Homo sapiens	Human secreted protein, SEQ ID NO: 4499.	74	58
13152	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	108	61
13153	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	131	67
13154	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	113	54
13155	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	127	84
13156	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	167	80
13157	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	125	68
13158	D38112	Homo sapiens	cytochrome c oxidase subunit 3	514	71
13159	Y86248	Homo sapiens	Human secreted protein HCHPF68,	130	66

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			SEQ ID NO:163.		
13160	AF116661	Homo sapiens	PRO1438	152	63
13161	AB046048	Macaca fascicularis	unnamed poitein product	105	53
13162	AF107406	Homo sapiens	GW128	159	62
13163	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	132	59
13164	M15530	Homo sapiens	B-cell growth factor	97	80
13165	K02576	Homo sapiens	salivary proline-rich protein 1	67	36
13166	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	126	57
13167	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	95	53
13168	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	96	57
13169	AL049795	Homo sapiens	dJ622L5.7.2 (novel protein (isoform 2))	250	95
13170	G00366	Homo sapiens	Human secreted protein, SEQ ID NO: 4447.	116	56
13171	L10908	Mus musculus	Gcap1 gene product	75	53
13172	S73853	Homo sapiens	NF2=neurofibromatosis type 2 {alternatively spliced, form A4}	160	73
13173	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	134	76
13174	A52568	Homo sapiens	HMG1-C	84	44
13175	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	91	49
13176	AK025116	Homo sapiens	unnamed protein product	130	44
13177	AF090901	Homo sapiens	PRO0195	103	84
13178	AF090894	Homo sapiens	PRO0113	92	62
13179	AF130079	Homo sapiens	PRO2852	118	38
13180	AK025047	Homo sapiens	unnamed protein product	141	67
13181	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	87	59
13182	AC003058	Arabidopsis thaliana	unknown protein	220	74
13183	S79980	Bos taurus	ribosomal protein L37	186	94
13184	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	113	90
13185	AF155232	Pisum sativum	extensin	95	36
13187	U16359	Rattus norvegicus	nitric oxide synthase	90	78
13188	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	113	79
13189	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	158	53
13190	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	130	59
13191	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	131	66
13192	D38112	Homo sapiens	NADH dehydrogenase subunit 3	439	86
13193	Z66499	Caenorhabditis elegans	T01B7.8	127	35
13194	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	126	61
13195	Y13141	Bromheadia finlaysoniana	extensin	58	43
13196	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	95	76
13197	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	116	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13198	X58236	Homo sapiens	36/8-8 fusion protein with epitope for anti-lectin antibody	98	41
13199	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	102	58
13200	AF220264	Homo sapiens	MOST-1	141	45
13201	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	112	58
13202	Y17221	Homo sapiens	Human secreted protein (clone fk317-3).	115	57
13203	W50192	Homo sapiens	Amino acid sequence of salivary protein CON-1.	91	39
13204	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	126	65
13205	Y30822	Homo sapiens	Human secreted protein encoded from gene 12.	98	68
13206	M15530	Homo sapiens	B-cell growth factor	105	76
13207	W48927	Homo sapiens	Schwannomin-binding protein C-terminal fragment.	84	45
13208	L27428	Homo sapiens	reverse transcriptase.	205	49
13209	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	77	57
13210	M81321	Macaca fascicularis	proline-rich protein	104	48
13211	X55685	Lycopersicon esculentum	extensin (class I)	122	33
13212	M15530	Homo sapiens	B-cell growth factor	159	61
13213	AF130089	Homo sapiens	PRO2550	126	56
13214	AF210651	Homo sapiens	NAG18	125	68
13215	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	114	76
13216	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	157	70
13217	R59842	Homo sapiens	ApoE4L1 protease.	102	72
13218	K01664	Drosophila melanogaster	Bkm-like protein	123	37
13219	Y02785	Homo sapiens	Human secreted protein encoded by gene 51 clone HUKEX85.	101	55
13220	D14167	Gallus gallus	ribosomal protein L37a	126	40
13221	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	178	82
13222	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	141	55
13223	L10908	Mus musculus	Gcap1 gene product	114	53
13224	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	216	73
13225	G03259	Homo sapiens	Human secreted protein, SEQ ID NO: 7340.	104	76
13226	AF130079	Homo sapiens	PRO2852	158	66
13227	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	125	60
13228	S77772	Homo sapiens	aspartylglucosaminidase, AGA {C-terminal, alternatively spliced} {EC 3.5.1.26}	100	46
13229	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	156	72
13230	M15530	Homo sapiens	B-cell growth factor	162	72
13231	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	161	66
13232	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	80	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13233	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	126	51
13234	AF126163	Homo sapiens	HLA3 protein	131	78
13235	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	125	85
13236	AB001684	Chlorella vulgaris	ORF49b	55	45
13237	M15530	Homo sapiens	B-cell growth factor	114	66
13238	AL355929	Neurospora crassa	conserved hypothetical protein	99	46
13239	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	63
13240	S79410	Mus musculus	nuclear localization signal binding protein	110	40
13241	AF119851	Homo sapiens	PRO1722	167	63
13242	S79410	Mus musculus	nuclear localization signal binding protein	147	68
13243	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	95	65
13244	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	99	84
13245	Y14437	Homo sapiens	Human secreted protein encoded by gene 27 clone HSAWA27.	104	62
13246	AF161356	Homo sapiens	HSPC093	116	67
13247	X61046	Hydra sp.	mini-collagen	108	49
13248	V00662	Homo sapiens	URF 3 (NADH dehydrogenase subunit)	458	89
13249	M11900	Mus musculus	15-kDa proline-rich salivary protein	92	37
13250	AB017362	Bombyx mori	fibroin H-chain	70	43
13251	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	125	58
13252	G00360	Homo sapiens	Human secreted protein, SEQ ID NO: 4441.	122	58
13253	AF210651	Homo sapiens	NAG18	151	73
13254	AF224494	Mus musculus	arsenite inducible RNA associated protein	299	50
13255	AK026107	Homo sapiens	unnamed protein product	102	60
13256	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	113	61
13257	AK024455	Homo sapiens	FLJ00047 protein	115	59
13258	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	155	51
13259	AJ251579	Arabidopsis thaliana	cef protein	115	39
13260	L78671	Homo sapiens	CoxII/D-loop DNA fusion protein	360	82
13261	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	151	61
13262	D38112	Homo sapiens	NADH dehydrogenase subunit 3	413	87
13263	D23661	Homo sapiens	ribosomal protein L37	487	94
13264	AF130079	Homo sapiens	PRO2852	153	43
13265	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	109	61
13266	Y01154	Homo sapiens	Protein sequence Seq Id 54 from WO9901020.	133	79
13267	L10908	Mus musculus	Gcap1 gene product	103	43
13268	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	151	70
13269	G04064	Homo sapiens	Human secreted protein, SEQ ID NO: 8145.	97	51

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13270	AF130089	Homo sapiens	PRO2550	95	47
13271	AF130075	Homo sapiens	PRO2532	90	60
13272	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	103	54
13273	G00403	Homo sapiens	Human secreted protein, SEQ ID NO: 4484.	77	91
13274	AF130089	Homo sapiens	PRO2550	104	57
13275	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	94	45
13276	G02753	Homo sapiens	Human secreted protein, SEQ ID NO: 6834.	122	52
13277	AF113685	Homo sapiens	PRO0974	98	36
13278	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	85	68
13279	G02515	Homo sapiens	Human secreted protein, SEQ ID NO: 6596.	139	89
13280	G01129	Homo sapiens	Human secreted protein, SEQ ID NO: 5210.	243	79
13281	AF116715	Homo sapiens	PRO2829	108	56
13282	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	105	60
13283	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	194	78
13284	AL359782	Trypanosoma brucei	probable granule cell antiserum positive 8	104	47
13285	S79410	Mus musculus	nuclear localization signal binding protein	104	72
13286	AF130089	Homo sapiens	PRO2550	147	58
13287	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	133	58
13288	AF119855	Homo sapiens	PRO1847	115	45
13289	AF161356	Homo sapiens	HSPC093	131	50
13290	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	104	43
13291	K01664	Drosophila melanogaster	Bkm-like protein	112	49
13292	G00377	Homo sapiens	Human secreted protein, SEQ ID NO: 4458.	150	69
13293	M36647	Homo sapiens	mitochondrial hinge protein precursor	284	76
13294	D38112	Homo sapiens	NADH dehydrogenase subunit 3	444	85
13295	D38112	Homo sapiens	cytochrome c oxidase subunit 3	633	93
13296	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	164	76
13297	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	147	80
13298	Y13141	Bromheadia finlaysoniana	extensin	84	38
13299	Y01400	Homo sapiens	Secreted protein encoded by gene 18 clone HNHFO29.	139	49
13300	AF130079	Homo sapiens	PRO2852	98	60
13301	AF090894	Homo sapiens	PRO0113	114	52
13302	AF130079	Homo sapiens	PRO2852	161	83
13303	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	154	76
13304	AF118086	Homo sapiens	PRO1992	120	75
13305	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	100	73
13306	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	108	56

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13307	Y74110	Homo sapiens	Human prostate tumor EST fragment derived protein #297.	448	100
13308	G00588	Homo sapiens	Human secreted protein, SEQ ID NO: 4669.	85	65
13309	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	104	47
13310	AF116715	Homo sapiens	PRO2829	124	76
13311	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	142	63
13312	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	155	61
13313	AF116661	Homo sapiens	PRO1438	142	67
13314	AF161356	Homo sapiens	HSPC093	121	46
13315	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	169	52
13316	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	98	90
13317	AF130079	Homo sapiens	PRO2852	109	58
13318	G01931	Homo sapiens	Human secreted protein, SEQ ID NO: 6012.	113	80
13319	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	81	61
13320	AF130089	Homo sapiens	PRO2550	106	77
13321	AF090931	Homo sapiens	PRO0483	143	63
13322	D29833	Homo sapiens	proline rich peptide P-B	59	33
13323	D38112	Homo sapiens	NADH dehydrogenase subunit 3	417	78
13324	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	119	82
13325	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	168	59
13326	A31038	Nicotiana glauca	PRP3	88	41
13327	AF090895	Homo sapiens	PRO0117	87	55
13328	Y02693	Homo sapiens	Human secreted protein encoded by gene 44 clone HTDAD22.	88	51
13329	G03797	Homo sapiens	Human secreted protein, SEQ ID NO: 7878.	103	66
13330	AL390114	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	101	67
13331	AF090930	Homo sapiens	PRO0478	93	36
13332	AF159055	Homo sapiens	leucine zipper-like protein	118	71
13333	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	89	57
13334	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	121	80
13335	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	160	73
13336	AJ005562	Mus musculus	SPR2D protein	86	44
13337	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	169	66
13338	G00528	Homo sapiens	Human secreted protein, SEQ ID NO: 4609.	78	57
13339	Y08769	Rattus norvegicus	microvascular endothelial differentiation gene 2	102	91
13340	AF090895	Homo sapiens	PRO0117	137	47
13341	K01664	Drosophila melanogaster	Bkm-like protein	115	46
13342	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	100	76
13343	G03714	Homo sapiens	Human secreted protein, SEQ ID NO:	134	65

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			7795.		
13344	AL359782	Trypanosoma brucei	probable similar to ring-h2 finger protein rha1a.	76	76
13345	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	111	72
13346	G00552	Homo sapiens	Human secreted protein, SEQ ID NO: 4633.	143	69
13347	AF119900	Homo sapiens	PRO2822	93	58
13348	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	169	75
13349	W48353	Homo sapiens	Human breast cancer related protein BCFLT2.	83	68
13350	AF116715	Homo sapiens	PRO2829	134	64
13351	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	115	65
13352	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	118	59
13353	Y02887	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	139	77
13354	AF116661	Homo sapiens	PRO1438	112	75
13355	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	170	73
13356	AF126163	Homo sapiens	HHLA3 protein	116	55
13357	U18339	Variola virus	D4L	101	58
13358	AF130089	Homo sapiens	PRO2550	127	52
13359	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	184	82
13360	Y02926	Homo sapiens	Fragment of human secreted protein encoded by gene 101.	78	50
13361	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	126	71
13362	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	174	76
13363	G02872	Homo sapiens	Human secreted protein, SEQ ID NO: 6953.	176	51
13364	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	99	41
13365	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	118	56
13366	U12390	Cloning vector pSport1	beta-galactosidase alpha peptide	158	50
13367	Y19467	Homo sapiens	Amino acid sequence of a human secreted protein.	65	64
13368	M15530	Homo sapiens	B-cell growth factor	132	77
13369	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	119	63
13370	AF130079	Homo sapiens	PRO2852	108	61
13371	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	150	76
13372	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	117	65
13373	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	118	57
13374	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	121	63
13375	AF118086	Homo sapiens	PRO1992	147	74
13376	AF130089	Homo sapiens	PRO2550	149	48
13377	G00637	Homo sapiens	Human secreted protein, SEQ ID NO: 4718.	123	55

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13378	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	120	53
13379	AF090894	Homo sapiens	PRO0113	101	52
13380	AF107406	Homo sapiens	GW128	126	51
13381	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	156	84
13382	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	119	80
13383	Y14437	Homo sapiens	Human secreted protein encoded by gene 27 clone HSAWA27.	84	70
13384	S79410	Mus musculus	nuclear localization signal binding protein	107	53
13385	S79410	Mus musculus	nuclear localization signal binding protein	107	53
13386	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	141	65
13387	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	113	63
13388	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	155	77
13389	AF130089	Homo sapiens	PRO2550	159	62
13390	AF161356	Homo sapiens	HSPC093	154	74
13391	AC006135	Arabidopsis thaliana	putative vicilin storage protein (globulin-like)	171	28
13392	AF113685	Homo sapiens	PRO0974	226	57
13393	AF118082	Homo sapiens	PRO1902	69	68
13394	D23661	Homo sapiens	ribosomal protein L37	498	96
13395	AF130079	Homo sapiens	PRO2852	109	54
13396	AF119851	Homo sapiens	PRO1722	107	57
13397	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	165	68
13398	AF130089	Homo sapiens	PRO2550	145	68
13399	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	134	54
13400	J03798	Homo sapiens	small nuclear riboprotein Sm-D	451	93
13401	D29833	Homo sapiens	proline rich peptide P-B	64	39
13402	R96800	Homo sapiens	Human histiocyte-secreted factor HSF.	99	76
13403	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	159	76
13404	AF090894	Homo sapiens	PRO0113	152	70
13405	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	101	45
13406	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	172	72
13407	G00407	Homo sapiens	Human secreted protein, SEQ ID NO: 4488.	135	84
13408	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	125	63
13409	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	138	58
13410	AF130089	Homo sapiens	PRO2550	101	70
13411	AK024455	Homo sapiens	FLJ00047 protein	112	73
13412	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	145	48
13413	G00328	Homo sapiens	Human secreted protein, SEQ ID NO: 4409.	95	50
13414	AF090942	Homo sapiens	PRO0657	171	72
13415	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	120	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13416	M15530	Homo sapiens	B-cell growth factor	121	45
13417	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	115	58
13418	AF026689	Homo sapiens	prostate-specific transglutaminase	146	70
13419	Y01181	Homo sapiens	Polypeptide fragment encoded by gene 12.	85	64
13420	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	77	73
13421	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	149	62
13422	AF130089	Homo sapiens	PRO2550	111	39
13423	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	106	42
13424	AF119882	Homo sapiens	PRO2492	110	70
13425	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	104	59
13426	AF118082	Homo sapiens	PRO1902	129	48
13427	X70771	Chironomus tentans	Sp17	95	56
13428	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	164	66
13429	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	149	80
13430	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	103	63
13431	AF116661	Homo sapiens	PRO1438	128	54
13432	AK024455	Homo sapiens	FLJ00047 protein	117	69
13433	Y13141	Bromheadia finlaysoniana	extensin	91	40
13434	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	118	64
13435	AF090944	Homo sapiens	PRO0663	115	50
13436	X55687	Lycopersicon esculentum	extensin (class II)	73	32
13437	AF090942	Homo sapiens	PRO0657	77	50
13438	AP000061	Aeropyrum pernix	104aa long hypothetical protein	82	41
13439	G00481	Homo sapiens	Human secreted protein, SEQ ID NO: 4562.	94	51
13440	AF161356	Homo sapiens	HSPC093	115	53
13441	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	125	44
13442	Y59784	Homo sapiens	Human normal ovarian tissue derived protein 61.	1096	100
13443	U33547	Homo sapiens	MHC class II antigen	120	73
13444	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	106	71
13445	W54966	Homo sapiens	Synthetic human type III collagen SYN-C3.	115	34
13446	G02256	Homo sapiens	Human secreted protein, SEQ ID NO: 6337.	486	100
13447	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	155	60
13448	AF130079	Homo sapiens	PRO2852	167	56
13449	AB047890	Macaca fascicularis	hypothetical protein	171	62
13450	AK025326	Homo sapiens	unnamed protein product	111	67
13451	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	93	76

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13452	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	109	91
13453	U65650	Arabidopsis thaliana	blue-copper binding protein III	103	35
13454	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	123	69
13455	AF090894	Homo sapiens	PRO0113	122	56
13456	D38585	Homo sapiens	TSC-22	710	99
13457	Y02999	Homo sapiens	Fragment of human secreted protein encoded by gene 121.	113	45
13458	X55686	Lycopersicon esculentum	extensin (class II)	64	51
13459	AF107406	Homo sapiens	GW128	162	54
13460	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	145	65
13461	X61045	Hydra sp.	mini-collagen	107	34
13462	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	130	46
13463	Y35970	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 219.	189	80
13464	L47668	Homo sapiens	alpha-2 collagen type I	64	39
13465	G02490	Homo sapiens	Human secreted protein, SEQ ID NO: 6571.	155	65
13466	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	159	76
13467	Y14437	Homo sapiens	Human secreted protein encoded by gene 27 clone HSAWA27.	109	70
13468	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	144	69
13469	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	121	39
13470	M15530	Homo sapiens	B-cell growth factor	144	57
13471	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	116	85
13472	V00488	Homo sapiens	alpha globin	704	96
13473	AJ012166	Canis familiaris	brain-specific synapse associated protein, Bassoon	56	45
13474	AF116661	Homo sapiens	PRO1438	128	45
13475	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	99	78
13476	V00488	Homo sapiens	alpha globin	278	91
13477	W65762	Homo sapiens	Human HDCAP protein.	490	98
13478	AB033767	Homo sapiens	brain-selective and closely mapped on the counter allele of CMAP in cystatin cluster	2184	97
13479	AB033767	Homo sapiens	brain-selective and closely mapped on the counter allele of CMAP in cystatin cluster	2184	97
13480	Y42382	Homo sapiens	Amino acid sequence of fx317_11.	613	95
13481	D29833	Homo sapiens	proline rich peptide P-B	61	58
13482	AK023277	Homo sapiens	unnamed protein product	488	98
13483	X67703	Drosophila melanogaster	Mst84Da	53	60
13484	Y27907	Homo sapiens	Human secreted protein encoded by gene No. 119.	135	54
13485	AF210350	Sceloporus siniferus	NADH dehydrogenase subunit 4	149	79
13486	Y14544	Danio rerio	Hoxc8 protein	98	36
13487	AP002032	Arabidopsis		111	27

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
		thaliana			
13488	AB047846	Homo sapiens	gamma1-COP	4463	100
13489	M37194	Rattus norvegicus	clathrin-associated protein 17	739	100
13490	Y59743	Homo sapiens	Human normal ovarian tissue derived protein 20.	138	96
13491	U01317	Homo sapiens	G-gamma globin	198	90
13492	W04180	Homo sapiens	Cellubrevin-1.	459	98
13493	AL121585	Homo sapiens	ba504H3.1 (SNX5 (sorting nexin 5))	2058	100
13494	X53777	Homo sapiens	putative ribosomal protein (AA 1-184)	970	100
13495	AJ271881	Homo sapiens	bromodomain containing protein	3378	99
13496	AF132970	Homo sapiens	CGI-36 protein	878	100
13497	V73498 cd1	Homo sapiens	21-AUG-1997 Human S100P1 DNA.	273	100
13498	AL121585	Homo sapiens	ba504H3.1 (SNX5 (sorting nexin 5))	2058	100
13499	X82456	Homo sapiens	LIM and SH3 domain protein	1420	100
13500	AJ277932	Homo sapiens	RPB1a protein	588	98
13501	Y53569	Homo sapiens	Consensus sequence for human RAD1 binding proteins.	633	84
13502	W73434	Homo sapiens	Human secreted protein encoded by Gene No. 2.	1903	100
13503	AJ005981	Sus scrofa	cAMP-regulated phosphoprotein	577	100
13504	AF116715	Homo sapiens	PRO2829	143	65
13505	U97553	murid herpesvirus 4	unknown	84	35
13506	X06323	Homo sapiens	put. ribosomal protein L3 (AA 1 - 348)	1903	100
13507	W82397	Homo sapiens	Human UBP protein #3.	4264	99
13508	M86246	Homo sapiens	EHS-2	110	71
13509	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	121	50
13510	AF073519	Homo sapiens	small EDRK-rich factor 1, long isoform	91	44
13511	G03812	Homo sapiens	Human secreted protein, SEQ ID NO: 7893.	591	100
13512	Y04369	Homo sapiens	Human HUCEP-14 protein.	1389	100
13513	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	136	60
13514	AE000232	Escherichia coli K12	orf, hypothetical protein	1480	100
13515	X76717	Homo sapiens	MT-11 protein	382	100
13516	Y00919	Homo sapiens	Human Rab protein, RABP-2, protein sequence.	1039	100
13517	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	136	67
13518	AF090895	Homo sapiens	PRO0117	109	56
13519	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	109	65
13520	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	145	71
13521	G00577	Homo sapiens	Human secreted protein, SEQ ID NO: 4658.	93	60
13522	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	140	72
13523	G04072	Homo sapiens	Human secreted protein, SEQ ID NO: 8153.	130	73
13524	M15530	Homo sapiens	B-cell growth factor	112	67
13525	AF119851	Homo sapiens	PRO1722	135	57
13526	G00541	Homo sapiens	Human secreted protein, SEQ ID NO: 4622.	98	82
13527	W48351	Homo sapiens	Human breast cancer related protein BCRB2.	117	41

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13528	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	105	100
13529	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	79	78
13530	AJ000536	Arabidopsis thaliana	COP1 protein	98	32
13531	U50403	Homo sapiens	breast cancer suppressor element Ishmael Upper RP2	101	62
13532	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	156	56
13533	Z80779	Homo sapiens	histone H2B	628	100
13534	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	151	62
13535	M11759	Lycopersicon esculentum	cell wall hydroxyproline-rich glycoprotein	82	63
13536	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	93	56
13537	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683).	139	81
13538	AF130051	Homo sapiens	PRO0898	90	53
13539	X16832	Homo sapiens	preprocathepsin H (AA -22 to 314)	1835	99
13540	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	100	80
13541	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	131	82
13542	G00452	Homo sapiens	Human secreted protein, SEQ ID NO: 4533.	94	65
13543	W88627	Homo sapiens	Secreted protein encoded by gene 94 clone HPMBQ32.	141	86
13544	AF130089	Homo sapiens	PRO2550	107	72
13545	M36647	Homo sapiens	mitochondrial hinge protein precursor	435	89
13546	U63810	Homo sapiens	WD40 protein Ciao 1	505	100
13547	AF090931	Homo sapiens	PRO0483	126	73
13548	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	143	65
13549	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	82	62
13550	AF113685	Homo sapiens	PRO0974	126	48
13551	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	89	53
13552	AF116661	Homo sapiens	PRO1438	109	69
13553	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	101	85
13554	X16832	Homo sapiens	preprocathepsin H (AA -22 to 314)	1835	99
13555	Y73435	Homo sapiens	Human secreted protein clone yd73_1 protein sequence SEQ ID NO:92.	528	84
13556	G00352	Homo sapiens	Human secreted protein, SEQ ID NO: 4433.	126	65
13557	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	103	67
13558	G03093	Homo sapiens	Human secreted protein, SEQ ID NO: 7174.	189	75
13559	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	131	53
13560	AF118086	Homo sapiens	PRO1992	157	71
13561	Y00320	Homo sapiens	Human secreted protein encoded by gene 64.	101	64
13562	AF159055	Homo sapiens	leucine zipper-like protein	119	74

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13563	AF118082	Homo sapiens	PRO1902	83	86
13564	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	234	97
13565	Y59778	Homo sapiens	Human normal ovarian tissue derived protein 55.	66	100
13566	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	103	60
13567	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	152	96
13568	X83703	Homo sapiens	nuclear protein	1633	99
13569	G02473	Homo sapiens	Human secreted protein, SEQ ID NO: 6554.	242	45
13570	G00521	Homo sapiens	Human secreted protein, SEQ ID NO: 4602.	105	90
13571	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	80
13572	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	46
13573	X92744	Homo sapiens	hBD-1	290	83
13574	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	107	68
13575	AF107406	Homo sapiens	GW128	356	100
13576	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	101	48
13577	AF220264	Homo sapiens	MOST-1	95	73
13578	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	129	68
13579	AK024455	Homo sapiens	FLJ00047 protein	81	76
13580	AF130051	Homo sapiens	PRO0898	128	64
13581	AF084256	Homo sapiens	beta glucuronidase isoform d	142	58
13582	AF118082	Homo sapiens	PRO1902	85	51
13583	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	114	52
13584	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	66	54
13585	X52164	Mus musculus	Q300 protein (AA 1-77)	109	64
13586	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	109	77
13587	AF090901	Homo sapiens	PRO0195	114	53
13588	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	95	66
13589	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	117	58
13590	AK000521	Homo sapiens	unnamed protein product	1313	100
13591	AL357374	Homo sapiens	bA353C18.2 (novel protein)	421	100
13592	AL357374	Homo sapiens	bA353C18.2 (novel protein)	421	100
13593	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	139	62
13594	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	103	56
13595	U16359	Rattus norvegicus	nitric oxide synthase	109	76
13596	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	127	88
13597	G00325	Homo sapiens	Human secreted protein, SEQ ID NO: 4406.	275	100
13598	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	108	63
13599	AF116661	Homo sapiens	PRO1438	128	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13600	X55682	Lycopersicon esculentum	extensin (class I)	58	43
13601	X52164	Mus musculus	Q300 protein (AA 1-77)	106	45
13602	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	122	92
13603	AF149419	Oryctolagus cuniculus	eye sodium bicarbonate cotransport protein NBC2	126	75
13604	AJ005567	Mus musculus	SPR21 protein	63	40
13605	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	150	96
13606	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	121	60
13607	G02867	Homo sapiens	Human secreted protein, SEQ ID NO: 6948.	85	60
13608	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	57	35
13609	AF107406	Homo sapiens	GW128	108	42
13610	D82345	Homo sapiens	NB thymosin beta	167	100
13611	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	161	59
13612	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	50
13613	Y32193	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 044150.	490	80
13614	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	115	57
13615	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	124	58
13616	AF119900	Homo sapiens	PRO2822	95	53
13617	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	124	58
13618	S79978	Homo sapiens	prion protein, PrP {octapeptide repeats}	88	42
13619	AF220264	Homo sapiens	MOST-1	130	81
13620	U16359	Rattus norvegicus	nitric oxide synthase	95	65
13621	AL132841	Caenorhabditis elegans	Y15E3A.3	168	85
13622	K01664	Drosophila melanogaster	Bkm-like protein	118	65
13623	M86246	Homo sapiens	EHS-2	100	63
13624	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	104	46
13625	AF067205	Homo sapiens	vesicle transport related protein	198	69
13626	U39529	Echinometa mathaei	bindin	72	47
13627	S79410	Mus musculus	nuclear localization signal binding protein	102	52
13628	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	123	54
13629	K01664	Drosophila melanogaster	Bkm-like protein	113	46
13630	AF161536	Homo sapiens	HSPC051	582	100
13631	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	158	87
13632	AF130089	Homo sapiens	PRO2550	105	66
13633	AF116661	Homo sapiens	PRO1438	116	53
13634	AF116715	Homo sapiens	PRO2829	101	60

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13635	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	139	63
13636	U33547	Homo sapiens	MHC class II antigen	154	79
13637	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	107	75
13638	AF090895	Homo sapiens	PRO0117	87	62
13639	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	131	69
13640	AF026689	Homo sapiens	prostate-specific transglutaminase	128	60
13641	S58722	Homo sapiens	X-linked retinopathy protein (C-terminal, clone XEH.8c)	128	81
13642	AC003058	Arabidopsis thaliana	unknown protein	210	67
13643	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	287	76
13644	Y73483	Homo sapiens	Human secreted protein clone yl18_1 protein sequence SEQ ID NO:188.	376	88
13645	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	130	85
13646	Y87212	Homo sapiens	Human secreted protein sequence SEQ ID NO:251.	423	97
13647	U50403	Homo sapiens	breast cancer suppressor element Ishmael Upper RP2	103	86
13648	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	128	55
13649	X58521	Homo sapiens	nucleoporin p62	2610	98
13650	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	141	69
13651	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	111	81
13652	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	140	60
13653	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	121	46
13654	U13066	Nicotiana glauca	arabinogalactan-protein precursor	92	33
13655	S79410	Mus musculus	nuclear localization signal binding protein	134	50
13656	Y07766	Homo sapiens	Human secreted protein fragment encoded from gene 23.	156	100
13657	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	124	48
13658	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	171	80
13659	AK000017	Homo sapiens	unnamed protein product	611	100
13660	U90446	Mus musculus	RNAse L inhibitor	3100	99
13661	AE000882	Methanothermobacter thermoautotrophicus	phosphoenolpyruvate synthase	88	38
13662	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	65
13663	K01664	Drosophila melanogaster	Bkm-like protein	97	34
13664	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	77	41
13665	Y94890	Homo sapiens	Human protein clone HP02798.	325	98
13666	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	65
13667	AF090930	Homo sapiens	PRO0478	119	88
13668	AF130089	Homo sapiens	PRO2550	120	77

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13669	AC006693	Caenorhabditis elegans	Hypothetical protein W02H5.e	165	85
13670	W80293	Homo sapiens	Human translocation associated protein designated Gp25L-H.	1003	95
13671	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	113	91
13672	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	160	60
13673	AL132841	Caenorhabditis elegans	Y15E3A.3	178	75
13674	AF118086	Homo sapiens	PRO1992	85	75
13675	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	132	55
13676	AF220264	Homo sapiens	MOST-1	133	85
13677	Y19730	Homo sapiens	SEQ ID NO 448 from WO9922243.	122	51
13678	Y65416	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1577.	467	98
13679	Y16589	Homo sapiens	A protein that interacts with presenilins.	2286	99
13680	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	104	52
13681	AF090931	Homo sapiens	PRO0483	117	67
13682	X55686	Lycopersicon esculentum	extensin (class II)	60	56
13683	AF090944	Homo sapiens	PRO0663	93	90
13684	AL096770	Homo sapiens	bA150A6.2 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein (hs6M1-21))	178	52
13685	AF116661	Homo sapiens	PRO1438	115	60
13686	U62039	Elephantulus edwardii	reverse transcriptase	86	53
13687	Y13141	Bromheadia finlaysoniana	extensin	77	36
13688	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	114	60
13689	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	103	53
13690	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	107	51
13691	AC003058	Arabidopsis thaliana	unknown protein	178	85
13692	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	94	35
13693	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	143	78
13694	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	98	50
13695	D63163	Rattus sp.	cyclin C	111	86
13696	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	118	95
13697	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	124	80
13698	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	129	70
13699	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	93	58
13700	W48353	Homo sapiens	Human breast cancer related protein BCFLT2.	100	73
13701	M76744	Homo sapiens	BGP	112	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13702	Y15155	Homo sapiens	phosphorylase kinase beta-subunit	206	100
13703	AF090901	Homo sapiens	PRO0195	100	70
13704	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	131	79
13705	R95913	Homo sapiens	Neural thread protein.	106	36
13706	M15073	Homo sapiens	MHC HLA-DR-beta-1 chain	74	77
13707	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	110	35
13708	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	150	56
13709	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	89	77
13710	X70775	Chironomus cingulatus	Sp12 gene homologue	85	38
13711	X80265	Hordeum vulgare	structural protein	96	41
13712	AB007922	Homo sapiens	KIAA0453 protein	147	64
13713	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	124	60
13714	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	108	65
13715	AF116661	Homo sapiens	PRO1438	120	77
13716	AF118086	Homo sapiens	PRO1992	127	64
13717	AK024455	Homo sapiens	FLJ00047 protein	93	56
13718	AF116661	Homo sapiens	PRO1438	137	55
13719	W48352	Homo sapiens	Human breast cancer related protein BCFLT1.	93	59
13720	AF119851	Homo sapiens	PRO1722	94	58
13721	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	124	45
13722	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	117	58
13723	AF161361	Homo sapiens	HSPC098	115	50
13724	Y95829	Homo sapiens	Native human Tie receptor signal peptide.	108	100
13725	AF118086	Homo sapiens	PRO1992	166	75
13726	AF116636	Homo sapiens	PRO1488	95	70
13727	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	70
13728	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	60
13730	G00673	Homo sapiens	Human secreted protein, SEQ ID NO: 4754.	118	63
13731	U33547	Homo sapiens	MHC class II antigen	123	69
13732	R59843	Homo sapiens	ApoE4Lx2 protease.	135	88
13733	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	138	75
13734	AF026204	Caenorhabditis elegans	C30E1.1 gene product	102	51
13735	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	117	63
13736	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	112	87
13737	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	115	58
13738	AF130089	Homo sapiens	PRO2550	122	70
13739	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	124	74
13740	AF130051	Homo sapiens	PRO0898	85	70

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13741	AF093748	Homo sapiens	KH type splicing regulatory protein; KSRP	91	51
13742	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	150	77
13743	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	124	82
13744	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	91	48
13745	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	116	64
13746	AB001684	Chlorella vulgaris	ORF54d	70	66
13747	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	140	60
13748	AF090901	Homo sapiens	PRO0195	92	39
13749	AF090895	Homo sapiens	PRO0117	148	67
13750	AF119882	Homo sapiens	PRO2492	91	45
13751	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	60
13752	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	129	65
13753	AF161356	Homo sapiens	HSPC093	99	48
13754	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	124	70
13755	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	120	51
13756	AF130089	Homo sapiens	PRO2550	142	96
13757	AF130089	Homo sapiens	PRO2550	132	86
13758	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	163	50
13759	Y19609	Homo sapiens	SEQ ID NO 327 from WO9922243.	92	60
13760	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	154	52
13761	U62040	Elephantulus edwardii	reverse transcriptase	134	51
13762	AB001684	Chlorella vulgaris	ORF49b	100	45
13763	AF118082	Homo sapiens	PRO1902	129	50
13764	AF220264	Homo sapiens	MOST-1	129	66
13765	R59842	Homo sapiens	ApoE4L1 protease.	135	50
13766	AF220264	Homo sapiens	MOST-1	115	71
13767	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	139	73
13768	AF130089	Homo sapiens	PRO2550	97	34
13769	U80739	Homo sapiens	CAGH26	564	100
13770	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	128	55
13771	R10755	Homo sapiens	Non-A non-B hepatitis specific antigenic protein encoded by phageclone lambda HC2533.	102	68
13772	AE004507	Pseudomonas aeruginosa	hypothetical protein of bacteriophage Pfl	93	44
13773	AB044885	Canis familiaris	dopamine receptor D4	78	52
13774	AF026246	Homo sapiens	HERV-E envelope glycoprotein	108	53
13775	S71805	Homo sapiens	RNA-binding protein=TLS/FUS-ERG	126	100
13776	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	156	82
13777	AB015727	Mus musculus	truncated granzyme M	86	37
13778	G02832	Homo sapiens	Human secreted protein, SEQ ID NO:	74	52

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
			6913.		
13779	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	137	61
13780	M14123	Homo sapiens	neutral protease large subunit	246	55
13781	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	99	67
13782	AF132972	Homo sapiens	CGI-38 protein	902	99
13783	G02469	Homo sapiens	Human secreted protein, SEQ ID NO: 6550.	147	63
13784	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	128	68
13785	AF130051	Homo sapiens	PRO0898	138	72
13786	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	95
13787	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	92	53
13788	U12206	Homo sapiens	unknown	84	42
13789	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	118	58
13790	S79410	Mus musculus	nuclear localization signal binding protein	102	50
13791	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	137	76
13792	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	104	72
13793	AB006006	Bos taurus	neurocalcin alpha	1000	100
13794	U63332	Homo sapiens	super cysteine rich protein; SCRP	183	95
13795	W34499	Homo sapiens	Obesity receptor C protein.	120	85
13796	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear <i>ma</i> -binding protein)	127	67
13797	U41038	Caenorhabditis elegans	Similar to cadherin-type repeat	182	83
13798	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	112	71
13799	U63332	Homo sapiens	super cysteine rich protein; SCRP	91	84
13800	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	105	67
13801	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	154	72
13802	AF119900	Homo sapiens	PRO2822	131	50
13803	AK024435	Homo sapiens	FLJ00025 protein	117	95
13804	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	142	53
13805	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	48
13806	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	98	66
13807	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	98	66
13808	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	150	54
13809	M37679	Mus musculus	Ig heavy chain precursor	70	100
13810	AL451015	Neurospora crassa	putative protein	96	55
13811	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	88	77
13812	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	128	71

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13813	AF130089	Homo sapiens	PRO2550	93	75
13814	K01664	Drosophila melanogaster	Bkm-like protein	119	60
13815	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	64
13816	AJ011435	Blackstonia imperfoliata	maturase	93	48
13817	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	130	76
13818	AF119851	Homo sapiens	PRO1722	141	50
13819	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	74	60
13820	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	76	72
13821	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	135	50
13822	K01664	Drosophila melanogaster	Bkm-like protein	95	52
13823	L10908	Mus musculus	Gcap1 gene product	103	50
13824	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	146	62
13825	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	125	83
13826	L10908	Mus musculus	Gcap1 gene product	96	43
13827	G02971	Homo sapiens	Human secreted protein, SEQ ID NO: 7052.	102	64
13828	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	135	53
13829	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	142	70
13831	AP000060	Aeropyrum pernix	101aa long hypothetical protein	79	50
13832	AF119900	Homo sapiens	PRO2822	94	46
13833	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	145	40
13834	AF218028	Homo sapiens	unknown	117	57
13835	L10908	Mus musculus	Gcap1 gene product	79	45
13836	Z26876	Homo sapiens	ribosomal protein	129	93
13837	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	124	76
13838	AF044311	Homo sapiens	gamma-synuclein	603	99
13839	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	100	82
13840	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	154	46
13841	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	64
13842	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	92	62
13843	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear ma-binding protein)	93	60
13844	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	63
13845	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	145	79
13846	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	102	50
13847	G03469	Homo sapiens	Human secreted protein, SEQ ID NO: 7550.	101	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13848	G03240	Homo sapiens	Human secreted protein, SEQ ID NO: 7321.	107	43
13849	U05313	Trypanosoma brucei	CR3	98	40
13850	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	100	65
13851	AF159055	Homo sapiens	leucine zipper-like protein	103	55
13852	R59842	Homo sapiens	ApoE4L1 protease.	99	71
13853	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	142	65
13854	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	119	79
13855	R59842	Homo sapiens	ApoE4L1 protease.	93	69
13856	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	114	76
13857	W48353	Homo sapiens	Human breast cancer related protein BCFLT2.	94	57
13858	U63332	Homo sapiens	super cysteine rich protein; SCRP	105	58
13859	AF289022	Homo sapiens	formiminotransferase cyclodeaminase form C	467	100
13860	AF078844	Homo sapiens	hqp0376 protein	488	100
13861	AB032436	Homo sapiens	brain-specific Na-dependent inorganic phosphate cotransporter	2968	100
13862	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	91	72
13863	AF130079	Homo sapiens	PRO2852	131	63
13864	Z29701_cd1	Homo sapiens	29-MAY-1998 Wild-type human c-Src tyrosine kinase cDNA.	2380	100
13865	L77967	Ovis aries	small proline-rich protein with paired repeat	80	33
13866	AL050318	Homo sapiens	dJ977B1.5 (myosin regulatory light chain 2, smooth muscle isoform)	904	100
13867	U37690	Homo sapiens	RNA polymerase II subunit	358	100
13868	X13923	Homo sapiens	cytochrome c oxidase subunit VIb (AA 1-86)	491	100
13869	L13848	Homo sapiens	RNA helicase A	6669	99
13870	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	133	46
13871	K02064	Bos taurus	cytochrome c oxidase subunit IV precursor EC 1.9.3.1	96	72
13872	D31763	Homo sapiens	ha0946 protein is Kruppel-related.	4606	96
13873	Z14014	Nicotiana tabacum	Pistil extensin like protein, partial CDS only	83	43
13874	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	117	70
13875	Z52203_cd1	Homo sapiens	17-SEP-1998 Human PRO217 protein encoding cDNA, UNQ191.	2135	99
13876	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	106	64
13877	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	143	50
13878	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	104	60
13879	L25404	Brassica napus	cyclin	124	42
13880	AL390114	Leishmania major	extremely cysteine/valine rich protein	139	59
13881	AC003113	Arabidopsis thaliana	F24O1.6	70	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13882	AB000098	Rattus norvegicus	MIPP65	905	50
13883	Z95114	Homo sapiens	bK212A2.1 (TNF-inducible protein CG12-1 (similar to apolipoprotein L))	1639	100
13884	AF132984	Homo sapiens	Nuclear pore complex interacting protein NPIP	551	82
13885	AF121862	Homo sapiens	Sorting nexin 13	1453	99
13886	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	83	69
13887	K01664	Drosophila melanogaster	Bkm-like protein	109	77
13888	AF217197	Homo sapiens	FBP interacting repressor	2725	99
13889	D38112	Homo sapiens	NADH dehydrogenase subunit 6	187	94
13890	AF118086	Homo sapiens	PRO1992	85	62
13891	M58664	Homo sapiens	Signal transducer CD24	371	97
13892	AK023443	Homo sapiens	Unnamed protein product	125	45
13893	AB040972	Homo sapiens	KIAA1539 protein	2271	99
13894	U03750	Escherichia coli	DeaD	95	48
13895	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	73	53
13896	AF078851	Homo sapiens	Secretogranin III	2384	99
13897	U62039	Elephantulus edwardii	Reverse transcriptase	109	48
13898	X07816	Human herpesvirus 4	Epitope CI3 (57 AA)	55	53
13899	AF116661	Homo sapiens	PRO1438	146	48
13900	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	77	60
13901	Y28643	Homo sapiens	Human serine protease inhibitor from cDNA clone HETDK50.	2191	100

TABLE 3

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1	13902	A	1	114	434	AI PKC VEGMFRIAMVNVCVSSGSLLY* PLTY/GVYDEWTHFAYMTIDLEIPITG SHPVVLNALFCLRAP/WISFNTGSFAYP VYPKSLIAHDFAVEATMPYIRLSST
2	13903	A	2	124	466	KSNIPNLGDCGWESLFNR/QSWRSSLA V\NDYSSKKSNAETFTFHADLCTLS DKDRPITITQTALAEVLKHKPKATYEQ LIAVLDEF/ANFLKKWKAYDKENLFCE EG*KLCAASN
3	13904	A	4	1	427	EGFLELLRTRNHSNSQLQTTGIGLFLN EGLKLVDFLEDV*K*YHSETFTVNFSD TE*AMKHINDYVEKGTQKIVDLVKELD RDTVFEDLANYIFFKGGKWRPFRVNDTE EEDFHVDQVSTVNEPIMKLLS\MLNIHPC FKL
4	13905	A	5	1	464	KIKSFYASKDTIKRMRTDWWKIFAY*I SDKELIFTLRLTKT**K*GKQPNLKNQ EI*VPISPDQIQAHK\HLEGWSTSLVS ELAPCEAPV/RHPLTGLTIAGLQGFGEA GRLVRGRWGC*W/VHPP*KYI/WQFLSK LHISLPYDPTTPLLGTCSR
5	13906	A	6	308	3	HFVIHSHKDLAIAHLGIY/PREMKT*VH TKTCT*IFTVALSVIARAWNQPGRPLCS BWL\KYMVHTME*HSAIKRLNYRYKNNC VNLEFLGITLSEKSTQTVNI
6	13907	A	7	587	2	FLTRETGDPTGRSSSHANTQSRFFPDDP PG\PLNNLGNTHGCGRRAGRCPTGPDG P\AGCGGPRCWPSGHLAATGD*GPS CGRLGANRGEAGPAGFTACSPLSGCRT PYTHHFPASRMSCHLNCASPRTYRSQGN RGCE RVAQGSQAGGERGAKSQVFPVPA PARNK DPAKCRKPRNRRPGNSGPVVR AYRRQR
7	13908	A	8	1	474	RI LNEEHGKYEGLHE*EVKWHLYIKSPA FTDLHLCYQKDMNGISTSSAPVGTVG MDMDEDDDFSKWNFYSPHSYDPK*LT IFKTESRVRESDEVTOIKVNWDEEVI SGL L TSLKDNVLKATGVLYDYAYK\Y LCEHT RSTLKEESLKLERNLQNH
8	13909	A	9	3	539	SQCSFPFISPA CSLTALEETEALRVH R LCLSPNLAPSSGPPRPPELAPCPPSS QA GLRTCHSWVKGLHQPLFVAGMKST FCN KTYTCPPPPP/PPLCPNHSPNAL TLPDS VTHAVPFE/L*SPSAPPSSTA* ILGSFS \CGASPCNHPSHPGICPTPP GLWPVCP CAPRAWQRDGTQGT
9	13910	A	10	2	453	RL*LGLEYALLVWGTPKV*H*GGFP PIYY YIVLLLSYALHQVTEYSMYVS IMAFNAK VSDPLIVGTYMTLLNTVSN LIGNWPSTV SLWLVNPLTVKECV*TS YQNCCTPDAAE LCKKLGSGCVTALD GYVYESIICVSI AF V/W*VFLVHKFK
10	13911	A	11	20	475	KMGVPPLLMSDPNRFLLPKNFLREK TIS PPKTF*PLKIWVGQWVNLFLGFP PGFKI FFPVFKFFFFFFFFFF/RDRV SLYHPGWSA VSQSELTAALTSEGS GDQVILPSQPPK* ENHLNLGGRGCSE PRLPRAEFLDLRSFS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IIIVIFP
11	13912	A	12	392	63	HIRADPGLEPRPSARTGLGPELGCTMN KLG DAGSATSLSGGSQSLWSLRRREQBL EQARWEAQ*QVETLGRVAREKEALAKBH AGLAVQLAA\ABHEGRTVSEBATHLQ
12	13913	A	13	18	338	APHPOYLQMPMLLPRTGPGQPSLPS RHGGHLE/GKEHETSVTLCGGEPPTPT PRDPDPGP*ARRAPCPRRPT*AHPRALS RAAPQEPRALAGPRARHPICPGSL
13	13914	A	14	2	371	TTKQ*KDNPIQTGAKDLKRHFCKEDMQM ASNHT\KRSLSLVSREMIKTKRMAGI KKSNDNNKH*GRGEIRT/LLRCWWDCKV VQLLWKTWQFL*GLYQYIPHDPIVISRL GISLILYIALRTF
14	13915	A	15	443	1	SRTFLDTDMKSMRGFKAS*NRQTLLGA NAAGD\KLKAMLTNHSNRKILQNYVKC TLPMLYKWNKAWMTAYLFTTQCTEYFK PTVETHCSEKKISF\KILLTIYNAPGHL RALMQIYKEIHVVFPVNPISILQPIVQ NVISTFKS
15	13916	A	16	375	38	HQONGFLKKTDPDLLCLQETHFR/CKDT KRLKVRRY/QPNSNQKRAR/VPILIEDK IDFKTKKIFMMIKDLTIINI*ASNTRVP KSMKQKLAGLKEENDNSVIMVGGFSYPV SIRK
16	13917	A	17	448	189	NRDRVSLCCPGWS*TPGLKRSFHLGLPK CWDYRRDIY*LL\FARHTQMISTHS*QT TNTCSYPAF*KSRP*EPGYNTTHTPHSS DML
17	13918	A	18	1	426	GMSHHARSLIINQLFKKCTLFVL/REM QIKSLLASSSSSSSRNSVSGQGFETVGT HCGQKCKLVQPP\WKAVW*YLLKLVFI LFLIYNRNAHLEDTCENVDRALFVIVKN WKLKSKYPGVKWKIKLWYSHSVESSTAV LPKV
18	13919	A	19	2	423	YFETFQPLRLRLGYQGTFFFP/KPWSSC LGIEYNSSGPDSCA*FFLQNIQLVNSAN IRLMAMTLKTNQVAIAQFLECKESDQOF CIGVTHVKARTGWA*F*SAQGCDDLQNL QNVITQ/GAKIPLVV*GDFNARPTQEA*K HF
19	13920	A	20	10	443	LRVDSGDSEVRYVFILOHITLLMCSAYM NQLLNIFVRPSLLAVALHMTPGFTKEDV YSCFRFLRDVFADEFIFLPGNTL*DFEE SCYLLCKSEAIQVTTKDILFTEKNTVL *FLVGLFKPF/VBSYHIICKSLLDK*A PFIEEP
20	13921	A	21	11	426	VLVETNNLRMGQVTM*PELPDM/SPDAW TLDSPSPQKIGHAQ\KYSIIKWKWYTE DWAQACLEDTSKYEQVTQIPMAFNDATL /PSS/AHLAFTAS*GAPSDS*LRLTLGL ICDGST/KPSSIN*KQTVIALQSHAGLN MKEC
21	13922	A	22	1147	1768	QLGMSHGYSKSMPOKLMCFLNHHLQK GHECLPKVLNSNPPPIIKYLAQDLMLL SQSPSRREQEVFSLSQPGGHPHNWTAIS RECLNLLNGMTQKLILYQEAATNGRVS SSYPVEPKKLNSPEETAFTQPKSSQMPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PSVPPLVKTSLSFSSKLSTPDVVSFPGT PGSSVMNRMAGIFDVNTCYGS*AT*HSE W\LLNLSLLYHVWLCGVFLLTTWYVSWI LFKIYATKAHVFPVQPPFAEGS*VPSKS VK*QSSP\LIKYLALQDLMLLSQYSPSR RQEVFSLSQPGGHPHNWTAISRECLNLL NGMTQKLILLYQEAATNGRVSSSYVPEP KKLNSPEETAFTQPKSSQMPRPSVPPLV KTSLSFSSKLSTPDVVSFPGT*PGSSVMN RMAGIFDVNTCYGSPQSPQLIRRGPRLW TSAS
22	13923	A	23	421	3	KIIFRAFKG*KSPSPMGFKA*KDRLLIL LGTNADNDFKRKPM/LLYHSKNPRALKN YIKSIQPLYE*KKA*MTAHLKVVWTEY FKPIVGTYC*KI/SFKILLNDDAPG\H PKALIMYREINIFMSANTLFILOPMEK GVI
23	13924	A	24	226	2	THERTHSKIIHVIIKITHPLNPSILRP QTTA*IKWRDLGSLQPLP/PG/LKRFSY LILPSSWDYRCPLRPANFCIF
24	13925	A	25	2	611	FFFFLLGLLHQIPDVSPGKYTTLLPL MIILMISGIKEVIY/DHK*HGRQNS/VR NTKLL*QDSWDTFKWKEVNVGDTVKASN GELLPADTVPMC\YLATSNPDRETN/VK TRQALPETASV
25	13926	A	26	1	443	ATQWRPGLVPASAENVKARSFAAGIHA LGGTNINDAMLMAVQLLDSINQDELVT* GSVLLIILLTDGEPTAWETNLMSIQNNV REAVRGRYSLFCLGLGFDVCYAFLEKLA LDNGGLARRIHEDSDSALHMQDFY/QEV AHLPLVTAV
26	13927	A	27	2	359	KAQSKQWLPRGGSGPVK/ARVDEESAKV IVRVYWEAQGILLIDFLKGQRRTIYAYS ENILRKPEL**RNAWGSFSRVLHHDRA AHFSHQ/TRAIG/RBF**KTIRHPHY/S PNLNPLDAFCF
27	13928	A	28	2	427	WRKTVRGHFTDQCRKHKAM/LGN*THEL EYHIHKHSIQYSGIQATQEKFGGLKTSY CSKD*YITVLDLTLKISNKDVSN*HENP ISMYKN/IPTVIYGSVKIKDRKLKA*I* CP/HRNKKF*YFDYFVLLNTMTFLKLW RIITEI
28	13929	A	29	47	412	HCDVLLASSRYTCILPYSDDDDGPDQQL KMSVDFRSRRTGS/WFPQNSWGHMVGCG WGGAGRTLDIHLRIPMRGLRSGGFLCR RKLVSSESYG*EPSPL*K*KGGWGSEPS/ LTTVPSQL
29	13930	A	30	336	419	RLCSGMISAYCNLSLPLGSDPSNSASR
30	13931	A	32	1	408	KIALKLRSNYSKISGY/MANIQKLIIFL YTSNEQIEFEIKNTIPTFLAPPKIK*IG TNLTKC/VQELYEKIYKSVMKNIKELNK WRSSYGGKSKIKIKINK*MDIACSWL RRLKIVKISVLHNLIRFNIVPIEIP
31	13932	A	33	412	2	QGHLSLQKFL\LPFVQLCPAPRGGVYRG RQDSLSCGGLHPF*ASGLLCLPTQASAM VGTPPFASLLLCSSILDCCASNERGVS VEPPEPGTGHNLLVCRLLRPLEKRSIRW KSAVGVARFSRCRPSWLPLARKKNSP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
32	13933	A	35	304	33	KVWGEKVWYQKMTQIVQWDRTESPQID N*SLTKEIQWRKDSLEFNK*GNNWTAPF SS/RSLNLNKDLTAVTKIKSKWVTDLNV KHKTIKLL
33	13934	A	36	2	424	SKTYSIGHFTYEGKGTITSLWGKVNVED AVGETLGRLLVEYPTQRFDDSPGKLSS ASAIMGNPFVKAHGLKGLTSLGDALQHL DDLKG\TFAQLTELHCDKLHVDPENFFL LG*VLVTVLALHF/SRRFTP/ELQAS/W PKM
34	13935	A	37	2	433	NKRLPGPGF*KRPNPPGEGGPARYFNPL GGPNREIPLGPEV*THFGPQMRPVPFLK ILKISGAFWGPVGPPTWGG*EGLNPRG PGYN*P/R/PPAPPWG*SQAPFPKPAP PP/TGIKPNP
35	13936	A	38	3	425	GAAQLLPVSLPSAQRAIDLQILTFPWN WTSIASLQHKTTIGRSWLITGPISATSS TPTSCTVASE\TRGHV*RSASWKYDVLQ HSSHMWVHTAVYLGEAFHQVHATGSCH HRVLSCCPITGRSGRDAL*QLLPL/HAL TEA
36	13937	A	39	2	463	LNEVRDIXLSSDHWPSKINSFLHSPGFL SRFBPQPASVA/PRP*SQQQSLPGKAST SLWPNPVPFVTSSLSLSALPGLFLWLP SIPPLPGSPFFSP*PEVPLPGPTYHN PSPPD/PTVLEAHPDQAPLP/PGVPTAE QRTPAP*AHRRPS/LPLPP
37	13938	A	40	223	408	RNTV*NIGTDKDFMT*TPQAIATKAQID KWNLEPMSFC/TYRETIIGVTDTRYTRD KIFESGR
38	13939	A	41	3	427	NLKMKSRTSKENIGEHIYDFDIGRFVNT *SKPERKLSFKTSVQKTP*L*GKHK* MKLEP/LPYPKINSKWIKDNVRSKAIKL LEENRSESSIWQRL/SIMPKAQAIKEK VDNLDFFKIKNCVSKDTIKKALDRPSE EKI
39	13940	A	42	30	448	FEMREIIVAFHSILIRYHGLINLRKFQ* MDRRYSKEVQDLETKLFARIVGPL*H DKFIESHALEFELLREIKRLQSYRTAGI TNFCSARTYDHLKKTR*EERLKRMTLSE VLQYIQDSNACQWLRRETY\IESGPNP
40	13941	A	43	1	928	LRQRMPPQGLQPCPWPYP/PSPLGC PGGLA\PPNSPSWPKLASLAGSRGSSAP PGVWGLVATGA*PLQRPSPAPPCPR/LC PGREPCMCP
41	13942	A	44	2	409	SKSPDPTQQPLRGSLTHSAPGPSLSQP LAQLTPPAFGPSTSSLFNLQKSSLSARH PQRKRGGPSEPTPGSRPQDATVHPACQ IFPHYTP\VWHILGPQRHTP*SVD/HPG LDRLLPETPGPCYSNSQPVWLCLTP
42	13943	A	45	3	136	LPMTLFTLE*ATLRFIWNHITQIAKA ILINQK/NKARGITNIC
43	13944	A	46	365	2	AWGSLRAPRSAPVPEPGTPPVMGNALHR QFSPCLDGLSCPSFLRG*NSPPHPGSPG LPKHA*APAAVSPWVDPDRTVQPPPPAP PST\D*PHCSPPCTPWCPRRLGSAPVMP GCPTASYPRR
44	13945	A	47	1	456	AELSELYEESDLQMDVMPGEGDLPKW\

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						EEATGTRAAIPWVPATGAQQLLEEGPM EE\BEAQPMAAPEGKRSLANGPNAGEQP GQPSPGRRTSRAEDEA\BEPDDWEDDYD F\PREEPVKGARLRFLPPS*KTPPSFWE NRNTPWGGGLKIFY
45	13946	A	48	116	442	PQNMGMERKPGPPKGLSWAGDLEDNLG VMSVGFLLLSPDDAVIWRGPRKTGLIKQ FLRNGTGKVDYFMGDTQLGTSDHLSS VATWAKAHLGEPGAFTFPQVRSLRE
46	13947	A	49	434	3	FTVPGLLTVPITPISKVPFKFSLQIF NFTPFQFPFQIRV*TIIPISLRFRPKKP LFFFF*NKVPLCSPYWNISARSWVPAAS VFQV\KESFYLNLLSVPPQVPLNVFLTF FFFFFLGRDR/SLPLLPRMVWNSWAQAI LPLWL
47	13948	A	50	1	482	EKPYQCSDFGKAFNMKTQ\LVVHQGVHT GNNPYQCRECGKAFGRKEQLTAHLIAHA R*KPYGCSECGKAFSSKSYLVIHRRHT GERPYECSSCDRAFCGKSQLIHQITHS TENHYECNECENTYPRKASLKIHQKIDL GKKPF/ECNEWGKALLK
48	13949	A	51	1	470	REFLWQEGHRAFATVDEAGEEVLQILD YADVYELLAIIPVANGTKTDKDLAGGD YTATIEAFICASGRAIQGGTSHLLGQNF SAMSEIVLEDPEIPGENQPAYANSWGLT TRTTWVMTIGHGDNMGL/LLTPRVA*VQ /MVIIPGGIPKAFLKRQKT
49	13950	A	52	26	448	SPGTEREYRIGQQSVTGVTSVDDNSY RIRGKSATVCERGTPIK*GQPIRLTHVN TGRNLHSHHFTSPLYGN/QVAL*GDIVI IL*RRKQRLKGFTTEGIKLRFKEVSFG DEGEDYLDWTVLCNGPYWVRDGEVRF NT
50	13951	A	53	3	495	AMEVKAFATHIRGFTLNDAANSRLIIT QVRRHYLKEAATTLKTVLDHQHTPSRLA VTRVIQALAMKGDV/DNI*VFHKMLNGL EDSIGLSKMDFINNIALAQI*NSNLDAS V*HIENMLTS*NNVIEPQYFGSAYLFRQ VLEEQLEPTVEKISIMAERLAKPLQ
51	13952	A	55	1	428	QERGTTKEMEDRMTLEETK\EQILKLEE KL*ALQEEKHQLFLQLKKVLHEEERRR KEQSDLTTLTSAAYQOSLTVHTGTHLLS VQGSPPGHNRPGLMAADRAKQMYGPQV LTTRRYVGIAAAFAGTPEHGQFQGRPGG VYG
52	13953	A	56	2	453	EDGDLDAFSSDEGLTMAMSYLKDDIFRI YITETOECRRYHRPPCAQEPACNMVHP VICYGCYGPVGTRYTCVCPDYDLSSS CKGKGLHRGHTKLAPPSFGHLSEGFH SRWLRNVKHGLLRWS*WEMGPPGNWSPR TSCA/GEARLGP
53	13954	A	57	3	435	ELNTSIFRSRPIEGLGLNTVLTNDNSNL VI\NRIGIV\PSVTEKEYTDPSSDGTYA WKIPSHETITKAQILKFLSYDYAVNNP WLAYPHYKSPKCPSSIILHDLRYLNLGL *CAASAMVMAIVTYNVALLAYHRWNGL TYMID
54	13955	A	59	409	1	LCCEHRGKTVCPVRGKFTTLNASINKER

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SKISVLSFRLMKLKKEYVK*K*\EKEKINNRIEIKINKAKS/WFL*HNKIE*TIRMINHOKRENIQITDFRNERTELPPDSTD IKKAIRKY*K*FYFNFYFYNPEEMNKF
55	13956	A	60	1	393	GNVSSCGDHPCEG*LCP\BDKVMs*GI*VPEEACTQCIGEDGVHHQFLESWVPDHPCHICTSLNGRKDNCTTQTCPTGKASTGLCELARLRQADQCCPENECVCDPESCDLPPVPN*ERGLQSTLTNP
56	13957	A	61	250	1	REDCKRVLYKDKVSLCCAGPCsVA*SCLKAASFQ\VKHFSLOSSWYRHAPPGLANFFHFLQRQVLTTPPGLVLSWVHAI
57	13958	A	62	365	3	IKKKLIWRLFTFPKPSWGKTKKGIPFP*GPKKIPGKIFPQGIKKAFFGNR*TLGKGN*KKKKKKKECGPGGDIPCS*IG/RNIVKILIIIPKAIYSFNTIHIKIPKTFTEIETTILKFL*NH
58	13959	A	63	245	558	FLPTQVISYVKRALAEGAQI*CGEGVDKLSLPARNQAGYFMLPTEITDIKDESCCTEELFGPMTCDVPFDSEEDVIERANNVYGLAATVW/SSNVARV
59	13960	A	64	106	532	ERACQSGTSGGGVPRRAIGAPR/E/DAFTGAVYIYHGDAGGIVPQYSMHPFA*SLYPSGQ/SVAARGNLSGDSFNCHN*GLQG LLLASSV*RPVMLLNDPIIYTTKN/ISGPKCHE
60	13961	A	65	2	548	VQKYPQQRSCVPPVAEWA VPPQSSRLKYRQLFNSHDKTMSGHLTGQARTILMQSSLPOAQLASIWNLSDIDQDGKLTAEFILAMHLIDVAMSGQLPPVLPPEYIPPSF/RRVRSCSGISVISSTSVQRLPEEPVFERDEQQQLEKKLPGTTFEDKKRENS*RGNLELEKRRQALLEQQRQG
61	13962	A	66	72	952	SSRTYTTSLPLLKKEVTRKIRKYFILANN*NTTYHNLNDLTKVVFSGKLLF*RSR*EYRKDKISDLCFYIQMLE/QRQVIKPKVSTRKEINKSRTO*SGKETMERPKLEDKFLVNINNINNP**LNL*RKKEGHHCIFYRH*KDNKGYYIANNFNILDQMDKFFERYVTKMD\QEQIVSLNIPIADKSNA*LNNFSSSSSSSSSSSS
62	13963	A	67	139	422	VNGNEPEPL*KGISRHEHRRQPHNGFRPKNKGGAQNQ*ASLGMKTPEAPAHSDKPRRRQHAAYSS*AMPFLGICISFSQCNL/CPPKLV
63	13964	A	68	274	1	NLKNKAVITKTA*H*QKNTDQWNRKINPEIN/HPFYGQLIFDKDARNM/WKR/DSNFK*CWEN*ILTCKKMLHP/SLTTNTKLNSQWIKDL
64	13965	A	69	22	419	KTIIGEDGDT/PLSEMAKSQRQIFSKDLVKLDSTINQVDIIDYKLLHHP/KWTVYTFSSH*GTFSKIDHILLDKTYPNNL*RTGIMQHMLSDIKVFKLBISTRKVTEKS*HTMSLCNKLTLEHPSGNEDASAYLK
65	13966	A	70	57	423	KDKNSQVTSEEEBQEGKIKENLNSWRDTR/CH/WIGR/NIVRLSFLPKLIFINTVPIKIRTQPFMKNLKPVLKFIY*TKRTRIAKSLKKK/RQEGKISPTNRRTYEAYS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TLESIGASMPSLDLG
66	13967	A	71	394	1	KHFRCLQEDCRILLWFFSETGSPCAV SPRIECSSKIIVHSLKLLGSSDPRASLS *VAGTIGVHHHTQP*GI/CNI*GSGRRR SEKQWIKENVSSEAKRRRTF*NE*SV* KGDVNDQGLRLGTVAHAYN
67	13968	A	72	485	1707	SALGLSQPRPPGASDAAPDSTPAGV*TA SSSAPAGEKDANQMEWARDPGPLHQAA PAPH*SHLVRDKRAQERLAKTSRGPPHS HRSGPVDLSPRSSHSRDSTPVHGPYFRS APDPRGSAPAFRGP IATRGR/RPRAPRA TASHVPLSSSSWKEPEEATAPRF*ASAC MKWRLEAGCPGHRGVWPGPPSRRLFWA TATGEKSTPSFPTGVWRGVEACT*AGS PTAHIQHSQRTWQPVPPCTNGSRSPWTS SYPKNQSKVGTVPKRGWACQPI PETAVR QATISQ*ARKGAARPHQARQVEHSTQ/ QRPSGDSGKFDQRLCEASTLLQPERPE VQGIKCKFRV/GERRRTASPN SAVPEKR TRTQTMVGTAFIGCSGKWRVYSVRR/R SSPRI PPPGVGSS\ PLKT PPPP
68	13969	A	73	1	462	QDHRSSKSSHSNKRPSLASSLSSENFQRA AKPLQVNWKKLYSTPLLAIPTCMGFGV HQDKYRFLVPLSLGRSLQSALDVSPKHV LTKRSVLKACRLNALKSSLKMSWVYG RVT*KYLL*F/YRTNRRGLL*SMGFAPR YLPBGDNPAHLERGN
69	13970	A	74	307	436	LP*VGCITEGIPQDMVRGKHKLLRQEK TRLIGPNC PGVINPGECKIGIMP GHIHK KGRIGIASRSGTLTYEAVHQTQVGLGQ SLCVGIGGDPFNGTEFIDCLEIFVND SA TEGII LIGENGA/NAEDNAAECL
70	13971	A	75	1	435	EISDSKAQLAAMALYIDTWRMNCFS* NHEPLRTHCALAASKLLKKPD/QAE\RE HLCTSL\WSGTNTDKNGEELHGGKRVME RLKKALIIAHQGM DP SLQVRVFIEILNR YIIFYEKENDAVTIQVLNQLIKILEDL PNLESWK
71	13972	A	76	58	366	EFPDLVKDMNLHIQEAQCIPNKINLNKL MNRHRII/RLNNTTKRILKAAKQK*N I/T/IRGSSICMMDFSEITEDRRKWH SI*KILK/EKTONCLPRVFCPVKI
72	13973	A	77	1	445	YHETGCFLMGAIVDITLTFNTYVHFQ GK MKGFSLLADPQEFWVDNSTSMSAPMLSG MGTFQHWSDIH\DNLSVTHVPFTDSACL LLIQPHYAFDLDKVEGLTFHONSINWMK KLSSRTIHLTMPQLALQSSYDL*DLLDQ A*LSDILTP
73	13974	A	78	53	444	ERGGYGAGPVAWQFLVPSTAPMLQSPPL GFAIDHTPPVPAPAN*APCPLPYAA*RT TGPPIAHLDTTFTGTDPHPSPASPP STPWLPDAFPCLPTWD/RPPCLQPLLS SLPTERLPFLCFLLLAPYAP
74	13975	A	79	1	353	HIRTELDYYGLTVVYIYSDT*EAYNYIY IMVT*NVYKPOLWNI FDRATMHSQDVRH HLLCIRLMKKNPKHHAV*/VLNGHYAFV SR/SFKHALVQYVQAFRTHPDEPLYSFC IGLTFIHM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
75	13976	A	80	1	350	LYFYALLFLSSG/CVAYVATRDNCCILD ERFGSYCPTTCGLAYFLSTYHIKVDKDL QTLBDILHQVEDKTS*FKQLIKAIQLTY NPDDSLKPNMIDAATLKSMKML**IMTY EASILT
76	13977	A	81	76	386	PAYPQVRGPASTPASCIRPTNARVLSTT PRGKSVAEASVSPSAHRGVTSVIKLWS AKRLH*YGA\KVRPNS\GCTP
77	13978	A	82	1	360	ESILQEDITVLNVGAPNNRASKYMRQ/M LVELQRQIDESIIICEDFTLISEMDST RPKISKDIVGLNGTIN*LDIIDIYRLL* PTTAEKTFSSSRGAFT*MDHILCYETH IYKFKLHE
78	13979	A	83	39	344	WGILEGGEYIWHVGGGKSLRASGGLWSQ PPRPDDSRPLVLPVCHLLPHWIGPTD LGHKRQW/MGPGAVAHVCNPSTLGG*GE WIT*GREFETSLANMVKPC
79	13980	A	84	1	427	QOAHLAGHHRHTGEKP*KCEACDKVYR GKSSL/MK/HRRIHTGEKAYKCECHKY YSR/N/SQTVKDRRIHTGEKP*KCKS\C DKAFGHDShLAQHARIHTGEKPYQCNGC GKAFSRQSTLVYRQATHGVGKLY*GNDC HKVFSNAT
80	13981	A	85	88	307	TWTQRRAKLVRRIGWALLPFPSPGSKP PP*TPPALPPCVP/PQSSPWTTPQPPAP DSREVSQDWTQMRSEKEN
81	13982	A	86	5	375	NSLLNTHSRGPGASHCTFWLHERASSRD LTGAESYGICRLRLISLSIVFSKSIHG LACISILFLFLFLFFVKTGSLCCPG WPQAPELRQSSLLSLLSSWNYRR*PPHQ LIF\OFFCRN
82	13983	A	87	2	342	VIKNEDHYIMIKCLI*QEDQTILNLHSF NKTNINIYKPHMTNLQKAVDKITITV*T CGTSLSIIVACRLKLVKL/VEDLSNIIN KLDLM/DNIYKTLHLNIRDYTFKHTWN IYKN
83	13984	A	88	1	338	CNEPRSHHCTPAWRQSKTBSKKKKQKKK LTTS/CIKASMKSRVQG*LR/CWAQVMG **GGVLWLPVK/REFFTLINLSKEGHS RRVPCLGCLKKKKKKKKKKKKKKKKKK KKFF
84	13985	A	89	931	2	VASPNALPE*LLPVSGHTDLERVGVAR LGQPHHTELACRARMESRDTCPGVTLH P*PPSFPSSSSPSPGGPRTRLTHQGAGL EGSQGPLQSQNPAA/PLGACRGWEP QPGSGS*GG*LMLRELRE/WQEAQVQL PTPG*PS*ESGRPLSSASGPTPPGSP/ SP*PGTQGLCGCHPSGLCATAAGPDGS GPTTPH\VPQPSCRDSGPGQLSPTPS LTSWENTRPSPTGPGPGGGRATW/PG S/PSQRESPPQLPCCTPGSFAGHPCP AP\AAPSSVACPLP/PDGFPRAPASSGI TTAPSPGDP
85	13986	A	90	66	464	LWVYSSFPRLPLHSGAESPEGDILWPGL TLFLSPSPSPLS\CHSHLSPTCRRPRES PRFSLCWRPHPPSKPPG*VKRDCCPSP DPVRLSVSENPISAGPR/VFLRPP
86	13987	A	91	197	2	NAETIPAPQKVGPFIKIWINFFPPFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFF*DRVLLCHPGWSAVVQS*LTVASNF*F\K*SSCLT
87	13988	A	92	317	2	SRTPDFR*STRGLPKCWDYRCEPPCPA TSSF**HLSLC*QGNL/VVGPPDSIRMG AG\TRKTKCWEGCHFLPFLRRSL/NSVA QAGVQWRDLCPQLSLTPRFKRLS
88	13989	A	93	1163	0	FAFGFEM*YCSVAQAS\VQWYDLTLLOP PLPGVQSDSPASSLPNKLGLQGTSHHAW LNFL
89	13990	A	94	3	363	VLWFCRPA GSPSLGLNFPYLSWLRLOTF AIRPGSTGRRLCLPNWVPTNLSLFFH*L VC/CSSRHNTYLQECTGHREPTYQLNIH DIRLLFLRFAMEQSFSADTGGGGRESNI HLIPYIIHT
90	13991	A	95	17	353	PEPRYVGFISGGKVDIKKTWKTKQRLER TVYVTGMYFINCH\VLKNTDSSWGTSP* *IQQHAGKRDNNYQLL\KLQG/QFSRAY TKCYSNPDSTHDVRKVYQDCPLLAPLND TS
91	13992	A	96	3	355	ANYPRDLCKVTDEGGYTKQOIFNADQTA LYWKMP\SRITLMEREKSVSGVQASKD RLTLLLGGSVAGDVK/LKPMLIYHSENP RIC*SYSLPVLCKWN/NKTWMTAHLPTT WFTCLNPL
92	13993	A	97	367	2	SLHRARRGKGVGVRMGERLPSFQSWRLR L/RRRKL CRRWGQGPNG*Q*QKPDGGA RASQTDGGGERRRGVQTGSQAERDTSRE TYSFRGIQREIVRVSKGKGTGRWQSQR QIQREKRVGR
93	13994	A	98	115	359	LNFFFFYLLNFMLLFHRYYALKVSYFKSS LDRKLELLWNKYWVNTLSSSSLLTVS/ DYTCKECI*ILSKLHSLISETLFHRK
94	13995	A	99	1	490	CVDPRVRTIFKKDKVGGLELLNLCTIYYK ATVT*TVWYWHKD/RTDQWDRIKSLEIN PCIYQGLIFFNYFFSQ*QDSSMEGNS LFNKWC/CRPLTLYTRIGSKWIKYLM*E LKLYRLSLHDPEFGNGFLEITSEVEITK EEIGKLD\LAKLKTFC
95	13996	A	100	195	3	SRCKQRHLVQWNRTEKPE/YGRLIFNK GVKTN*WGKNNLFNKWYWDN*ISTCKRM NLVPYLSPYT
96	13997	A	101	1	371	FSLIKISMMLLMKMEK*NLQFIWN/HRR LQIAKARLNKKNKTEGITLPDFKIYYKA VWYWHKKRHIDHWNRLSNSNINRHICS QLILTKVPGANTKDHFPNEWSWEN\VCT KMKFDP/YLSSYTK
97	13998	A	102	6	370	KKGTIPNYF*RE*TDRSKPN*NYATKEN YI/PIS*NKKIL*KLANKIQOHKKKPD NSLFYKIQFGSILETFITINQISKPKK NHIISTDAENA\FDKIQH
98	13999	A	103	298	24	KCWTSIYLLLPFRDEVSLCCPGCAQTPR LK*SFCLSFPPKWDYRREPLVPLDQ/L FLESNRSVSVLKKNP*WFSNSSGSKSG NHDAFCGIS
99	14000	A	104	2	352	GTIADFTQCCQAADKAACLLPKLDEL QNGRLRS AKHRLKASLQKSGKRTFRAW T*AGLIHRFPPIABFAEVSNLPTLTTVH TECCHGDILLECADHRADLAKSICENHDS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond- ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						ISSKL
100	14001	A	105	139	361	KHTEAF*MPCKAYYLFGGLNQICALPE KTPVSDRKTCCCTESLVNRRPCFSALEV DETYVPKELNAETFTFHAK
101	14002	A	106	3	350	ELEMIMLSEBVMKAKIRQKLGLL/QPV S*VVNAKEKFLKEIKSATPVNTQMI\KN SLIAD/MEVVWIDDQTSNVPLSQSLIQ S/K/ALTLFSSMKAERGGEAREEKLEGS RGWFTRFKER
102	14003	A	107	225	1	QGIMMDTVEYVGKGPVRCWWCKLVAL L*KTTWKLLRLKLI*\YDPAVPLLDIHP KEIKSIYQRDSCISMFTA
103	14004	A	108	390	2	LGYSGVRAPLERAVCRFSDLKLRAGRTT TLFKADROGHLSQLRLLTFDSLCP/AP RGGVYRGRQASLSCSGLHPVGASWPRCL PTQASAMAGAPAAASLPCCSLISDCCAS NE*GSVSVGPSEPGTGHN
104	14005	A	109	304	33	KVWGEKVWYQKMTQIVQWDRTESPQID N*SLTKEIQWRKDSLFKNK*GNNWTAPF SS/RSINLNKDLTA\YTKIKSKWVTDLNV KHKTIKLL
105	14006	A	110	135	1	KQAILWPGAVAHA/WSCNPSTLGGPGGQ IT*GQEFKSLTNMVKP
106	14007	A	111	140	338	IMSTILYYGSICYCYWLDL*LILRWTL ALVAQAGVQWRELGSLOPLP/PCLSLSS SWDYRPP
107	14008	A	112	26	361	RSFFWVFFFEKKSLLGIPGGKKGPPIN* LEPLAPGPKGFSGLNPLENGNWGPGPPC RGDFGFF*KKTPFFP\GPGGVKTPNPG TF/RPKPPKGVGFPGETPGPGGENLYQ WK
108	14009	A	113	11	330	ASINLHIFLFLSYFLEKGPVVAQAGLN LLGSTGPLSASRAAGTTGALHCTQL*TY LLLPHKGKAVFF\QETLLLRSTHFPPLK HVYTPTYELLVWDRDSLRRP
109	14010	A	114	350	2	GCCPCLFPGSPTVFGSLYSIRLVAFVR AVPPVWKA\VP*PPVKM*FHLFIYLF KQ/VSLWHPGWS*LAQSQVSRFFPRSLP SNWDYRGAPPRLTLFFFFKQSQGIAM VLAL
110	14011	A	115	3	341	RMVSIS*PRDPPAFASQRAGITGVSHRA RPVYSFLLLSNPVMDVPQDIYPLVDG YLSLPLVCCV*V*VLLCYPTWPPGLKRS SCLSLPSSWDYRHEPLKPA/SCCVLLSS G
111	14012	A	116	1	384	PSYPGDLTEIMDEGGYPNQIFSIDDTT FYWKMPSTRFTL\TEKSS/GF*ASKNK LTFLEANVAGDFKLKPVFTYHALRNP TLKKYATSTLPVLCKWNNKA*VT/AHVF TTWFTYFKLSVETCCSE
112	14013	A	117	43	347	CAAGFGLL*TPPRT*TRKERRNGTYKPI SLMNINAKILKK/ILANRIOQHIKTK\L LQSDQVGFI
113	14014	A	118	351	23	FNK*CWHNWIFTCKGMNLEPYFTPTNTKI NAIKAIQLLEENKEVNLC*LGNGGF/S RLPKAQMAKETIDKLDIFIKALCSK\N TIKKVKSELEKIFANHIHGTSTQNI
114	14015	A	119	123	340	AADSSSTHSLTKPAYLEKQNFFFQMEYC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LIPLAEGPWENLA*MQPPPTGFKQSSCL SLPSTWD*R/HWSPRLAN
115	14016	A	120	1	371	PSYP*DLTEIMDEGGYFNQIFSIHDTT FYWKMPSTTFLTTBKSS/GF*ASKNK LTFLL*ANVAGDFLKFVFTYHALRNPR TLTKYATSTLPVLCKWNNKA*VT/AHVF TTWLTEYFKLSVET
116	14017	A	121	82	367	YSKRNTIVAGD/FTPLSALDSSSRHRI NKKTSNCTIDPMDVIGIYTVFHTVSTBY TFFSSANGPFSKTDHLLGYKTSKTF*T KLK*HQ/CIFSDHN
117	14018	A	122	27	253	MKTENILGENIGEVFGVGRDSDLMSPKA *TIKEKNDKLFFIKVKNFSYSKHTI*KI KNQATVWQ/KLLTVHKSDR
118	14019	A	123	3	305	GTRQGCPLSPL*FNTVLEILVR*ISQNK *INKT/SLTADP/MVLHIENPKGSIK*V LELINEFSQVAGYKINM/QKTVAFLYTN N*LSKKEIKKTIQFIASKRT
119	14020	A	124	1	327	QVIFCLGLPKCDYRHEP/RMPGLRGAD FFSLI*ILWEHMF*VMCILPHPCGDFWA MLNF*EREGMFF/CLKRWKSHNVQA/G PQTPRFKRFSLTLSSWDHRHAPPHLA K
120	14021	A	125	74	334	IFEPGVLVKITCLSVSSHEVGKLCPPFF FFKNGV*FCCPGLQGYNGS*L/TLELLK QSSCLSL*CTQDHRCLPPCLANFNILNS SIH
121	14022	A	126	381	60	TVSQVLAHTCSPSYLKAKAGGSLEPGSC YPGCSEL*SCHCTPAWIT/SQTPSL*KI H*KKIIVKRAIVECVVYVYTIWLLIL KFSDSIPFAQIWGFHEEPYWNQC
122	14023	A	127	323	2	RGFLGLSDEVSGQQLFSILSEIENQFKN NLEGCGGSCL/SIPKCDYRCQPSRLAY A*LIFVFLVE\TKNTGFRHVGQAGLELL TSSDLP\ALASQNAWLGTISHAEFY
123	14024	A	128	2	354	ENCQINNLRPHLRKPKKEEYTKPTASRR K*IVNIRIERNGIEQK/TIEKINELKSW LFENINKIDSHSGKWMVGEE*CVFVCVC VRERQSDRERETRLIKI*NERGDITADL TEIK*LLILQKLNNY
124	14025	A	129	74	327	GELAMLPRILNS*\PCNPPA\SASLVT GTTDTPLYPAYYYY\IIIIIIIEMEFH S\VAQAAMQWCDLGSLEPL\PPGFRFRF CLSL
125	14026	A	130	83	382	YEFHASDGGSRLLSQHFRPRWRDYLST EVEGQPGQHSETPSLSLSLSF/CFLEME SCSIAQAGVVQWPLYLSLQPLPPRFRF *CLSLPKCWNYGHEPQL
126	14027	A	131	749	2	RQSLALSRLSSTISAHNFCLOGSS DSPASASRVAGITGVHCHAKLIFVFLVE TRF\THVGQ\AGLELLTSSDLPALASQS SGITGMSHHVQARCVIF/CGPTFKNQDM KY*NKKEKNQSTFLEHLQNNRHAH TLRHHTAS/LKSSEFLFAIRTSFLIS*K RSGTGMF*YN/WTIGNVEDRFVLGPP FGLGVQWYHHSLLQPSGLKQSSLSFL PSS*DYRHVPTPSFLKFLRRWGLAILLR L

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
127	14028	A	132	371	1	KKNLNLNLTL*VKINTNWIMDLTIKYKI IT*KKQEKVGNLEQKKEPSDLTPKV*SI KGNTDK*DV*KPFSL*KPM*GNRQATD *KKMSAKHVSNNKYP\LSRIYKPNDAKN KPIRKWAKQMN
128	14029	A	133	2	318	NHKIILKDAKAFDKM*HPFTMKILNK* GIEQYAT/DIIKAMCDRPTADIILNGEK LKAFPLRSGRRPLL\FH*IW*VLARTVR PRKRNGSQEWLMLALIPSTLGG
129	14030	A	134	3	362	WSELGSSDPPALASQIAGIIDMKHYAQ EGTDF/STSVYFTLPTQIRL*ALKRKF L/EFK*IFASI*QFAKCSMSRNFPAQ PYHHWHFPNEETEAQGNFSLWAC/LRE DWIPTD
130	14031	A	135	12	398	KCSTSIIVIREIQVKTREIYHTPTKMAK IKKPDNAKC/WSGCGATKTLIHCW*NN\ SLEIWLFLMKFNICLPDPEIVPLDLYL REMKTYIHENTYTKVSIAPLFK/QPKSP STGESINCSIIIPMECII
131	14032	A	136	309	1	QSEAPSQNTKKQKTKVGGTTS*FQTYH NATVIKTVWH/W/YIGIDIDQWNSIQSP EINPHIHGK/LISNKAATNEWGKNSLF NK*HKDNRIPTCKRMKVDSQPHI
132	14033	A	137	2	251	QCGKAFRAASVLRMHGRTHPEDKPYECK Q*GKAFRSASHL*MHGRTNHQEK/P/HE CKECGKPPRSAQNLRIQ*RTQAHIRMHS G
133	14034	A	138	396	3	LELLTS*SACGLPKCWDVRRPPEPAK MIL*SKSS\LPFLCSKCLNTIWALLLLL CSLVPLLTLPKEFYAAH*SPDSLKYPV LQKLSKLEMLVLHETVQRKEQLTYSLYK PIFGFLVGYSFPLFCSYKTS
134	14035	A	139	3	384	LDFIKMKNCCSSKELCGKYEKP*T/MBK MFAKHISNK*FIFRI*K*LSKLTKKK*A KDLNRYSLKEDIQMANCKM/KKCSI*LV IREKQTKNTMYRY*NGLS*RS/GQTK** QGWG GTGPLIHCWWEYPMI
135	14036	A	140	63	388	FMYLFIY*LER/CLTLAQTKVQWCDHSS LQPTPGLKH\PPASASGVATTTIMP*G FLFFF*KRGPCWVAHARTT/WNLGSP
136	14037	A	141	370	3	GPGHFPALFFKGPGLGPWPVPIIPALLE G*GGGFPGP/RGSGPPGQPCFFLKQNF PGFV\GAPVVPGFPGNLGRGTALNPEAE GSINLKGPPGLQPGGKTKLFFQKKKKKY QHFQKTQLILCF
137	14038	A	142	363	2	REKATEENFATS*DWLMMFKEGSHFHSI KVLGETPSADVETVSCPEDLAKIMDED GYTRQIFNVGET\PSRTLITRKEKSVPG FKASKLQIRIG*LLLGVNAGDFKLQSVL MDYSENHAE
138	14039	A	143	99	375	KNKNQNISPLVRYTLLSPLLLPFIINS FFFFPFSF/CFF*KKS RFBKVAFOGGN LS*LNPRPKGSKBFSCLSLQSTWITGGP PPHWADDFD
139	14040	A	144	39	399	LQITYNIWLYIWLYIFWLVSKIYKELL QINNKETNKGQKT*IDVSSNNMYMNG* *LHEKIHDI VIR*MRIKTTVTYHVMSTR MVIIKETENKYW*GYGE\KLIYCWEN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FEK/SVWPFL
140	14041	A	145	358	3	REHTAEDKYEASRSWFFPRFKEK\SPLRN IIVQGEAATNGEVAVSY/PEDLAKNID EGGYTQQIF\NADETF*YWKMLFRTFLA REKS\RLPSRDLTLLLGANAAGDFKLK PMFIYHSDSC
141	14042	A	146	3	376	AVMGMYKINVVPVPTNTSILQPID*GVI LTFRSY*LINT\FNTIGAIGSDSSDGS GQSKLKTFWKGFTIPKS\IKNTCDLWBE VKISTLMGVWKNVIPALIDLPERLKTLL EEVTAYMVNIGRRL
142	14043	A	147	374	161	EFHRVSQDGLDLLTS*STCLSLPKCWDY SKWQRRI*TQ/DLCSED*SSIKPIQLC QELMS*MAEMAHGP
143	14044	A	148	373	2	FFFFFFCDLLLFKPQRSHASFSLPSV VPFEMPSSSLTFLYLFVYNLR*YL/N SVTQAGVQWHDHGSLLQPRP\SLSSWDH WCTTPCPAN*IFFL*RVGLAMLPRLLN SWAQAILPLWSPK
144	14045	A	149	3	282	ILKRIIHPDQVFFIPAMQGFNI*K*IN TV\NHIIRIKGK\NRMIISLDTVKAFGK IQQPFMI*KLGIGKNFLNLKGTYPNP QLAGHSGLC
145	14046	A	150	3	360	DII*BSKFQGHHTGVOKGLQYGIILFI I*EVFFAGFFWAFYHSSLAPMPELGGH \YPPTGIFPLKRLEVP/LLNTSVLFASG VSVTSAHSHSLIEGNRKQIILALSITITL GIYFTLLQI
146	14047	A	151	349	3	KKSSGSHLETKSNRLPGPSQGPWCKEIR KGS LAWQEKSWPFYKPFLLLEVGGGRVIR GSRMTRHGHLIRSSKTLIKHHVPK*TVQ FNFCLFIFLEMESRS\VAQAGVQWCNIG SLQP
147	14048	A	152	500	0	MPSRLECSGA/ISDAQCNLQNSGAPSEP SSALSNPCG*DYRDTLPPLPGYFLKFFVK TRSRVTPAGL*LLASS\IPPTSA/FSK HWDYRHE
148	14049	A	153	373	2	QAGFTLLTSSDPPASAS\QSAGITGMNH RTWPGNF*PQKSCDSFVTKMCTCHKNH IYAQSLVT*LGHSYIFF*DSLQSPPRF KQFSCHSLPSSWDHRHTPPCPARTQLHF GYEYFSRHFLRRR
149	14050	A	154	332	3	THKFQRLTSKSKKLKRKLIFHQGAQKSN SLNPDIKKNLKRQORNME*EKIFTDHL SRIYRELLKLKAK/INLIKMGKGYFYEG DT*MAKHIKRCISPIIREMQIKTTIR
150	14051	A	155	337	21	LGLLFFQRCPAKRGGI*RGSLAAVALL NCGELHPV*ASWWLCL\PVRGKLPTEAS VMGDAPPPTKLECPRTSDCCDGSKNFB SVDLSLLGSVGVGSVDLDPVAP
151	14052	A	156	21	491	HPGSRGCSEPRSGHCTPAWGTRVKTTPAS TKTKQNKKKK*RTVCLTPWHTLL/RVWC DGGDYSSSL
152	14053	A	157	3	394	REDLLSPGFQGCCBL*LCHCIPAWVT/S ETLSQKKK
153	14054	A	158	36	354	LSAAFTSQLLGRLRQENGVN\CSEPRLLH HCTPAWATE*DSVSKKKKGKPFWIPNPL SSLSPAFISGQGFWESHLKNPGRALQGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GFQPLICPRPGRTHMSLKSPWRP
154	14055	A	159	78	340	VVFHKAQRGILLAEYPSGSAGHSIEPK TITLFFLGKVLCCPGWSAVA*S*STV ASN\FGPK*LLCLSPSSSDSRYARPHM ANFK
155	14056	A	160	2	362	HLSPLSIPQNRHCHGPPSVSCWAHLPD GVVAGQRGSSLP/M*GRPGRGAPSPRR GGWPGGLTPHLPSGRGGWPGRGTP\PS Q*GRPGRGAPSPPGRGWPGGLTPPPP SQTGRLAGRR
156	14057	A	161	293	2	PHLAIREPTTVDKSALYWKMPSTRYKV RQKSMPPGFKSSKDRLTLFLGAK\AAANF KLKPLMLID\HSKNTKALKNYAKSILPVL CKWR\HKA*MSPHLF
157	14058	A	162	2	136	LIVPILIAMAFRLTERKILGYIQLRTG PNVWTPPTGATYRLLS/P*QP**LFTKE P\LEPVTCTITLYITDPTLALTIALVL* TLPPIPNPVGNLNLGLLFIATCSLAVY SIL*SNRNGIPKTYRTKNSRLYTTTTRP QRLDAAYWCYVQTPIA
158	14059	A	163	1	464	RQGL/DSVTQAGVQGRNLSS\LOPL/PP GLK*SSRFSVSNWDYRCAPPHLANFFN LFFVQRG\FTMLPKL*TRS\GPGD
159	14060	A	164	1	353	FNYSSSLGNKSETPPQKKKKKKGRGPG ENPGTPTFGGAKGGGNPGIKILKTTGPK GGNPFCKKKPK*PHRGGRP/HGNPVYRG GPGKKNFWPPGGGSGK*KSPIKPPPGG KKGDF
160	14061	A	165	45	389	FFVCTFCRERSLLCCRSWSGTPGLK*PS CLSLPKFSDYRHKWPCSARNFLPACLP CLPPSLPSFFPPS/SPSSSPRQGVTVIQ VRVQWRDYGSLQP*PPKTKRSFTLAFQD LGFP
161	14062	A	166	330	2	WDYRCAPPHFVLYLKM/STFNIFFL*RG VIMLSRLVSSDPPISASQVARIIDVSHW AQL*RSV/CYVFETGSGSLTQAGVQRYN HGSVQPHSRLS*SSHPSLWNYRYPPPC
162	14063	A	167	2	396	YSNVILGIYPKELKTLVHWMFICV*NTC IWMFITALFLA\ES*CSSVGE*IGKTY IPTMKYYSVMKRNAISSHEKTWTRLKCI LPSESRCDRLQTV
163	14064	A	168	486	2	LIFGRIYKINNSSKTDNKRKGTQIQILG MKTGDMITY\QOTSKEYYAHEFNNLEEM DQLFKKHKRP/RIHQYKHHLTGPMNTIN EFEFINVKTPKNQSPGWDDFIGKFYQMF EEFLSENKTGELIL*S*YYSLTNSFYEA SITY*PKPDRQ*KKQSCGPISFM
164	14065	A	169	200	3	GRVDLEPTQESRPPGPPSPDPGVQAPRP SIVRNCGILTRGSPGPD\PSPLSS*AQL CGSPPPPSFS
165	14066	A	170	2	327	PGGIGCGELR*HHCTPTCATERDSV/WN KIIHYIIMLASPNELILPLNICLEIL* AGPLTAICISMFMTAL\FTIAQMGKQPK CPSTNEWIRKMWYIHIMEYYLHFKMK
166	14067	A	171	2	343	PGWSQTPDPR*STCLGLPKCDYRR/AA TVPGFLFLTALC
167	14068	A	172	367	3	FIRDVQFISALRYLLTPERMA/MIKSK NNRYRCGCGK/RG/TLLHCW*KCKLVQP

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						L**SVWRFLKELPLNSVPLLGITYPK/D KEVIYEKDSCLVFIIVQFAIA/RNIHP TYCPINE*IKRMWYIY
168	14069	A	173	102	345	YQLQNI PRWVYSKLQNLSPAFVLL*RDR VFLCHLGWSSLL/QLKRSFHYLASSWD YRQVTPRPAN*ILFRD/RGLALLPR
169	14070	A	174	22	401	STRGLGPECWDYRCSSCPATYLPF*HS IPFLSQLKVQVHRRYFHLFPELSNLPL LSKNVS*TY*KSFLS/WPSLRVLCFVVL FCFVTGFHVSQARVQWGNHGSLOPPPS LK*SIHLSLFPSS*DCR
170	14071	A	175	2	388	SDLQLRAGRTTALFKAVRQGHLLTLQRF LSF/V*LCPAPRGGAYRGRQASLSGGGL HPGRAYRLSCLPKQAWAMVGAPTPASLS SCSLISDCCASNHRDSVGVGFPEPCAGC NLTEHRFLSPSGAVVSC
171	14072	A	176	334	1	KLLELIN*FNKVAVYKINTONQLHCYTL IRTTQKGS�KTILLTIAPKRIKYLGI/Q /LTKEVKDLHSESYTLLEIK*DINK*K DIPCS*MGMVFPFVCLFVYFCFEMAFRS
172	14073	A	177	339	2	KNSPYNFPKGNPGNL*SLKSRI/CWG STFAHIGELFFPKMGKKFPPI/RPFFFF EDRVLLCRPGCSGVVRSWLI AAST/CLG WDYRCTPPCLANFL*ROGLTMLPRLLSN SGLQ
173	14074	A	178	3	303	DLRRAACILPKCWDYRHVPPRPADNSG FLHLII*VCLPLLCHAQLVFIPIETG FCHVAWAGLKLGLSSSPLTLA/FSKCWD YR
174	14075	A	179	342	1	INRLNIFTMAIFSTLIYRFNTIPIKIPA GFVEMDKLILKLWVKFAHGIGKTTLKK NRVPNSKAYYNATVSKT\YWNEDRNINQ WN*IDNLKINPCVCGQLIFNKDAKTNEE R
175	14076	A	180	2	323	STSYPI TGSHAFL*PQNVVDAETNS*HI NNVNLRLKIIKLEBENTKNCIDLGLAT DYY/SVTPKA*ATTTKIDKLELIKIKNF CTSKDIT*KVKRQLIGENSCKSF
176	14077	A	181	326	3	RRKKRRRREPKKDEERKRLYGKDIK KRRKDTM/DWEKILQKGVQRMCI*KI* RGVTQELKANPIRKGNNLNKVHQRI*M ANKHMKRCPKS*VIREI*IPTIMRYH
177	14078	A	182	5	326	TKTIEKAAN*IRRSRRKKIKFKPEIKNR KTTTKINESKSCFYKTKNTDKLLVKKLI RKKTKKIITKDEKNHTI*DCTEVKGM TECYEQVYANKFDNS\BKMDNFLER
178	14079	A	183	3	378	TVLCSFTVWGLDFFG*IHITIYS*VFCYK WNCVHNFLFRFFSAYI*YLLIFVY*S*I MHLCLICY*LLL/CSIFFWIFYMLYFS FWL/CFLYFYFYILCPFIFF/CIFICLL FFVYLFLLFIFFFIFF
179	14080	A	184	365	3	MQLKCI MKSISVQAGVQWNNFGSMQGP PW\LHHFPASASLVGTGTTWARHQGRVIF /IFFFFLMRRSL/DSVDQAGA QWHDPGS LQPLLP GFK*FA/CPCWDDRRAPQCPAN FVFLA\RHGFTILAR
180	14081	A	185	51	293	PYVUNQASVL TNSFYQAS/I*KKSNYRP ISLMNIDAKILNKTQIKLNKVND SRQT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GEDQIPKYCTVSDGRMMRDYFPLFSS
181	14082	A	186	326	3	TKICQWILNLGKKREFGFKKKKIKCPN KRHLRANGIKK*DPTTGCLQDIFRSD AQRLOIKGWKKIFQKTGI*/GVAULTS DNIEFKIKTVTRDRVANYI IKGSIHQ
182	14083	A	187	17	330	KDNEM*IKRTMRCYTSFTMAKINLKIN NIKC*QG*GTGT/L/LYC*WKHKIVQP FSKTV*QFLMRSNKYLRYPAILLLGIY SN*VKI/C*KTYMRMFIVLITKDWKQP NYSS
183	14084	A	188	124	357	SLWGGDLEGGGKKERGENPFGPKPKGK KKKGGNGLGARG/VFKRGRPQKEKPGK KGEKGGP*GAGI*GGGGNGVKKK
184	14085	A	189	333	124	RLRQENRLNP/GSRGCREPRSRHCTPGW ATE*DSVSKTNKKMYKSI IARDCHAENS IVSFLSKRGCVFLF
185	14086	A	190	1	327	KSWLIGDNI PSSQSLIQKGVNPSFKSM KADRGKEAAEBKSEASRSWFMREKERSH LHN/IK*VQGAASYPEDLASI IDEGGY TKQ*IFNEDY/MWKKM*FRSFLTREKL
186	14087	A	191	53	400	VNILGPFHLEFFT FVNALSPNIYTHML TSLGPLHMSLQTFPKPSYLKFPSPH SVPVGF/IPGMQR*FSIHKSNNVIYHVI RMNDISHMIISKDT*KAFDKIQHIGSLF PALSL
187	14088	A	192	65	321	RARTEIYLIHTLLGVYAGETKTGPYTD M*MFTTAPTTLVKTWI*PKSLSIGERIN KL/WILICTYMEYSAIKSVLTHLTTW NPH
188	14089	A	193	127	241	IIKNDSTRICNLTEKLPLRKINS/WPGA VAHACNPSTLGG*GGESRITYNESRNKG EQTONNK
189	14090	A	194	1	337	DLPASASQSAIG*ESIRN*NKLVKRT LKCSQKDPKEDLNK/WKDIVCSWLGRLS LTKVSI LPKLIYKFAKIPTKLYD*KKN RPGAVAQAYNSSTLGGGGQI
190	14091	A	195	2	333	NFNSLFFVFEIEKLYLKFILNCK VARR ILQRKNKVGRLTLPNFNTDYKATVIKTA WH*HKDTHMDQRNRTSTKINTYKGAKT I*WRKNSLFNK*CWDK/WITTCRKKVD P
191	14092	A	196	299	2	PHQORDVQSPSPSICRIFSPSSIPGIQ SWFNQKSINVFYHIVILNTQHRSSSSS SSSSSSSSSY*LMIKF/LNKLGIENF LILIKAIHGKPTVNH
192	14093	A	197	2	199	LALSPKLECTGATTAYCSLELLGSNDPP TLASKVF/GITGMSH*AQPQVFLLLYY FIFFFSSSVL
193	14094	A	198	226	2	KKFFFPNPNLKNFPLGRVFF/CSFG*KF FAPLGFVLVSFLRQKVPHLGSPGKTTFF FFFGDRVWTCPCWSAVA
194	14095	A	199	338	93	PQHNGSL*SQLPERLRAEDPLNLRVQG CNEL*LYLCTPSWNPVSEKKSIOEKNA NLDFREY/RDKRENWTCV*NSIERSSSE
195	14096	A	200	1	361	PRSHLSQLRVRLSQ/IKINQKTIGKGF AIG/MGKKF*GKTLKVPFTRGKVNQKWF LKLKSF LPRKKKTEITL*TLGKHFRRWE KFFATYPSTRE*ISKICRDLNHFTGKKI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						IIPIFQRAKGL
196	14097	A	201	2	358	ENKTTMRVH*IPIRMAEN*VLAVGTL/L QPWWEYKRV*PLWKTNSLAVTLLNINLP CNPTILLVGIYPRERKTYVYTVACTQMF LTVLFTVAPNWKQSQGPSTGE*KNK*WH IHIMGHYS
197	14098	A	202	110	357	IWVFIWCHFLPEKTSFFPGFPQCLDIS *KTLFVHVSLEFFKDRVLLCHPGWSAVA Q**FTAASD/FOESSCFSLPGSWDYKRM
198	14099	A	203	2	374	ILRLHAFMAETPGACKTPCDLRQVFIF IFTYLF/MRLSLTLVAQAGVQWRNLGSL QPPPPGFKRF*GRCLFYPKDGLVCPGLA GS*TGQIGKGIRTSPDLCLSDGFCGSK PKS/ASASQGHVG
199	14100	A	204	375	3	LSSILIRGSFNLSLTITQEH*LLLPS W\PLAII*FISPLAETNRTFPDHTGES ELVSGFNIEYAAGPFAILFIAEYTNIII INTLTITITIFLGTTYDALSHELYTTYFVT KTIPLTSPALMNS
200	14101	A	205	393	3	SARLGLPKCWDYRR/ASTVPGL\SLMLL LKSYSVKMKKCB*LVKPLKAKL*DSCKE L*VGNNLIMPSTYDQENDRVDSLTWLC VLLLLLLLLLLFWRQSFALVARAGMRW RDLSSL*PLPPGFRQFSCI
201	14102	A	206	2	377	FRAVLQGRWSLQKFLLPFVQLCPAPKGG VYM*RQRS/SLSCGGLRPVRASWLLCLP TQASAMVNAPPPARLLPPRSISDCYTSS EQGSVSMGPAEPGVGYDLLVCCLLRPLE KHSIWRVSCFSRY
202	14103	A	207	327	1	ILTGNFKQIRMLIYHSVNPRALKNYAKS TLPVNYKWNKA*MTAHLFIAWPTGCFK PTVEPYCSKKK\IPFKVLLIDNAPGH PRALMKMPEEISIVFMPANPASIL
203	14104	A	208	310	2	FCWVAPGMGFPLGEWGLILGPGSPFFLK EGFPGVGQPGPPKRWGLKG*PPGAHWKG F/IFFFADRVSLLCHPCWSAVAQSLTAN PASQVQAILLPQPPDYRIR
204	14105	A	209	374	3	GVRDP/LEEVVCP*DLKLVARRT/SLF FKAVRQGHLSLQRFLLPFVWLCPAPRGG VCRGTQASLSCSGLHPVRASWPLCLPTQ ASAMVGAPSPASLPCCSSISDCCASNER GSVGMGHSETDVG
205	14106	A	210	3	196	LENLKF/LDKFLETYNLRLNQEETEL NRPMTSSKI*SVIKNLARAMAHAYNPST LGGKGRRIA
206	14107	A	211	34	339	IIKSKRINYMSCELYPNINIDNFFFPET VFRSVI\KLKCYGAFMVHCTLNLPSTN LSTSAQVSGAINRGYPGQF/IGLEK*F LVKIGFCHVA*AGLEPLGSG
207	14108	A	212	200	312	HYGQFHVLFCSLF*MESHVST/QAG/VQ WP/SLALQTPPPGFKQFSCFCLVSSWDY
208	14109	A	213	300	124	NHIFFYFQIHRVCVCVCVCVCVCVCV YRYTYCVSPW/RN**SL*KECLSLVLLT PTC
209	14110	A	214	1	357	QVDHTSDRKANLNM*KKIKVIQTMFSDY NGVKSENRRKTGKLTNIQKLNST/L*I SNETNEKQEIIRKYFEVNINENTTYQDL WDEVSIQAHPSTLEAEAGRLLEPRS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LRSAWTTE
210	14111	A	215	360	1	LTITTYCSE\KKTFFKILLFIDNLAGHP RALMEM*KEMNVFMPAKTTSIMLPLI\S SFNSYYLRTRIHRTFVVVAQSWLQCPTT AISDIQIGPVAMGLLLIPSAFVLCWLSI QQVSKLKH
211	14112	A	216	3	347	SSRSRADGLFFYQCK*QTLYW*HLWYKT QKEKKKTQMKKKQRINKAR\GDKLPEC EAVCGKPKNPANPVQRILVGHLDAGSP PWQAKMGSHHNLTTGATLINEQWLLTTG KNLL
212	14113	A	217	75	347	PPIFKRTARGKVTGPWEYPAKG/CGGTF LGNRGLFPNPGFSGPFPKQVWEGALCA PG*KVCTLKF*FI\SLAIPGNGSKNFFT LFEGPSPIL
213	14114	A	218	3	397	GGQGYSGTGHGGIWHKMEH*R*PLPPK KKKKKKKKKKKKKKKKKKKKKKKKKK GGQNLKGGGKKEPPQKGVKKKTLSGRI IKKDGREKHTRGELWKKTFIW/EGEKIG EKPPKKI*DHEGKKKVLRGKG
214	14115	A	219	3	401	DSWATLHGNIMK*SAAVL*ALGLV\FGF TVSGPTGIVLSNS*LDIELHDTYYVVAH FHYVLSIGAVFAIIGGLIH*IPLFSGYT LDQTYAKIHFTIIFIGVNLTFPPQHFLD LSGMPRRYSDYDPDAYTT*NIL
215	14116	A	220	162	3	KPAQRNL*SNPEKEDINILKRNQS/WPG TVAHACNPSTLGGQGGKQIIRSGV*EQP
216	14117	A	221	374	2	WCDRERERERATERERERERERQTDRO TDRRREEA/EGWAAWAIN*GRAPGTSLE AALBCSCPRRPPQAPPEQGPFPRRTAR GQPRPKLLQPEAPSQTRPHGYPWPLRV LPQSGPEVRPRE
217	14118	A	222	3	264	DHMRPKVRGCSEL*SCHCTPAWAT\SES LSQKKKKKKKKKKKKKKKKKKKKKKKK PFFFFKKKMNKSPVGIAGVAKNTRWIL KHRG
218	14119	A	223	2	410	ATSPIIEELIT*HDLALINILLM*FLGL HALFVALTTTLTNINI*HAEETQT*TI LPAILVLIRLPSLR\ILYISDEVNDPS ITIESMGHWY*TYEY\TDYSGLILNCY ILPPLFLEPGDLRLLDGDDQVALPI
219	14120	A	224	399	3	GVGKPGFPWAKKVALPPYSKGYPK*VQN LILKVKLLLLKKNPGENSLEATGTWGLP PKARAPKLKPNW/DSPKRNPGAFKKKK KRQPTWEKIFANHASDKRLTSRIYKEL QQ*KSKQPIFLPIYHLNHFKG
220	14121	A	225	360	71	NRTTWVPFKTPPLLYHINTKKK*HTGNK KHKTKRAKRRKTKNAKK/EKKNHPHQ RPQRRK/EEQKPKRGKKRGKKKPKPK EYSYL*K\YIHTNLQ
221	14122	A	226	3	386	PSTHVSINLAMGIPL*ADAVITGFHSKI KDALAHFLPQGTPTPLIPILAIETISL LIQPIALSVRLTANITAGHLLMHLIGST TLTVSTINLSSTLIIFTILILLTIL*IA VALIOAY/VCPLLVGAY
222	14123	A	227	3	372	YSLDSPSLTRFFTFHFMLEFFISAALAL HLLFLHETGSNNPLGITSHSDKSTFHPY YTIRDALGLLLFLLSLMTLTLFSPDLLG

[illegible]

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LEL
237	14138	A	242	3	339	RKDSRKRRERKNKEKRKGRKEGRKKPIRM TVHFSSTKIMVAK/ARRQ*NPVFRMLEE* KN\FPPRILYSEIIFGSESIQIKKPSGD GNPKGSFPPELFFLRIPMEVFNLKEAYLR KS
238	14139	A	243	216	3	NSTGTQTQSQKFMLSLVKLLISPIYL*D GVLLFAQDGVKWRDLGSLQPPPP/GPTL FKQPSCLSLPSS*GSRI
239	14140	A	244	408	2	VLTS*SNIAST\WYGLYQ/TQLR/KILA YSSI/THIG/WNNPVLQYNENITILNLT IYIILTLNA/FLVLNFNSSIGTILLSRT *NEIT*LPSLIPSTLLSLGGLPLTGFL PKWAIIEEFTKINSLIPTIATITLLN LY
240	14141	A	245	3	243	IIMLKAGQMTVFPNEDVVMAYKHTDRYS TSLVMNEM\QIKTTMGYHYAPITVAKLL N/SNTRYWP*RG/CSRVHCWRKCR
241	14142	A	246	2	337	FLIMDLQKYINPKIKEPQGETNHTVSP MNINAKILNKILVIQI**PPKKNVSKF G/FIP*/SQGCFNINQCYSILDERKMYI ISKNIKAFNKIQHSSPMIKTKNRKKLP EL
242	14143	A	247	347	1	HYTPIRMTRKIQNTDNKICW*GCGNP/GT LLHCW*ECKMVQAL/WL*TVWQLFTKLN LLLPPYNPITFFGIYPNEGRTHVHTKTCT LIPIIAALFIIARTQKQ/PRCSSVDEWI NKLWYIQ
243	14144	A	248	319	2	KKIILFIICTERVFLCCPGWSQTPRLKQ SSSLGLPKC*DYRESS\PGLNVIL*CL KFHLRVAMLFYVFEV*\IVIFFFLRQSL /DSVTRAGVQWYNLSSQLPPPGFK
244	14145	A	249	329	3	KFPFFHTGEAKNYAVFVINKRIKKQHI HIIYNYGGHQKAECKEIEAHVHCWWEYK MMQ/SL*KTAW*FLKK*TMELPYDPVIL LLRIYSKELKAGTRTDVCTSMCSFLFL
245	14146	A	250	316	3	KTHKTMGTNHIPEKIDST*LKNLNIR AITIKLL\KNRVSLHDLRIGHGLLDMT PRAQAACKIKR*IDEFIETKNFCASKD NIKRV/NRQHK*DTMFANHIS
246	14147	A	251	152	364	QLTSLNHINNQIKYK*TRHS\NHHHHH HHHHHHHQ*KRLPE*SYKSQSQEHYTY GMDITGPKNLRTIPL
247	14148	A	252	230	1	PCWICEFIVSSNFCWFVLETGSCYVAHA RVQWCDNRSL*PQTPGLKRYSCLSFRSG WD*RH/VP IANF*TLPRGGVL
248	14149	A	253	3	345	DVGLAGLELLTSGDPPALASQIAGITGV SHHSWPLLFFFFFFF/CFFEGGFFFLP V*SQGGDLGSREWPYGFPGISRLRFPN EGKIGPQPLAPDNFCFFDKTWLSTVVP WFH
249	14150	A	254	194	1	GRVDTKWANTHERFSKCS/TTVD*WIFK SNYLCTMEYYSTINKKEILSFVTWML EDIMLSEVS
250	14151	A	255	327	3	VKTAEFVNKQKNSTKLWNSQAQIDKKK IVNQINDLRQTEIWMGDRIMNLESRIQ QCDWNTSDPCVTPQ\YNTEH*WKKVKR HLEGREENLTL*IVKLKEQDFEASQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
251	14152	A	256	314	3	KNFPSSLINFLRQSFAPNGQGGVQRVDLG SPQPLDSRVSDRIRLCFKTKKKRFP* QTILKLSKV/E/MTERVLKTAREKHLVT YK/GKPIRLTMDPSAETLQARRE
252	14153	A	257	2	308	RWWW\EEEEVEVDCGGEV*FFFFCFFF FFFCFYVFFFLFFFCFFFFIFFFLFF LFLFIFFFFFVFFIFFFFFDCEFFFFF FFFFFFFFFFFVFF
253	14154	A	258	52	186	CFGKLGWDDCLRSGVQGCSET*ACHCTP AWAT\NETLSLKRRRG
254	14155	A	259	1	269	LKRSSHLSLPRSWNYRCMPPCPANF*TF FVETGSHHIAQHLKL/PPASA/PPKCW DYRHESLCPALDSPPTNINSATIITILQ GKCWHYC
255	14156	A	260	387	3	PLLQVAKINPKRILDLNVKPTIKCLQE NTGENCWDFGSGKDFLDMTPKMQSTK*Q ISKLIKIYNFSSKTQ/SFCTTDHENFLE DIVKRIKIQSHKLEKRFVNHIPDKRLIS RIYQELFRTQHEKPHITK
256	14157	A	261	62	72	LRIIKFSEESMLKAEMG*KLGLFHQAVN KCNLSLTVNEVVNAKRFLLKMKSATPVK THMIRK\DMKVLVWIDQISHNISLSQ SLIQKVLILFSSMKPARGEEAV**KNY
257	14158	A	262	2	193	GGRGCSELRSCHCI PAWVTRAKLSLKKK KKKNSKF/RELGNKGQFMGP*LRKGFTC YKKRSPLIF
258	14159	A	263	3	330	QLKKKYYEELYANKLGNPDMDKFLIC ILQKLQHKH*KKFKDSRRKSKMNRPI NRLIQ*PKELPKRKTLPDGTGELYHK HFFFKLTKPLHKFF/AKIKEEPPFNS
259	14160	A	264	326	43	TQTEAGESL\DPGGRGCN*LGSCBCTP AWATGMKLPKPKKKKITSPLPRLFSY TCSSSQNFLYNDDTI IHPVAQAKNLGD LDSSPTDPIQ
260	14161	A	265	311	1	FFPPF/SFPLERKEKFKGRKRGTKRG FFPPFFPSSPLPLGFP/SPQRA*FLLFR FRFLKFFFFPYLPKPGLGKFFFF FWDGVSLCRGWSAVARSRLTV
261	14162	A	266	5	323	DSTKAQKNTVVSIEPGEVGTILHC/WVQ PL*KTWWFLK/DVK/LBRYDPAIAHL GI/YPKKNT*TCTQVNITLFIIMTKM* K*PKD/PINNEWVT/KLWYMTMEY*ST IN
262	14163	A	267	3	293	GSLQPLADPRFK*FSCLSL/SAGEWHRP WRRSLQRSCHCTPSSLGYRAGLHLKNN NNNNKSEVSRICITIGIFLLFIY/CIYET ESHVST*AGVHWLDF
263	14164	A	268	3	332	HLSTINLVNQLNSPLKAYTLPVWI*KK KWPNY\CCLQEIHFASKNTYKLVKELK KKFQANEKEKHADKTGFKSKTVK/KKNG HYIMIKRSVQKENIYIMFLIADPDIC
264	14165	A	269	3	326	KVLERHDVLKLTQ/DKICNLNM/PYTKE MESIVNNLPKKKTPGLHSFTGEFYQTFK NEMILTSYNFSQKFEAREILNSFYEASI LL\IPKLDKDIIRKEN*R/PNAKILNKI L
265	14166	A	270	1	318	PYPAKLSSLSKGBIGTF/LDKQMLKEFV TTRPALQEILKGALNVL*/LERKDHVQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						QMCKH
266	14167	A	271	1	318	LKLLTSGNLPASASQTAGITGINHRAQP HLSFSL*LWNET/CVPG
267	14168	A	272	108	322	DSHVIPLLCGNLTVFVCLFLRWGL/DSI THPGVQWHHNSL*P*TPGLK*SYHLSL SSIWNYYRRTPLRLAFFL
268	14169	A	273	341	3	GFFFFPFFFRQGFPLLAQVK/VPWGNFR SLQPLPPGVKQFSCNLNLPKN/WGFSLKG FFKKGCHFPF*Y*IFPVGKKPDIKFSI FTNPFFFFFETESCSVVQAGVQ*HDLGS TRP
269	14170	A	274	41	328	FWLLTPGQETERERESETERESEREREA GEAERGRETGDIDSLYSLKLYSKTIHLK ILEYI\ATYFKRLPYNWEL*T*AK/TRI IEKPSVRHQCQORS
270	14171	A	275	3	322	EAQELL\DPGSGGCSELRSHCTSAWAT KAKLRFKKKKKKKCPGRYLGNTVLQ*FN IIAKCDKYHIVKLIF/CFSSAYTASIQL LIQVSETVTTHRNKKTRQVYILD
271	14172	A	276	175	313	STLISYFRDRVLLCYPGWSAVGQSQFTA A*NFV\VK*SSSLSS\PSSW
272	14173	A	277	254	3	RPRRQFGIEGSFLNQIKNIYKKSTANVI LYVDRINAFSLISGTRQGCPLSRLPFNI VL*LPVNIIRQ/EKVI*GMQIVKEELNL SL
273	14174	A	278	186	1	PETMQARRQ*SEIFKVLKEKN/LQHRIL YPEKLSFQSEREIKTF\QRLKKFITSRP ALQRMKE
274	14175	A	279	288	3	GRLRGKKGFNPGENSKKEFFKPLPSGLG AKTQPVFKKKKKKKTRNP IKK/WAKDP NRYLTKEAI*MASRHMKRCSTSCVIREL *IKTTMRYDYVLI
275	14176	A	280	3	329	LKSSRLSLLCSWDHRFALPPMLSGLVW NSCPQ/CDPSASASLSIGITGMSHTWL *WLF/C*ETGSHPVTAQGMQWYDPSPLH PTKKGVYLT/RRFWRLGSPSAW
276	14177	A	281	233	3	IITKDKEEHFIMIKRSIHQGGITITNIC VPYNRGSK*MK*KLTKLMGENR*/HSII IAGDFNTTFSIMDRAIRKSAKNG
277	14178	A	282	32	309	LPDITPRDHLSPGTMDFIQETGCSKCWR GCGTPVCC*WECKL/VIVQSLSRVWRF LKKLKIGQVRWLMPVISALWDVEVGSGP EARSRPAPW
278	14179	A	283	1	302	CKRNNKAWMTVHLETAWLSEYFTPTVET YCS*KTIPTIL/LDDNAPGQPGVLVE MHKDMNVAFRPANTASILQPMNQGGIST FNSYLRNTFPKAIVAIE
279	14180	A	284	155	1	PRRFFFFFF*DRVLLCHPG*STAT*SCL TTKSASQV\RQFSCLEPPSSWDY
280	14181	A	285	131	15	DRSNPGRFLWTSNSSLYERPREIRPSSQ APPFVNDPI*T
281	14182	A	286	1	359	FFFFFFSVVFWCFSTFFFKKGGAPGGG GPPPPKKTPLFSPQKNFLLQKKPPGKG FKGPGLPPPNFGPG/RNGGPKLPDHP PDFTPPRWLFKPPF*KRGEPPPPPGFP KNLFLKKVP
282	14183	A	287	52	419	LEERAGTSWPKKBNKKQHFCMKKKKKKK KKKKKKKKKKKKKPFKKGAQIFS*GGV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NL/H/SGPGPVLTGGGGRHSPPPPSP PSSLFPPSSSLPSLPFLSLPLPSFLPSS PPLLSS/CPPPLFSS
283	14184	A	288	236	325	LNIRTPGSWLXAVAHACNPSTLGGRGRR IT
284	14185	A	289	218	409	KVKGNKADLIRSANGS*N/VKGVLC HQY LEKSFCLTEFHSCLPQLVHWPDGLLQ PMPPGIARF
285	14186	A	290	3	426	HEETGSPRLCSGMITAHCSLDLPKLR* SSHLGLGS/RHVPPCLAHFLY
286	14187	A	291	382	1	ANFYVTLVQ/QGFTMLRSWRPA*PCDPP TWSQSAGITGVSHAWPKMSTITLGVY SFGSEVFSIFKPYFLETGSSFLPQAGA **CNHSSLYP*TPGLKQSFHLSLLSTSV YRYLPPCPLCPVLV
287	14188	A	292	3	309	HEVPYFTLNQOLEMIKLSKGGVLKAKMG \ISQIVNAKEKFLKEIKSVIPVNTRMK QNSLIA\ETQEVSLVWIEDQTSNIPLS *YLIQSKFLTLPNSPKADM
288	14189	A	293	2	415	ARDQYKKSTKK*AKDLYRHFKEAI/HM ASNYK/KRCSIS*VIRKIBIKSSMTSCY THLQN/ALKLSDNFKC*QKCTAMGIIL SWWECNLVQSLWTW\QNLLMLNTHKPY* SAI/PTSGLYPTMYRNIEQASLRMFVA WRGG
289	14190	A	294	335	108	IPTPK*PLSSPPIHTPYTTIPKP/RPPF P*HPPHIHPPPPPLTP/PLPHTLPTPT PTNLPHIPLYSIPPSSPKIS
290	14191	A	295	266	2	GFPKKVFSFPIGPPKLGFPNSVFS/LFT FFNPGLCLKFFQFPFSAFLPLGFSFPF FFFFFFFF*DRVLCHPGWSAVVRSWLT ATLV
291	14192	A	296	347	1	DSLQP*TRGLN*FFHLSFLTRWEYRCAP QCPANFC/VFL*RWGFAMLPKLVSSDLP ALASQSAGITGVSHCAWLVLFLFSLYFI HFSKASETPWAQNSQTPSEYPATYNFK IYSC
292	14193	A	297	284	2	CRQGFVLCRLVSNSCDQVLCVRLCV*VL GLQACAT*LGAEVSIIEFSCPHKGRGCL CRHRSS/HSMFSAWC*PHTHTHTHTHT THTFSPMQLV
293	14194	A	298	1	96	GTRLCIGAITTLPAAVCALTKQDLTKIV DFST*SQLGLILVTIGINQPHLSFLHC THALFKAILSMCYITIIHILNNDQDSQT IRRLNTMHINSTS\LTIDSL*LGK FLN/GYY*QKDLTKIVDFST
294	14195	A	299	3	134	HEGRD*PGNHGDTLSLLKIQLAGSGGV CL/KLRKLMCENHNP
295	14196	A	300	2	333	GVGREGGSREGGEEESGWNNGGIRERRSG KREEEGKEYRDEVDRKEREGEGRERER GRGWEBEQKGAS*C/EEGRVK
296	14197	A	301	354	1	TENELLSRIYKNFYQIN/RKQKNSIKK *RK*QAI/TTETIQTVNKHKKCSISLI IRELQTKTR*ILYT*LVEKKLKTNGIYC WECCRELGSC
297	14198	A	302	1	282	GTRGMVAGAYNLGLPSSNDYR/*CLPPC LANFFVSLVERGFTRLTLVLVS*LYDS PASRSETAGIPLIHTSCIVYWSLRNNAD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IAILCKAQAV
298	14199	A	303	361	3	LPKWWDYRHEPLCLATFFFF*AFPPVPL CMYVPPN/RVVAFFSLSSF*ICCTFTL YIFPQLMDG*AVSSFLFLQPVGVKFKKK FFLSFFK\KRRLGMLPRLILNSWAQVI HPPWPRRA
299	14200	A	304	2	352	ARMVSVS*PCDPPA*ASQSAETGMSHH AQPIIIS*TIAYVSFLSSSLGT*ISSVR SFTKMSQLLYFYFVSL/PSFW
300	14201	A	305	334	1	KNSFFFFFKRSLGLLAQI*/VQWDFKT LQPLPPGVKQISRLNLLKKWDY*RGPSG LGKFW/IFL*KQGFPLQFVVLNFFFF/ CFFETESRSVAQAGVQWHDLCSLQAPP SSC
301	14202	A	306	270	2	DWCAGGGGDGVPRROVIFVILVETGFWR VGQAGFQLLASSYLPA/LA/FPKCLDFRH *PPHSALKALFFF*DGVSLLLPRLCNG ASSPRA
302	14203	A	307	306	2	HIFQCVVCVCVCVCVCVCVCVCVCVCV KLVISQT*LSPLCSGP*/A/CTFFSVVCV VCVCVCVCV/CVCVCVCVCVCVSDLTNLS TLCSGP*/A*HFFSVVCVCSC
303	14204	A	308	117	332	SPPVLLRCSLSLSVQLNGKTIRFLK*LK MEL*FHSALPLLGIYPKGGKFLYQKDT/ CHSIFITALFIIAK
304	14205	A	309	1	351	GTRKTNN*KWAKDLSRHFSKEDIRNGQ* V*/HMKRCSASLIIRIM*ISITV/RYNL TCIIM
305	14206	A	310	1	352	PSPNSPPSPPLPSRPPQPPYPPPPPRP PRSP/L*YTPPAPPY/PSPILTPSP/PS DPPEPRSSRP
306	14207	A	311	1	405	FKPSP*PLTGALLGLMTSGLAM*FHLH SIT\LLILC\LLTNT\LTIIQ*WRDVTR ERTYQGHHTPPDQKGLRYGIILFITSEV FFFAGYF*AFYHSSSLAPTQGLGHWPT GMTPLNPLEVLLNTSVILAS*VSI
307	14208	A	312	3	176	HEILGSNF/CGETQVSIHCPG*S*TREL KQSSHLNLPKCWHLRA*TTVPGLTTFPH LGKPKHKRVR
308	14209	A	313	298	327	SLTSLPRL*KIKK*RKK*NKCWQGCKEI GAFTHCWGCKMVQPLNKS\W*LPKKVK *KLSYDPAIPLV
309	14210	A	314	344	3	HSTSLVIREM*IKTRMTYPTTTKMAII *KNRS*\WLGCGKTGSLIHSW*KC*MVQ SLWNTFGQFFIKLI*ELTIPLDLYLRE MKTYDHTKTCI*MFIVALFIIAQNVKMS LV
310	14211	A	315	18	321	WALFVYCLEKKEFGQPPRLACFFFWDRV SLCLPGWRVAVMGSWVT/VRPKLLAFN*S SHLSLPSSWDYRLIPPCSAKDSICEKNR VSTVDGADKKVRGKEGD
311	14212	A	316	289	52	ETSCDVPSKGIHFGKRNTHIMPEKNAK GMR*YFH\KEDK*MAHIHVKRC*TSLVI MKMQIKSSTPYHFIPRLTKPLKSANTK CW*TCIWAIIYLSSSMKILSHALCPFFWH DVCISLTEVKNAFTGHITRFS
312	14213	A	317	57	324	YCVTFFFFGKQSFVLSPLNCGPFWVN CSLSLLSTWNYGLVPGTQPPF\EFVQR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						GFHYVAQVGLKLLTSGDLLP*GSKGAGF TGLTHC
313	14214	A	318	65	341	QWLLKSRSCYFFFL*DRSWAVAQA*VQW R/NPPPPGFKQF/SCVSLSSWDYRCLP PHLADFWIFSRDQPDQHSQTSSLLKKKK KREIPNLPGLG
314	14215	A	319	2	182	ARGDYRHMPPT\H*LETGSCFVIQAGL ELLDSSHPPALTSQCWDCTCEPQSWAP CVSI
315	14216	A	320	345	3	MPPRQAHF\VFPIEMGFHHVARAGLELL GSINPPTSASQSSWDHR*SQSAWITGVS HHAQLGTITSYHILLFLKKGRAHAC*SQ HDPTTCLHVNLCSSLLLAISRPTTTLN PRA
316	14217	A	321	122	466	QSFSTYC*KNWVTI/CFLKSIDSYLVPY TKIDSKWIIDLVNPKPTIKLGGNMGEN LCHMLSKDSSDVTQKA*SIEKQINKFN SHGGTRLRSQPLKRAEVGRVRLSPGGRS YSDL
317	14218	A	322	3	345	HEDAVSAPCNLHLPSSNCPASASRVAE MTVPA\PCPANFFFFFLEREFGCCPG /CK*K*VFQKKPKGKKKGRIEKKGVWG PKLKERERKKRKKERRKGRKERKEVRTE MNGG
318	14219	A	323	206	446	GNLHQCPCYKWLHLAKYMCEKQDSIC*IL KECYQKPLLEKSHLIAQVENDEKPADW/ PLLRGEYVEWND
319	14220	A	324	62	327	VERLLRDLRENFCRNPDGSEAPWCFTLR PGMRAAFQYQIRRCTDDVRPOGEAQAWG LQSRAGSLEPEGRGEVSA*W/SARTHR
320	14221	A	325	441	1	RKKK*ILQGL/EFRLEHVVASPHRDHRV WPRQEGKLPSEGNKATRMVLYPEE/S SKKLGSR*GSE/CTSVFRITLSVGYVA YTGA PVSISERPSAAIYHRMNK*HQHR RHLLGFSEQEFVQGVPELQSSQGPKPE QSPSPNPAPRA
321	14222	A	326	2	358	ARARTLRIMVNLNYAKSTLPVLCKGKNK VWVTAHLFTASFAEYFKPAVETYLEKI FFKILQLIGDAPCHPRPLMDHKEVNVF VPARTSIQQPMD\ISPFSYY*BITFOA GCCGSC
322	14223	A	327	1	430	ARENMPGHLHRCIEQDWRHMLIPKLN TQMIKIV*YWKDRYVDTE/YNNIESTE VNLYICGELIFSRSAKIQWGWGRIVLN KWCWDD/WNL/SCKSM*MDSYLTCT\K ITPWIINPTGRATMRLLP/EKTGVSF DFG
323	14224	A	328	146	374	KCLMLTKPYNIMRLT*PYEIR*/CGDTF P*SYA*TGTAVRTWGLTPVIPALWEAE AGGSRGQEMETILANTEKPR
324	14225	A	329	2	322	ARASRTFIVRKTOCLASKDKLTIVRG*C SCDFQLKSLIDYSENPRALK/NMLYKR NNKAWMTLGLFTAWSTE\KPTVETYSQ *\KITLKIWL
325	14226	A	330	350	47	EMGFLHAGQAGLELLTSGDPPASAFQSA GTTGVSHRARPAN*KKKF/CLKT/RVFL CCPGWS*TPGLK*SSCFGLSSHWYRHE PPRPAQPLIDFYLRHYRES

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Methiod	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
326	14227	A	331	753	458	FFFVE*GVL\HVAQAGLKLTSRDLPTS AS*VAETTSTHHHA*LHLFNFKEYCKE QILLCCPGWSRTPALKRYSHLCLPNSWD YRHEHCNEPEBISLI
327	14228	A	332	256	3	TLVLMQSCLSLSSWDYRHKPP/*LSNY FNLPMGLSGHNPIINGGISVSLDRVVVL FLFC/LCFETGSHSVAQAGVQWHDHGS L HSC
328	14229	A	333	25	358	TPDLR*STCLSLPKCWDYKHVPPHPANI FI*QKLFFISDGQYANVLTWFEGGTFHT *A*RPNHHSYKLRKDQTIIFIYLF/LR WSL/NSVAQAGVQ/WHNLGSLQSLPPEF K
329	14230	A	334	3	329	HEDVVSPPFWPGWSQTPDLR*SACGLPK CWDYRREPPHLALNAFLT*NIFNL*W/C LSGSNPIIRSICIRFLGKGG*LLFIFIF VVFLTQSLTHSVTQAAMQWHDGSLQ
330	14231	A	335	26	330	SQLLGRPRQENHLNTGGEGCSL/CKIIL VCFWLGHLLPVWFR/ILYLF/CVVS LG FNFCFSLVL/CWFLLCFFCAFMFLFY* WFI CHLFFFLFYFFVFLFF
331	14232	A	336	3	348	DEVFKS/YH*HPMLKC*GDYSLLFHGES DLDTTQILTHPSTTAMFYFVHCQSP*IL YGTIDT*PPVIHRNP IIRTPYPCLOAS TAINLQLSHMNCNSKATPHSLGYHQTYP PLTV
332	14233	A	337	2	329	AAAAAARVTGIAWAYHLIGKLEPFFF MALLFLR*GL/NSVTLARVWYHNGSM* A*PPGLRCSLCPA/NFLYFLVE/IGFA TLPRLQAICLGSSDLPTSTSGSABITGV S
333'	14234	A	338	60	354	NGKECKLIYLSIYLSIYLSIYLSIYHL C*YL/SCLSI*LSN*LAVYLSVCLSVS VCL/VASCL*ISIYLSIHLSFYSIDRIL AHHCVEPTCSLPHATH
334	14235	A	339	1	351	RDADVMLLQILVIFQALALGVQTEGMAG VTHHDRVLVNWRFPQCL/HRV*NGT\ P*VGTSASERPGLKQSSHPSLPSSWDYR CEPPCPVNF/CFPV
335	14236	A	340	190	358	FGSWLVFFF/CFLETDSRFAP*AEMQGP NFG*LNPPPPGLRGFFGLSLPGTGDYGP V
336	14237	A	341	306	119	LRWENHLSLGN*GCSEP*FRHCTPTWTT E*DSVSKQKQKQNNLELKKPGSS/CVVF LPETLFT
337	14238	A	342	1	122	GTRGCGEPRSRHCTLA\W*QSKTPSKKK KKKKKKKTGFFFF
338	14239	A	343	92	316	VCWDIPHRKSRTICILFYPLVIFLFETK ICSSFSP*KGCM/WLGAVAHACNPSTLG GQSGWIT*GHE/FKTS LA
339	14240	A	344	83	329	ATAPAPCYFLILCICMVCVCMHTSVCT /CVILCMCMGLCHIL*TCVA/CTCLGMR FLLPAHIIICVKRFLCMCGSGNSGSLCL
340	14241	A	345	127	357	YGVLRSRGRVLPWPG*SRTSGF/SSPEA NSWPPLANILYLVETGFCVHAQAGLEL LDSSHPPTSASQSAEITSMN/HRA
341	14242	A	346	312	1	LMNLNRSVGALLTRGVKCHKAFRSTISL LIGALK**QKSDLGISLSKVVDLNN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IYRSLLRQSEEDTS\KWKDIPCS*TGTP NIVKMSILT KAIYRFNASC
342	14243	A	347	350	243	FHHVGDGLNLLTL*ST/FCLGLPKCWD YRCEPPRLAY
343	14244	A	348	165	338	HTLDPASHEGPTFLFSL/PVEQCLK*LT LKVATIVLFCFCF*DRVTLCHPGWSAVM QSQ
344	14245	A	349	328	2	SVCPHGSINLSPAETTGACH/RRLA*NI DSRV*AKTFKKG*TNCSYNNNNNNNN NNNKPFLLLRLAGDRHPDQLCPPPRRCH FNGATPAGPPSCLRRSHSSAVCSC
345	14246	A	350	3	338	HEIEELITFHDRLIGNILICSLVLYAL FLTTLTKLTNTNHLHAKEDTVRTILPA IILILIA\LPSLRILYITDEGNDPSLTI KSIGHQWY*TYEYTDYGGILFNSYILPP
346	14247	A	351	124	382	NTFKS*NSNKTKNART*AKDTKQHFTG EDIQIANKHMKRCLIPLGKR\SLNQEIS PRVRINKIRPGMVAHTCNENTLGGWGRQ IT
347	14248	A	352	3	368	RDRASLFCPGWS*HPELK*SSCLGLPKC WDYRR/AATAPGLLCL
348	14249	A	353	390	161	FSRDRISPRWSGWSP/DLRLSP/CLSLP KCWDYR/R*ATMPGTFHFNLKNQDARN QIITCPNLTKYIYMTSSFILVHS
349	14250	A	354	123	345	LAPQHFAFLRLARF/PAGPPCDRPLAPP RPS*FSPAPLPFGADRSVPLSPSPVPP*S LPPFAGAPPR/PPPPRDSRR
350	14251	A	355	37	393	TKHFVSTCYVPEFIAGTNQRKRNRISVL ANVKDKQIILLRVRTAITEGYRNYHVL LVFVCFSPPKQGL/DSAFQAGVWWNH NSL*P*TPGLKLSHLDLQSSWDYRRVP /RMSSYP
351	14252	A	356	2	335	ARETSKDRLLTLILGANAGGDF\KLKPV LYHSENPRPLKNYAWST/LPVIL*KWNKA *MT\HVFTEWLAIFYFKPTVQTYCLEN\K FSILLINNPLSHPRALMDRFKETIGVLM PA
352	14253	A	357	199	377	VGSSCFLKVCQ/C*AVCVVCVCVCVCV CVCLRCV/CVCL/CV\CVGFFFLVLGC CGCVCVC
353	14254	A	358	1	335	GTRTTCMYHVPPRSANF*LVLERWGLPM LPRLVANSPPQTILLQPPPTVLPNPRT SALY/YRPLLDLSPTSLSPRIPSSPLTS SLSIPAPPRSHLAPPPPPPPHPIRPS A
354	14255	A	359	3	369	KPSP*PLTGALSALLMTSGLA\M*FGFH SITLLILGLLTNTLTIQ*WRDVTREST YQGHHTPPVQKGLRYGILFITSEVFFF AGFF*AFYHSSLAPTPQL*GHLPLIVII LLNSL*FPTLY
355	14256	A	361	337	121	LWSQLLGRRLRQEDCLSPRSQGNKP*CH CTPAWTE*DSVSKKGKVVIYHNKSSSL KKK\NSCNMQQFGGT
356	14257	A	362	256	375	EKKTIQYQPHTYGINV*KNLPAKKTGPG DGFIDKLYNTFRGEITTS PHILFH*FKB VAVLINSFSK\AASITLTPKPKNDIMRK ENYSPISSYIWNQCSFFLEQIFPLSFKL NCPGLIIPH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
357	14258	A	363	170	1	SQLLRRRLRSQGACHAWLI FVPSVD TGS HHIGQAGLKLLS \ *AIHPCCPPKILARA
358	14259	A	364	330	3	RIMSASASQSAVISDMSHDVLIDY*HE P*FYQALYSFRQ*ITSSPSYR*SYLLSY KWQDEARC/AFVTAWQAEAGGMLEPSRL VLDS*PRDLPTSASQSAGITDMSHSC
359	14260	A	365	1	341	SQVGLDFHDLSDLPTMASQSAGISGVSH RAWPASG*FYVSREVICSYRL*GYTPSL LVLESGSSSVTQAGAQWHNHSILYPHTH GLK*SSCLSITTR/WDYRHESP
360	14261	A	366	2	338	ARMVIS*PRDLPTMASQSAGITGVSHR AWPATGKFYVSRGVICFII*KDTHLFF/ CFLETGSSSVTQAGAQWHNHSLL*PQTP GLK*SSCLSIKPC/WDYRHESP
361	14262	A	367	2	337	ARAGILKH*QRCKSIR/PLWNVGYI LKLNI GITHDPAIPFLVLPSEMTHAY *KTSMRMCITTLFIMAIN*KFKCS*SEE E/IGKFWYFT**LLYSNENEHLQLHTTW IN
362	14263	A	368	59	348	SAPGIQENEMPAGRGGSHL*SQHFGRRPR RVDHLRSGVDP*LGDR/GETPSKKKKKK
363	14264	A	369	350	3	GWSQIPDLRWSTHLSLPKC*DYRRGPHA QL*TLMYKYLFEHLLSVLLGICPEVEWC /DHMAILCLISLGT VILSSKALHHTYPS PVTCKCSNFSISLSTLVTFHCFINACYF PLFSRA
364	14265	A	370	908	30	ECSGTILAHCKLPLPGSCHSPASAS*VA GTTGVCHRARLIPLYFLVETGFHRLNL LTS*ST/SASASQSAEITSVGHHAQL/C LELELK*STCLNLPKCWDYPA*ATVPSQ FGSVFLRIF*PMFISNIGQLFSCSAFVW P*HQGNAGLIE*VRKYFLFLKFLKEPA\ RTGINFR*MSGRTDW*NHPVRGISLLKG F*LVI*CSY*L*VYPYLLF*EVSLLSP RLECNGVHSESAGITGGSHHAQLVYPYF FFVCDSVLVGFVLEICHFIWLFNLLVY LCLWYYLIITLIAVKSQ
365	14266	A	371	164	1	SCRQVESYGIKRITCISLASSWNYRHAP PRPANF*FPAEMG/FLHVDQASLDSC
366	14267	A	372	3	383	MVSTPAEDAVNIVDMTTN/D*EYSLNLV DKAVAGLERIDSNFEISSTVGKMLPNSI ICYKEIFHERKNQMLMQKSLLPYFNKLP QSIQHSALTTLISRQLSTIWQS/PPPTK /RFOLTEGSDD
367	14268	A	373	1	349	TLGNDHIYNVIVTAHAFVVIPI IIGGSGN*LIPLIIGAPVMAPARINKLR LRLPTS\ILL\LAYAILEAGARTG*T V*PALTRNY*NPEAYGHLSPSLHLTGV SSISR
368	14269	A	374	443	2	SSGSRSECRFLPLLFNVLLEILAGAIRQ /EKE/IKGIHIGKVVSIKLTEVINKFI KVA*YKIN/QKSUVCLYTNNQLEKKFK IPFKIASKRIKYLRIH*GKDLNENLK TLLKEMKENKWINIPCSWIRRLNNVNIS ILSKVTYKF
369	14270	A	375	3	201	LWIKKLDIPIIPS*LFFNTELDKLLK LWKFGRGP/ITQNSFEKPIVGGLILSD FKTYKATVLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
370	14271	A	376	11	324	DKFLEHPPLVLQAVAGKGSPLHCLSTL PTSLFI*DRVLLCSPAWSAVAQTWFTAT ASWAQ*SSNHSPSD*R/PHTTTGHFFCR DKVL/TMLPRLVSNSTQAI
371	14272	A	377	85	364	YQHNYSFCFISQYVYRLFFFF*TFFKKK GFWF*RLNFQGGNMG/SMEP*PP*IRQF FCLNPLN/SPDYRGPPRGANF*IFLKKK GFQVFPSSLSKIP
372	14273	A	378	1	382	GTSGTSYSTIFAGTLITALSSH*FFT*V GLEINMLAFIPVLHQKYT*P*YTHAAM HFLTDSGA/SVLLIEILLLYSNSLGE*S SIIELQLISIFLSMMLVIPNKFGAAYYS IHALCLDRPQLLHILLI
373	14274	A	379	24	323	IPGLKRSSRLGLLKCWDYR*DNFQHMCL KNFNWAAAYFVCKICCAVDPHGCSIKV SFFLSF/CFFFTKSRTVPQAEVQGGDLG *LEPLEPGLMPFSGLSL
374	14275	A	380	2	317	AGWFQTPDLR*SPCLSLPKC*DFRG*FP CQKLFCLPIKIF*TRLK/CYLNTL*QSL PLMHFKKNVIYFILIYKAALFFFLRRSL /HSVAQAGVQWHDLG/S/LQTPSPGFK
375	14276	A	381	1	323	VKRQPTWEKIFA/TLYPSGKGLITRIY KGLKQLEGKN/KSNNLILKWAKEDIQTA NRYMKRCSTSLIIREI\MQIKTTTRYHL TPVKMAFIKR*/GNNEC**GYSEKRTLI
376	14277	A	382	2	248	TQPLILRCLPPRSIYRFNSIPIKIQVNF F/*EKEKSLKFIQNLKGP*ITKTILRK KKVDGKTFPDFTMYKATVIKTVSWYQ
377	14278	A	383	178	1	HNPLAISFCFFPFFFLRQGL/NSFAQ AIVKWDHDLQ*PLGLKRFSHLSLLS SWDH
378	14279	A	384	312	26	FLRGVFFFLRRSL/DSVAQAGVQWPS FGSLQAPPPGFMFSCFSL/SFPPFFL VE/MGFTMLARKVSI*PGPPASASMP VEITGMSHCLANMFF
379	14280	A	385	1	849	FFFFKQTKFIKLSKYKNIIKKS/SAFLY ISNYLKMFKKIPST*L*FEVNLTKLK HLTFYSKEHYTN*VTHKWNITHS*TGI FNS*IFVLHKMICRYNATSIKIPVTFI DIF/EKAYLKFIWYKTP*IAKAIKTKE GI/LPDPEIHYKTIVTKTVWHLNKNRDI GQWSRRKREQKYISVFTAN*F*IQVTF FKGNNSIFNK*CLNFMSTCR\KKK*DP HLTPYVKINSK*ISHLNVRPKTLKLL\H QKIE*KPHNIGLGSKFFDLT*ISQDTKG RTSQSDHF
380	14281	A	386	3	318	LREMQNALESLSNRTEQVEETTSELKDK AFE*TQLNKDK\KKRI*KNE*RLQEVWD CVK*PDLRIIGVPEEGSKYLENMFF IIEQNFPGLARDLDIQIQAQR
381	14282	A	387	1	382	FTPRTAVVKK/SNDWCWRCGCSIGTLR HCSWECKMAQLLW*TV/WTFPRKIQPS DVCCDMVIGLPYDPAVLLLGICPERMKT YVHTADMSVITSVSLVII\ADSENNLNV PSADEWINEMWYIHTVDY
382	14283	A	388	1	341	HKLENLENIVKFL*TH/TLPRLNQEKIQ TLNRSITSSKIKSLIKTPTTRKHKK\N PGPKGFPREFFPRA\KKQGVPTLGNPFQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KFRBRGSLNLYFYKPGLPRIPLKLGKNPR GKKK
383	14284	A	389	168	1	KKFFFFSFFF*GDRVLLCHPGWNAVMQT RLTAAS\TPGLKQSSHFTLPSTAGYTG
384	14285	A	390	337	1	TGITPLNPLEV\PLINTSVLLASGVST *AHHSVIESIGNLIQALLITILLGLYP TLVQASE*FESPTTISDGIYGST*LVAT GFHGLRVIIGSTFLTICSIRQLIFHT
385	14286	A	391	1	235	LNFSYESSMYFALFTIVF\WVFLNF*KF FMN*YHLCYVL*YFLLV\FVCLLTWFM VFCEFFFEFFFEFFFEFFFEFFFEFF
386	14287	A	392	1	258	SCDRLFANHLNKLVSRYIYIF*KSQ DSTIRKQTDKK*AQELNRFPSTKDLQMG NKHMKRCSTPLAI/REMQIKTMLRYHCI PIG
387	14288	A	393	2	317	LAYCNLCPLGSSDPPTSSSRVAGNYRG\ HHDVVF*RAEDINMHEIQFISFLFLNRD EVS LCCTGWS*TPGLKRASCLDLPKCWN YRHEPLCLAFFFNWSWFQCCI
388	14289	A	394	91	408	LGAEPDVRAYLTSGRLTGPGVPPLTGFI SKDHII\ETANISYTNA*ALSITLIATS LTSAYSTRILLTLTGQPRFPTLTNINE DNPTLLNPIKRLAAGSLFAGFL
389	14290	A	395	3	165	RNKKLKNRHRWGC*EKGTLIHCCWCK LVQPLWKAVM*VLR*/LKTLPDPDAIP
390	14291	A	396	661	1	LCPLSSFYRKCALLGFWFVCLFVQIRV SLCCPRWLQTPGLKGSSHLSLPISWDYR HLPPLAIGAVPLIFVLMRTCLR*FADP ISLSFE*QQRN*LHILISLL*MVDICLT QPTKWIFL*PKNS**LKRQCKLPKITEL /PKNRIQIYPTD*MSSIPHSLSFYLVCL FVCLF*MBSCFVT/TMAAVQWHDLGS\L QPLPFGFKRFSCLSLLSWDYRRPSPC
391	14292	A	397	320	1	PDSKQQIFNVDENVFC/WKMPSTRTFLA REEKSMPLGKASKDRLLLVQANPAGGF KLKPVLTYPH/SENPRAIKNYAKS\TVL* KWSKVMWMTGHLFTALNVLSPPRAL
392	14293	A	398	1	158	CIGPMWENRILGGRGCSEL*SCHCTFA WAT\SKTLSQKEKKK*NMRKVMIOC
393	14294	A	399	264	1	LINEFSQVAGYKINKQKSLVFLYTKY\Y SKLSEK*IKKAIPFTIPAKKKEIKYLG NLTKDVKDLYNENYKILKKIBDT\KKWA DTPC
394	14295	A	400	3	343	HEQKRQSKVREVRELSQGLNMDRKRWSQ DLNPGCRTVALSPYHHTRLALNCPGRQW FVGVNFF*KKKIPFFPKFWDRLVLLCHLG WSAVVPSWLTAALISW\VK*SPRLGLLS SW
395	14296	A	401	1	345	GTRKNTDNTKCR*VCEETGYFIHCWGWY KMVYPLGKLVWHFLKKVSIHLPYGTSAL LSLMIEKLTFT/CHTKTCTQM/FHVLF PIVKWKQPKCLPVGELLNKLWYISHT IYSAI
396	14297	A	402	102	355	DRVIRLANFCIFGRDRVSPCCPSWARTP GLKRSTSLSLPKWDHT*ATAPG/LRAI LLYFWDYRCLSPDLVNFACHEFSVELVA FF
397	14298	A	403	156	3	NNKNGFP*SMLFQPSNGLVSI*NI\PLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						*QKWFSFFFEEVSLFHPGWSAVV*SWL TACSLDLPAQVILPPLSLPNSSC
398	14299	A	404	1	364	GTRSEVIYKLLLTQTFWVI*HMRTLLQ ACGAR*MMIL/MIILGLVTCRLTIYQ* WRDVTRESTYQGHHTPPVQKGLRYGIML /FITS*VVFLSCVI\WVFF
399	14300	A	405	3	365	HEQTSNHIPLSQSPI*SKILMLLNSMKA ERGEAAAEKLEASRGWFMRFKKRSHVH S\KVQGEAANADVEATASYPEDLVRTID EDGDTNKQIF\NVNKTAFCWKNMPSRTS TAREEKQCLP
400	14301	A	406	3	356	HERSDQLYAN/KLDNLDKRSKFL\EGYK LQKLTQKEIQNTNRPTTRI/EISKKKK KKKKKKKNFSPGGFTGEIPPTFKGQFKK IFKKFFKNLGGEKTLPI*YAG/IKLL PKIKK/DPSKKK
401	14302	A	407	116	362	YKYSLTPOKLYNHSYIKKNHNKQNNRH STTTTQKPPPPGFKRYSCLSPPLS*DY RCTPSCPVLN/CVELVETGFHHVG
402	14303	A	408	3	360	HEVRLWDFAFERNEGGGENEEDVDLWNY RMWFHLIF*AECSICRLHAYYSICILGP VLLLLFVLIILLPCCL/SFFDYF/VFMF FIFYSFFLLFSLFFSLFL/CFIFLYF FIF/CFFLYFFFF
403	14304	A	409	388	1	ALLKFPFPKVLKKPP*GSFFP*GF*LLS /LIFPPYFGRETLFFFF*NKVPLCPDW SSMARSVPAGSVFPVK\ESLSLSLLSV PPQVQVNGFLTFFFFFWS*ROGLPLLP RMVWNSWAQAILPLWPHAS
404	14305	A	410	1	386	VFNAAESAY/YWEIMPQRKFIR/EEKQA P*FRQERIS*YCANAVVTIRTTHICKP ANPQALKKKKKKHQLTVFWLYTKKS*T MRTFLDWFCQCFVPKVRKYLASKTLPL KVLILDNAPGHLKPHIFN
405	14306	A	411	2	417	AHHIFTARIDVDALAYFTVTIIDIPT GDEPFS*LATLR*INMK*SGAVL*ALRL IFLFTVRGLTGIALPDL*LDIVLHDTTY VGAHFHYGLSVGAVFAILGGFID*WPLF \SCYTLDPRYAKIHFTIIFIG/VDLAF P
406	14307	A	412	295	397	WQWPGTVAHACNPTLGS*GGRV/TLRS GVRDQP
407	14308	A	413	437	3	PGFGLIGNLIPASGNRGRKSKVCVCV CVSVCFKSCT*SLCEHLFTCLCPQICVR LQLMV/CPQNCVCWCPESGLFLDESVCV RLCVCAMMAVWMGGSGSG*VCGCGC/MC ICVGFLLDSELCLVC/LLGQSKDCGL RCRLPAWCV
408	14309	A	414	2	392	HLQFIFFWILKIFHYL/FLWFYFLTSM ALFYLQ*QKRNCMYEVFNRLFF/SCGE GVSGSPASSSSSPSCSSSTRGGGAVGG GLGFVCPLLLFWGFVFLFCWFLVVCV WVWCVWVFFLLGV/CCNCFEF
409	14310	A	415	376	1	GFOASKDRL/LLG/ATAAGDLKLPML IYNKSNPRVLKNFAKCTLPVLYRLYR*K NYAWMTAHLKSWFTEDVKSTIQ*KISF EMLLIINNVPGHPTPMEMYKELNFF\M PANTSIP*PMDQGIVL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
410	14311	A	416	409	2	FFPIKKKKFAGALVFFFFFRKIFFFFPK GEGKRGVLVSINLLPLC*KDFFSPPPPG EGVLWPPPPGPIFFFFFLKKGFCLFCQG GFYNPSLYLIPSPFKIW*TRGT/LP PPALFFYFFFF*DRVSLCHPGWNA
411	14312	A	417	425	3	RELLAFWQNFKLRPQGFPS\GPGGEK KR*SLPKTPPKGGPPGP/SPNGRLPSGG QLPPPRGG/SPQGPPLPKGPQGWGPPF P*RSPPCPPHRIGVPOVSSSPTGLVFP RGPLNPGNLGGTKKKKISSKAARDLEL VRTRG
412	14313	A	418	1	346	LLPDRNLNTTFD\PAGGGDLILYRHLF *IFGHEGYMLMLPGFGIILHIVTYSG KKEPFGYIGMV*AMISIGFLGFIV*AHH IFTV*IDVYTRAYFTSATIIIAIPTGVK VFS
413	14314	A	419	2	382	LFSTNHTDIGTLYLLFGA*AGVLGAALS LLIRAEIGQPGNLLGNDHIYNVIGTAHA FVINFFIVIPIII\GGSGN*LLPLIIGA PDMAIARINNISFRLLPPSLLLLASAI VEV*SRTG*IIYSSL
414	14315	A	420	261	378	KKNFFFF*KLNFF*KFFLIFFPPKKKIF FKKKKKFFFYKIFF/I*KNIFFSPQKNI *PFLFFFI*YPPFFFTTTTTTTTTT TTTTTTTTTTTTTTTTTTTTTTTTLN SLYFSGRVGGRV
415	14316	A	421	124	428	KPAATHACATIFMCLDQEAISN*H*AT TQTTEVSL\SEKLDYFSIIPVAFVLT WSIIIEFSL*YINSDPNINQFFKYLLIFL ITILILVTANNLFQLFIG
416	14317	A	422	8	355	PVFSYNHSTLLTFSLSLSTFFFFAPGK KGEKNGKPGPFRGGFFPKIKKPPPP/ GGPKKPPGPGFPQKPHFPKGGPWPSKT LFGRGKPNFGGPQKPLV*NPPSQGP/ HGPSGGG
417	14318	A	423	356	3	KPLGIDLTKKVKLSKKNYKTLMKKIED DSN*KDNSCL*IR/MTILEKAIYRFNTI SVNIPMRFLPDADAW
418	14319	A	424	2	338	PSVRLGGHWERSGITPLNPVE/VGLLNT IRLLASGVSTGAHRLIECNRHQIIQA LLITILLGLY/LTLLQAS*YFQAPFTIS DGIYG*TFGSGTGQGLHVIIGSTFLTI CF
419	14320	A	425	55	342	GPFTPWSLC*GDLQR*P/RAVRPFLKKK KKKKGNPIRN*RDISS*FLKNLETAVR NFWTFYSYFKSKKLIQKSDHPLKNVKKI LQNDKRYLKLDWG
420	14321	A	426	2	367	DRRFCTYHKDIGALYLLGA*AGVVCT AVSLLIRAEIGQPGN\LLGNDHYNVIV SAHAFVIMFF\MEYPIINGGFGN*LVPL ISGAPDMESGINNISFWLLPPYVLLLL ASAVEAGSRT
421	14322	A	427	359	74	ICADYTRKPPYMGAPIEFSCATCVL*LT STQRECVCVVCVVCVCSM*VALIPD SN/CIPLSAYVCVVCVVCVCSVI* VALLDSNSYH
422	14323	A	428	52	361	NYPQLSEI***VS*LHY/LFSFLFFYFF *LVSRFVARLECSGAWHIIAHCSLDLL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GSS/DSSPASASLVAGTTGMCHQNIIF LFKKVFGVRVQWLTSVIPATWE
423	14324	A	429	105	361	SRLFFFFFETNFGFVFKVGVK/WAF GLMEFFAFRVK*FSGLTHTPTWYRNP HCPVNLFF*VKTGFNLVDKAGPKLLT*K DFP
424	14325	A	430	1	379	HAYHIVKPS*PLTGALSALLMTCGLAM **RLHSITLLILCLLTNTL/SIQ*WRD VSRESTYQGHHTPPVQKGL*YWIWLPIT SEGVFAGIF*APYHSSLAPTQLGGHW PTTGITPLNALEGPL
425	14326	A	431	1	390	KKVKKWKNLIFMIGRLNNVMSVLHKVI YKFRALCLR/TFHFHRKKKNTWA*KHK KALIPKTIKKNGKSGGITLSDYKM*YK TTTTTIRFWKF/DINKYNKITTHEY FHIYQMYFFKIAKTFQGIK
426	14327	A	432	1	392	TRTRGRTOWD*T*LRPI/WTKKKKKKK GKKRKKKGVFFFFFLGF*FFLWVFFF FFFFLGGFFFWFFFWFFFWGIF FFFLLIYNFFCKF*FFFWFGFPNFF FFWFFFLDFFFFFFPRV
427	14328	A	433	382	1	RGGKFQNKQKRVSPPPKGGFPFPAA PKNIKGGGK*TPPKGGVS/PPPKK KSPPHKK/IGNFFPPRGKGGPKNPK PGPFFFKNPPPPFFFWFFFLFFFA HKDGLLAREQTQAEVKT
428	14329	A	434	375	1	KYSQLIFDKTAKIK*SKDCLLKWFVN KWTSTHKSLLD/SPPTKINSK*ITGLNL KCRIITLLENNIEENLDRLGFGNDFLT LPEAQSKTELISY/DFIQTNFCSANATV K*MKRQATEWEKIF
429	14330	A	435	1	459	PTREPTRPSTRTLGFTMLAKLSNARPY /DYPSYSASHSAGITCVKHCAVAIHDF NGVHRPLLI*BFLEISFIFDFLETN PGFITKGELQGHNLGSLQVSPGLTLPS CLSLQKSGFYG/HLAKYLVKF/CFGIFS KRGF*GGYPGGAQSPPP
430	14331	A	436	14	382	MARNTSQKDIRIDPNNKCLWLKVKKKK KKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKYNFHV/LKNKAVNNGSTITS TNVMSPLHRLIIILSLMIYKSTTE* VEKQTCYIILM
431	14332	A	437	3	192	TPGLK*SPCLGLPKCDYRR/AAAVPGL *DILAIFFHHILSECLFLLVFIHCFNA NLFLRWSS
432	14333	A	438	1	364	DRIALGTVDLPGRPTRP/AHPIILKVS LADRAI*NLWQIPIVAS*YIPLGF/WS KAMPCSVDIYSSFEKKKTVFFDRGQGP TPEIQVLGAEGVKPFEPGRGSKPSWRIM AKPKFYKRFKL
433	14334	A	439	336	2	GMIPMKGNAGP/SG/PRKPGFFLG*KG KVKAWLNFKPPFRAFVWPKKILLPLGFS GILGPGPKGNLSRPGPPQAPPLGFCQV LGP/SGPGVGFPKPGQIGWSNNPCLTLQ KNK
434	14335	A	440	1	333	HKLENLENIVKFL*TH/TLPRLNQEKIQ TLNRSITSSKIKSLVKNTPTRKEK/SKK PLVPGFTIEFSQLCKLRVPVFMKPFQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KYGERGLFLNGFYEPGLTLIPKFGKNPGG
435	14336	A	441	320	1	WGINNWLSP*EKKGRPFLL\SHPKINSK WIKDLNVKGKI*KPLEGQIG*YLMIFGV EKGLFKGGPKYTYLYKRY*NRELLFIKR YFSLTEKSPAIECHIKKLAKKK
436	14337	A	442	8	391	ERILRHQVGIIPGM/QGVVRI*ESVDE I/QHV/NQLPKITHITTSVSVGKARDKF NIYS*FKLGKTEKERNFLHWIKSICTSP AASILLEKESPF\PFRRSGTRKD/CLL* P/LGSGMVLEALGTAERRTRKEK
437	14338	A	443	363	2	HHVGGACLELLTSGDPSNLASQSAEITG MSYRAQLSIVTFSAYFLVV*KLSHARGL ML*QSIII/HVLHFHQVKAFHVS/PEN SQPLHNVEPEDWIF*EHQRKTVPIHTA RKLQDLEPCLV
438	14339	A	444	1	900	DSSAGIT/GICHHAQII/LFVFFVETGF HHVGGAGLELLTSGDPPASASHTGGDYR HEPPLLASLSFLNKLCTWPERRRKPIF SLPKLDPNKRKFSFPP*LF/IGS*TLIW SLFCFRNVCTQLADPTKSIAYQSSLMKP FGQKSI CFGSEKFPDKVYLFSSDRKAKE QVLVVVVVVEY*I*DMSACFQ*ALGFCY CLSIWN/YELPEKFEVLACSLPSRNNDL ILSLKKKSQNSFFVCVFFFFKTKSNFVP QAEQGQPLFG*KLPLPGFRNISCLNLP GSCQTGA VPPPPVNFGLKKNRVSP
439	14340	A	445	3	346	QIGKVKKLNK*VPHEPSKNKL\FLEASS LILCENNNEPFLSRIVTWENWILYDNH* QPAQLD*EAPKPNLHQKKKKKKGLAP FWGAFSRGNPFYFFNPQQKLHF*KFSSQ KRG
440	14341	A	446	2	246	FKCGKTRALMHCWEGKMLRQL\RKVWQ LLAMLMELPREPAAPLLSISPRERK/S TTARTCA*MCIA TVCITVKWKHRLLG
441	14342	A	447	38	393	VILHRQGLSL/VTQAEVQWYDYNLSL*P* TPGLQSSCLSFLKSYCHG*LFVVVVVF KWM\GFTMLPGLILNSWPQ/CNPPAVDA QIAGIRGFHS/VGQAGVQWHDLSLQPL PPGFKQFSHLS
442	14343	A	448	54	540	RIPFEHASGFLQSSHQKPHCLLHPLSGQ VSSDQ\FRKFGISRLGNSGIYKAAPPL HDCKFRQSEDPSCPNERYLLYREWAHP RSIY*KQPLDLIMKYGEKIGIYFAWL YYTQMLLLAAVVGACFLYGLNQNCT WSIEVCHPDIGGMI IMSAQDRDL
443	14344	A	449	2	310	FFFLRQSL/DSVAWAGVQWRDLGSLQPP PPGFK*FSCLSLPSSWNYRHAPARPANF FLYP**RQGV TMLTRMVLIS*PRDLPS ASQAGITGVSHHAWAKISL
444	14345	A	450	2	466	KQKIFSVDETAFYWKMPKSTFHS*REG TASKLHTAG*ILLGPNAAGDLKLPVFG DDSGNLRALKNYAESPLPVLYKWNNAW MTAHLFTANFTYFKPSLRS\PRKISWK I*LFMDNGPHHPRALMEMCKE/NAVFMP ANTTSILOPMDKGVILI
445	14346	A	451	670	212	SSSSP*GS*YQNRNTNTIPSPKKQTKK\ KNNHYKSIFFTDAILSNILANAIQQSI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KRFIRHEQLGFILVVLGWVNIQTPTNAT CYTNRLKKRNHMTILINABVLYKIQPSV I*KLFPLRGAF
446	14347	A	452	407	219	PLISLRWENHLGPGVQGCSEP*LCLCTP AWMT*YPISPSQNKTKKQ\HTRKQNH KNKCVKN
447	14348	A	453	2	395	WFLWFRERSHLH/RVQNRASADVEAAA SYPEDLAKI IDAG\AKQIVSVEETAFHW KKVPSRTFFITREKTTSAKG/RC*LSLV DNAAGHF*VEA\MLIYHSDNPRIL\KN/ YAESTLPVLYKWNKAWMTACLFST
448	14349	A	454	424	38	EETEPL/HRPISSAEVELVIKNLPT/KH KSPREDGFIAEFYKMQKE*LVPILLKLC QKIKEGGLLENSFYEASISLIQ\NSGRD TV/RKENFREIPMNIFAKILNKLILANC IQQHINKLIHHYQVLFSSLSHR
449	14350	A	455	2	309	PRVRSQTPGHKRSTCLGLPKCWDYRHEP LHPATASFLVAAPVGM/FADPP/CNMHL NE*MNE*MNGDDASEILSFEMRSHSVTQ TGGQWCSSHSPQPQPPGPPK
450	14351	A	456	3	441	DAWGLVLDREPPFFIFFFFFLGNGGYF RGPGRPGGEGPPMETSVSPVKILRGP GQGGGKARKPHPLGGPRGNHKTGG*KR AYPTGENPVLTEPKFTGPGGNGPETPV IGKAGAGKPLNPG\MGGSRNPKWAHCP* TGGKKGK
451	14352	A	457	1	234	PTRPNHGLGDRGCREPRSSHCTPAWAT ERDWVSKKTKG/EKF*KGRTK*MS*VE QGGSGGKGFITLAINSLPFF
452	14353	A	458	42	470	KRIPQLKKSPLPLKNPPGEWVGKINFPF PRERPKNFF*KKTKLTTPPKQKFLRKKS PFKKPHFLLYSKATKKQKRGKKRAPP KKKKKENPKIVIFRTEITVASPVLSWA VKPIIHIFFPREKKPHA\KPPPP
453	14354	A	459	2	393	DRPIEQWNKRERPRINLYIDGQMFSGK TTAF/WK*NLCKYVWNAWIC\NRNRN PYLTSSRKINLR*I IDIKVK/PAIKLP EQNIRCSL*VLGVGRDFLENMNYTRKK\ IGKLDFIKISQLGMVADTSNPI
454	14355	A	460	338	33	GDEKIEKSFFFPISSLCFVP/AYL*QQI RLLIPTNRSLFIY/CLFLEMGSHFVT QTGVQWCHHSTLQPRPLGLKQSSHLSLL SSWDYRHLPVVLKWTEACAV
455	14356	A	461	77	435	AKEVEASLSTLARPISTIQQQQQQONEK KNKN*PRIAKAI\LS*KGEITLP/ELQL CYRAMITKTAWY*HKNRHIDQWNRREN ETNPHTYSELIFDKGPKSI\SLFNK*CW EYWFICTR
456	14357	A	462	157	3	NGRVDLKIQLARCGGACLSQL/ROEN HLNPGKGCSES*LHHCTPD*VTQ
457	14358	A	463	363	3	PSVAQAGVQWCHHSSLQPPPRLR\HPP ASA/SQ*LGLQGQATALYHKYILFPCN VLISFIFFFFLEMRSHSV/SQARVQWH DGSPQPPPELKRFSWEAELAVSRDRAT ALQPRRQ
458	14359	A	464	3	396	LKETAERVKKIIFKKQLRL*MKKIINR YLKEN/LNQLLEIKGTLRELQNAVESFN NRL*QIEEGISKLEDKAP*WTESGKIRK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						INK*TK*TDYIKEPNLRITIDVPGGEEKA KSLKNLFEVIEENFPGLAR
459	14360	A	465	399	1	PPGVLLNGPPFFFFLILGPGWVFGQPL KTPLVFFPNFYHIFFPKISRIF/LPTR FPFQVPPLCP*PFSSPWGLKVVFILLSF FFFL*DRVSLCHPGWNAVM*SQLTAASN TW\VK*SSHLSLLSS*DYRCVLS
460	14361	A	466	279	1	TTNIFNPRRVGSTDAGPLNMKEKEKENV KRRQATGWEKIVAKDTSRGLLSKIYEE LLKLKNEKTNK*/ILCLKWSKGFNRYFA KEYIQMANK
461	14362	A	467	2	436	RGELPQLDKYLKKTATILNGEEL/E/A CPLRSRTRQGCSSLPL*KKFFPKSHI ESLLPFNIILEVLYSAVRQENIKIVEI GKEEMKMYLFDGNHLCKNSERIRN/YS KVAGYKVNVT*ITFLYTSREQVEFEIK KTLNMRFF
462	14363	A	468	2	420	RTTALF*AVRQGRSLQRLLSLFC\CLC PAARGEAYIG\QASMSRCGLQAVQASC LLCLPKQAWAMAGAPPSASLLPCSLISD RCASSQPDSSVGVPSEAGVGNLVVRGL LSRSEKR\NIRLGVTRFSRCV/LSPLSL TRR
463	14364	A	469	1	416	PSP*PI TGALSALLKTCGLAM*FHFHSI TLGILCLLTNTLTIYQ*WRDVTRESTYQ GHHT\QAVQKG\LRYGILFITSEGSFF AGLV*AFYDSRLPPTLQLRGHWPTSTG PLN\HLQVAVLGEVLLAS*VSI*ADH
464	14365	A	470	211	398	IFFFPKMGGLSII LCWRRKRHPQKLK* STCLGLPKWWEYRCEPP/VPGQKNFRP *KTKESPPLVSGGASSASNIKL*IALPP FLEKKFKKQGFKDPPFLFPTQNPQG NFFFGKI*YCPPIFFFFLRRSFTLVAQA GVQWHDLSLQPPPTGFKRF
465	14366	A	471	62	424	TLMHCWKKWVHLLWKTVLNLLIKIN/ RTLNHT*PCNPAIPLLGVSIREMITYVH KKPCP*MFIVALFMVTKNSHLKCSLTC KWINKLWSLYTMKYLATKRKELLNHNR SCRNYSSDMS
466	14367	A	472	427	20	LGLRLPFVEQEENKPYPLAPFSPPEPP MSLYKNSPIYPGKGLFPSPKNNKIPLN FLKMSNLF*/FALLGNKDFHLLLLGGP IGIMGDNMATTSMFYSRVPIFF/CFFE TGSHSVAQAGVQWCNLSLLQSLPRLK
467	14368	A	473	424	98	NWYLYYYYYYHLLF*ROGL/DSAAQAGV QWHHCSLQPRRHLKQILPPQL\TSW NYRHKPRLSPYVAQAGL*LLGSSDLPD SVSQSAGIIGNEPLHLASL*FLFAFP
468	14369	A	474	415	75	NHFLKFFPQTQANGPGGKNKFFFLKTRF CFFPPGKRWAYYSKLPNSGGQOI\S AATP*IKGAPKGGPPTRVKFFFFFLF/L RWSLRSVAQAGVQWHDLSLQAPPFGFM PFS
469	14370	A	475	3	413	PVQGLRYGI\ILCITSEV/LFFAGFF* AFYHSSLAPTPQLGGHWPPTSITPLDPL EGPLLITSVLLASGVSI*AHSLIEN\ NRDQIIQALLITILLGLYLTLLQA*EYF ESPFTISDGMYSFFVATGFHGLHVI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
470	14371	A	476	1	440	ITLTDRELSYY*ANRL*LAYTITFIV* IPLYGLHL*L\PKAHVEAPIAGSIVLAA VLLKGGFGVIRLTLILNPLTKHIAYPL LVLSL*GIIITSSICLRHKDLKSLIAYS SISHIALVVTAILIQTP*SFTGAVILII AHGLTSS
471	14372	A	477	2	397	LFVYNHIDVGALYLLFGA*TGVLGTGLS LLIRAEGLGHPGNLLGNDHIYNVIVTAHA FVILFIRIPIIIGGGF\N*LVPLIIGA TDMAPRINNISL*LLPPVLLLLASAI AEDGAGTGGTDYPLTGNYS
472	14373	A	478	442	44	SSSEFTTPRGKFFFKKTPRKFFS/SP GNKGFFSPLSP*KFFFFNPFFFGGFF PNFPPPKKNFFKNSPGFFFPPLKKKI FFFFPPLNFAPPKVFVKSPPPPPPPFF FFFFFFFFFFLRGHPWGREGI
473	14374	A	479	1	439	PTRSPTPLVLDREPPPPPPFKKGGP SVPPAGGGGANLG*GNPPPL/GVKKFFG PKPPKIGE*RPWPPPPGQPECSFFLKKN GLPHGGQGR*N\PPRP
474	14375	A	480	420	0	YSPFSPPK/YRAPGKKFF*KKPRKEKF* KKKILGFFPPLSLKFFFPKAFKFFGG VGPNCPPPKRFFSKNSPGGFIKPPKLG KNFFFPAPVKFGPPRGFFFKGPPSFFFF
475	14376	A	481	371	2	NKI*NKFSKLSKSSSSSSSSSSSSSS SSSSSSSSSPSVNK*IKCSTSLTISSS SSSSSSSSSPT*IAKIKNIDSPKCWQGC RETGLTV\LVQPLWWQFLLKLSMQII*D SANMILSMHARG
476	14377	A	482	3	335	HASGKDRHTDQRNRIKNPETDT*ITYSTF *QKC/RLI*WRKDSLVNKC*SNWA\SP MKKIKLDLSSSSSSSSSSSSSV*NV KLLGNNVGGNLQYRGLRVHTVDVKAQHI
477	14378	A	483	1	418	GVR*FSPLNPPSRWGPKHGPPNL/LNFF FFFFVFLVETRFHPVGQAGLELLGSRAP PASA/FPK
478	14379	A	484	1	356	FCANAVRSMIKTVLIDKATK/RAWKGN YKYHLPVFNCKTGRT\DSGNPLNWFYQC FVPEIRKYLARVGLPFNVFLILDNAPGH PEPHEFNTEGFRVVFLTPDMPLIQPLEQ GVLRTLTA*YQCFVPEIRKYLARVGLPF NVFLILDNAPGHPEPHEFNTEGFRVVFL TPDMPLIQPLEQGVRLTLTA
479	14380	A	485	166	406	FIFWGSVSSSAEGGWSVVSSLPRVTVR PDETVDVTIHLLEK*CRPGAVAHACNPS TLGGRGGRI/TLRSGVQDQPSQH
480	14381	A	486	107	429	FWVTQTFGFWLNPFGGLELWPPPCPG NFGGNFKKGGFPLWPGGVQTPGPRGIT PPGPFRGGK*RGGPP/SPGPGFLGKPKG GGP
481	14382	A	487	399	2	GSPAPGLPKGWGFRGGPPGPGKPVFFKL PKGGFPGAEIFLGEFFQKGGKGLGPIFP PVFLKTEGGTSL/NSFFKGRVFLVFKP KAGPKKKKKTKNYKPIYLNNTDTKFPNN MLANRI*QCIKEVMQYDRTRG
482	14383	A	488	419	2	PPPPPPPREKKGGLYFNPKIFLGKSFFP RNPDKPS*KPRVGIFFEKPKPKKKKF* FGPWGKPPGDG*RKNPFK\PPPPPPPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						*DGVLLCRPGWIAMAQSRPGLQEWNSIS KKRSGPCVLGISSKEVPDAWADAWADAW
483	14384	A	489	629	0	SSSSR*SLCKCFKN*GEKIRNPICKWA KVMHRLFTKRCINI*KDVRSTSLMVRT *ITTLRYHFSPIRLSKT*KLNRPLYG* DCGETGIFIHCWWECKMF*VL*RE/VWQ YLIKLL/LHIPVDTA
484	14385	A	490	2	351	KNRPMDPGM*GY*VNDEGDTTYQQNE ELRS/WCWDNRLLAKVKLDLYPPHITI EINSKWI*DLNIKNPPIHVLEENMN/I* F*HVGIGKHYLTI*LKI*NP*K*IWHL ENRMYCL
485	14386	A	491	42	507	NLAK*IQ**IQTIMHHDQVSFIPGIQGW LNILKSINIYYTNRL*DKTHITISIDA EKAFDKI*YLFMKGK\KPLSQLGIEGN/ YLKLIKGIH
486	14387	A	492	18	417	REGKKSRVHHFNKQGRVMSTKH*KTQL /SHSNAHSNKAQISKSQPHGLHDFKKK KKKKKKKKKKKKRGEKKKKKKRGGKKK KKRGGGPP*KGVREALFCFFWRKKFFF VGGGGGKTPLGCLQADTFLWGA
487	14388	A	493	413	82	FFSSPPPLPFFFFPHLPPPPNFFFFFS PPPPFF/PPP*KTFFPPPPPLFFPPPP LFFSSPPPPPPPPPPPPPPPPPPPPPP FFFFFFFFFFFFFFFFFFFFFFFFFWL
488	14389	A	494	1	413	PTRPPTRPPTRPPTRPVLDREHSPSNLP KKKKKKKKKKKKKKKKKKKKKKKKPKG GAKKKG/EKKKKFF*KKGEKKKPPGKF GKKKKIWGGEKRAKTPQKKKTP*GKKKI LKGEKKKNPKPRGGKKFFSGEKKKKK
489	14390	A	495	274	1	IYRIDCAYMKKVERSKISILSFHIRKLE N/QLNPK*/RRRREIKIGABINEIENRK *IEKINETKSYF\WKISKPLAKLIKSKT QITNTRNRAY
490	14391	A	496	336	1	VFQYTYNKLVSIFYCFPL*RWGLTVLL RLVNSNG\PSD\LPSSAS*VAGTTDAHR HTQLCFTTSLDLEPYFHLGSPFISLL* FFFLNTESHSVVQGV*WHNLGSLQPLP
491	14392	A	497	445	382	PRVLIFFFLTTPRGPPPPPPPNKVFPPPP PPQNPPPPPPPPPPSWSGGPAPK/PPPPK SFFPPKPPPVFFSPPPKKKFSFPPPPH FAPPVVFF*PPPEQ
492	14393	A	498	430	2	SPPPKPTRM*\KVKFGR*KKGGGGGGGS PPLSPPLWGSKPVP*VPKGR/PLPG*A GKPPFFLKFPFFPRPGGPRCPPLFGGL GQKNGFTPEVLL*PKFSPPSSSLVDR RIYCLLKMLEYKSVMMILLFASCLNLYT FPIV
493	14394	A	499	363	3	KKLVTPARVLGDII PRNRFLOMPQOREN FLCQVWMTKPPTTIFVKTGTGWYLISL KRFCPAKKK/IKILVNRVNRQPPPEWEK IPANYASDKGLISSLYKDLKQVYKRKN PITK*VKGM
494	14395	A	500	145	435	VFMCINSSFLFIPWYEYTTVWPVTCRR T*MFIALFVIARNWN*SRCPSTGNW/L KLWYIHTME
495	14396	A	501	162	1	FYNYTIIIFYLFIFIFLRRNL/DSVVHT GV*WRHLGSLQPLPPKPKFPRLSLP

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496	14397	A	502	343	2	IKKFRWGPKEPPLKEPPGV/SPDFFII/N FGNPGVPVPGKDFKFPNFPKKKKWGGGRAP PVVPTTPGG*MGRRP*PPAFGVPRGGDG SPPPGAPKEGPLSKKKKKENEKEKERKE KSARL
497	14398	A	503	23	405	KGRNYLWEKKKKMMLVRGKIGGGPPPRI PKF*KVIFKTPPGPPFFFGPPLNFFFF KTDAPLFF*NHPPKSKIWALAPPKKKIF LNPKKPPPPFFPPHFFKKNFPRAFFKNF AFSPRGASPSPPP
498	14399	A	504	418	247	PPKWGF\PPKPPRGFFFPKKGKFFFP PPG*FGPPQGF*RPPLFFFPFFFP
499	14400	A	505	26	426	GCTGLLHS*MYAKVCCDHPIT*VLSP AFISRISYSPTHQILFF*IFFLFLVE TESCHIAQAGLK/LEASSSLPVNASQSA
500	14401	A	506	337	2	IPNLKESA/CPNLPKGWGFKD*PPPPSQ ISLIFKYPKFLKFEI*KKKPLKGLFW WV*KKAPVGF*G\EMALGEKFFFPFF FFFFFFFFFRRSFAPVAQAGVQWRDLG S
501	14402	A	507	454	2	TSKTGQPGRRGSFFPI*WAAGQKRSSPP RRGSRAEALLTSQTGWPGRDTPHFPDDG RPGRGAPLFEDGAGQRRSSLPFRG/VP GRGAP\QSQMGCCQLGRGAPHFDPGVAGQ RCFFPPRWGSQVEALPTSQMGQPDRTGP HIPDGVAAGQRR
502	14403	A	508	390	13	RIPPPKSRWKGKGF*VS*NPRPQI*KN FLPPPP*K/YGDPGRGPPPIKFLPLKK KGAPPICPGCFEIPAPRESPPLAPPKS* NSRGNPPPPFFFKKNPLFWGGKTKKLE IFFFFFEAGSCYVA
503	14404	A	509	2	282	WQFLTKLNLPEYEVIMLCIYPNESKT* IYTKTYA*ILLAALFIMAKTWKQGVLEK V\TDKVWHIMTEY
504	14405	A	510	400	250	LLSVTOAGVQWHDHSLQPTPRLK\HP PTSAS*VAGTIGAYHHAWIIFFF\IFIY CRDAVLLYLWGWFPKGLLKCDYWCPE/ RMSGFLVFWSDLGRSEVS*ILSSWDYR CVPPCLDNFFF
505	14406	A	511	99	242	VTKEKEGHFIRIK*LIHQEDTTTINIGV PNNRTLKCMKQKLTLEKKEI
506	14407	A	512	139	374	SLWGKRIFFFGADPHFVPQAGGA\WGN HG*LQPTPVGLKSSLLTFPISWYYRLG TPPPANFKIFCKNGVKCCPACF
507	14408	A	513	23	401	STCLRLPKCDYRRESPLPACMLFL*M KGKYVYMGFFI\LFFFLFLHKK*LLQEN FVYVCLKKNKTKLKA*TKQKKNETG*N ILVDLNVLS*KKWKCLLWGFILFYF/NF LRQSL/NSVAQAGVQW
508	14409	A	514	7	386	FFVFSTHITLLFLFLFFFLFPRPPGFF LAGKKNTPAPPEKPPPP\PPKKRGPP FFFFGPPQKPPNSPRGGRGPPPPRPPR KMEKGGPPPPREIPPPPPFF*PKTTPP PPGGGGGKKTTPKR
509	14410	A	515	370	2	FVFFQVVLPE*NSFLFSFF*KGLC*RD AFKRFFPPPPNKKLWPSLF*GFLKNS*K FNPSLKSLEVPFF\CPKFFFWI*APF RFFFPFPFP*RG*IFFF*DGVLLCHP

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						GWSAVVQFWLT
510	14411	A	516	1	163	NTREKLSGGGGTQLS*/LLGRPRQKNHL NLGGGGCSEPRS\HCIPAWMTE*DPVSK
511	14412	A	517	1	390	RIVRVYKHL C/Y*GSVNPREKIDNFLD TFNL SRLNQBEIETLSTPISSSIETVI KSPPT\KQKSPGPE
512	14413	A	518	47	312	EYTGILRLRYE/LFTTQH*KQKALNQA K*LAKGLNKHFIKRGCMNDPKHMKSSA SLAIRKM*IKTMRCHYILT*MAKIENK TESTRP
513	14414	A	519	320	1	QNPINKQ*KKNKKYRLV*HKKPPPTT QPHQSNQHQ\PN**PQKHT*TKNHHTPP PPP*SPPPPSLSPSPPPSPSSSHPP LLSPSPPPSPSPSPSPSPSP
514	14415	A	520	1	368	LKTQEQANLILKWKADLNRYLIQK/VY RNVKHTKRCPTS\RELQIKTRYIYISIR *RVYKKRDNKTC*GRETGTGLVIHYS *EYKMN*PLWETV*QFLTKL/E*SY/P* DPAITLLGIYSKELK
515	14416	A	521	2	264	GKKIPMLYFAIEKCILKFV\KRS*KAK *ILPKNNKAGGLKFPDFKTYKAAASKH QVGLWKELRSTLQAQQTWVPRELRST SPS
516	14417	A	522	1	408	LEKMSTSLAI/RVMQSKTTMKCHYIPR KAKI*NNDNIKCWQ*CRETGPIYCC*E CT/LVQPL*KTV*QFLIKVNM\DPAFVL IFIPKK*KHMFTHKKNCKHTFRAALFVM ANTRII PNIPQFVWLNKLSYKHIVDY
517	14418	A	523	320	3	TYIYIKTCPRMT/AVMLTITKKQKQPK YPPTDE*NV\YIHSNAYYSEMKRNEVLI HATTWMNPKNIMLNKASSRKRPHIT*LH IYEMSRIIQVMVLCNCLLLPSMF
518	14419	A	524	426	9	AELPASPTPGTCTPQPLGSGRDQVP\GA VGGTHPGGSLAGSPP*GGLGMAGCKS* ALPRGEVTEAWRQFKCGERRQASTGGP GAPSAAGPGAKPLTAWGQRHQPAAPSA GPAEELPTONWCWPASNPGSRTLSLET
519	14420	A	525	13	461	ICIWKMNILLPYTKLNSRWIADLYVKG TTIMELEVSVREHLHDSQKKIF**DAKL MNQKE*LDILDSINIKSFVH*KAPLRBN KGKLOSAIHIYEKGLVSRIYEELLO\TY KETLKANKKKIDNP I EKWAKNLNRHFR GCPSIYKHVK
520	14421	A	526	288	570	ATGSLCCPGWSIVAIHGFNHSAL*LLTP GLKHPPASASQVAGTAGMSDCTQLCKIN FFVFVFL/RRQSLAVTQAEVQ
521	14422	A	527	3	438	AVSHDCTTGLQPG*QREILYQRKKKGT SPLPPSPGIGGKALPFWGPKTWPPPG IPPLFSPPPPSQSGGGRPLETAGSP SQNPWNLRDGAPPPGGGFFG/CPFPGP PGGLG/PPGAPPPPLKNFPKKGGGGG LFPPQAKG
522	14423	A	528	2	616	FFDTEWRSVAQSGVQWRDLGSLQAPPP GFTPFSCLSLQSTWDYRRPPRANFFL YF**RRGFTVLARMVIS*PRHLPALAS QSAGITDVSHRALQVCFITLL*LSK/H QFKKAGVT/PHLQCLHEIGLDCVLHGH /WSVHSP/HKTNVC

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523	14424	A	529	57	485	RHSSLGKNSSETQSQMKKKKKREKKKGKEI SFDPALSLSI*PKENKSLYQKD/TCICM FITALFIIAKTONQPKCPSTDE*INKRV \\YIYIYIYIYIMKHYSPIKKNEIM/SF AATWMELEAII ISETMQQKAKYCLFSC I
524	14425	A	530	399	3	FFFFFFFFFENPPPPK/WRGGGKKKAP FFKFFKYKK*LFFF*GGGGHQQKKKKK KSSSFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF F*FKGFLLGTTASAHASAHAS
525	14426	A	531	491	4	SKWIKDLNLRK/TKFVEET*VKIFMN LGLGNDFLSMTPKA/LKIDKSDFMKIKN /FCSSKD/TIKEVKRQHTWVKIFTSYI FDKGSTSRCKEL/RKQQQNKPIQKCSK VLNRFFFREDIQLSNKLMKGCSTSLNH
526	14427	A	532	184	509	PQWPAHSFLPALGSSGTGPY*VVRQIFD SKDKESSQ/WSHETSDRPPKADHRRRSR PSLATSP\PRLEPHPSLPNHSGLPILSS LPWGAVALAPTHFSALAWP*RPLPCNSQ GEKFPFWGFF\ERESH SATQAGVLGHD LGSLKPPPWGSKGFFCPSYSGG/WNQKN HLSP
527	14428	A	533	401	3	VIREMQIKPLHIQ/PGWL*SKSVKKY*Q GCGQS/NVLIHY/WLKT*IMGPFWKIVW QFLIKLPYGTVILLSGIYILWRMEKKPP KFCTQIFIAAFFIIQ*PKSENNPNIHQ KNQ*DVHMYIHTMEYLLAIRMNIH
528	14429	A	534	419	93	SLAIRQM*IKIPPRYTRVAK\IEKSHNT KYWKRGATGTLIHCWWECKMA*S*KIW *FLIKSNINLPFPNVILL*GIYPREMKT CLYKD\CM*MFMAVSFIEQNGKQPKCL
529	14430	A	535	414	2	NFLARGYINCGPQFFFFPPRKNLKWGP LSNFPKPL*KGGI FGEGPKVKKNFFFF FLFFFF*KKPPCSRLKAK/WKIFGPL KPPPPGLKKFSFLT PKKNGDKRGGPPRR GNFFFFFLVFLVKTEFFHYVGAGLK
530	14431	A	536	32	435	DRATALQLG*KSETSSYKKKKKKKKKK DGGAPLKKNPGGAKKPGKKNFSPKR GGKKNPPGNFEKKTNFGGKNGAKPPQK KKT/AWGKKKNLKGKRGKKNPKTLGAKK FPPRG*KKKKKPPAARPGKASS
531	14432	A	537	348	1	EYIKSTHOMGKNYPLKNTVSSGQVQWLS PVISAQFAIAKSWSPKCPSLNEWIKKL WCV/WCVVCVCVCVCMMEYHSAIKRNE LMAFAVT*MRLEII ISEVTQEWTKHR MFSL
532	14433	A	538	523	66	TDQTSHNIPLSQSLIQSEVPTLFNSVKA E*CEEA/AEHKFEASRGWPTRLKERSRL RNMSV\GEAAGSPEDPATV/INGGRTQ PQIFSVAEATLNWKTTPCRPFIGREKSM PGFRASKDSLTLCDRDFKTHLCLVFHYWN AKHVQVYILLKVTAKI
533	14434	A	539	413	2	RDKV*PCCRSWSQTPELK*STRLCPLPK *DYR/R*APAPGPFLL*VHRHVSIFKSG PLSCRCNSFQD/HDSIKPSFPTIQYAHG NKFQL*TPDTLIFFLKWSFTFVAQTGVQ WHNLSSLQLLPFGFKRSDAWADAWADAW

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534	14435	A	540	385	2	MASKHIKT/CARQLAIREVQIKTTQYHV IPTRMAKVKKI/DNECWGHC*NTLINCW WDCKMMQLLWKK/SVWHSSRGKMYQLP CTPAIPLLGIYTELKTCSHKN/T/CT*T FIAALLVIAEKWK/KCPSAEW
535	14436	A	541	44	398	RPPFFFFFKRPLWKKKQGFPPPA*RGE IPSAKK/PPLGPVSGPGNPPGP*KP/PQ NPPPLGGSPFGKPPPLDIPFGGPIK GK KWGGPPLAGGATTKN/PPPGGNFWKGGK APFFPSQKF
536	14437	A	542	370	10	FFLRITKVSLEPRVEG/KVQSOLLAAPPS WGQVIPPLOQSP*LRQKDFSPGG*GCS EPCSCPCLPAMWTEPNVSXS*KKKRKK EKN**KKKSPINTGKIRFRIH
537	14438	A	543	1	370	FLLRHILLCHPGFCVATAYCSRDPGSS D/PLPPQAPLPDQ*PRLQA/WHRLAPPH SANFF**RQGFTVLARMVISISQPCDPH WASQGATATKADDYQK
538	14439	A	544	50	395	IPGLTRQWLLDPCASPSTPPYT/P*VQP STPONSSSPKTHNQKGLMPLSPTPKP STAWKKAILEHTSSSSSSSSSSSTCRNR NGYTYTVPEHRPARGHTASQTRKQVLAA THKP
539	14440	A	545	1	370	LCSVTQAGVQRRKLSVQPPPPRFKQVS CLSLFFFFF*KRVFTLFPRLBGRGPII FNGSPTLRG*GDPPV*ASKELRTKGGPH QGQLINLF/CLGATGPTYGAQGGFKSPG LRRWAPLGPPRA
540	14441	A	546	178	365	YKKTDATKTKMDK*DSIKLKSFTVKET INKGNR/QPTEWEKIFASHTSDMGIISQ ICKELKQ
541	14442	A	547	11	236	KGTTKLVLKLSDFKSYFKAIVIKTVRN/ WHKYK/HIDQWNRIQNPEINPHIYGQMI FKKRAKNKQKKDGLHKKR*WSNDFQET CQEQTMEKGRSSQEKMM
542	14443	A	548	355	3	IKKKNLGRKRFCFQBEKTWP*TPKKKP LENPGGVFPNPGFPFFFKAKIPEGPPPG V/SFF*RGGFKGYPPLFFFFFL*DGVS SLCHPGCSAVAQSRILTASSASQVHAILL RHVDEGR
543	14444	A	549	1	373	CFLICRHTSHMWRIWFQTTAINQIWQ*K ESQVVVSQ/LYI*KLHLLYEVO*HFV*K YTQ*LLLENADTK*AHAVGKMVLIDLK AALSILFNL*KNK*NLKNWPGMVAHACN PSTLGGQGGWLT
544	14445	A	550	446	2	NIDKAPTVLGKMVSIFPFSRSPPLGPPK CWGHRREPFRPAYFGI*ILFLTPP*NFL NNSPQHLGKISGIFSDPSLVFFSSFF FAPPPKKFMLCF*PFFFFFF*DRVSLCH PGWGAVERSWLTAAPISQ/IR*SFHLSL LSSWDHRA
545	14446	A	551	342	26	WAPFIFFFPYKRSPQKPPPPGNNNR GF*IFG/RGGFFKKEGLSQFFFLKKV FFSPGGEFGYFPFKASFLKRIFFFP PPIKKGDPGRGSPPRGNNNPF
546	14447	A	552	3	167	QPHLQDCL*QONPVAVG*AFSSHPRDSL NNPW/WPGAVAHACNPSTLGGRGRII
547	14448	A	553	3	413	TLITALSSH*PFT*VGLEINMLAFIPVL

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						TKKINPRSTEAATKYPLTQATASIIILI AILENNILSGQ*TITNTTNQYSSLIIM ATAIKLGLAPFHF*VPEVTQGTPLTSLGL LLLT*QKL\APISFIYQISPSLKKK
548	14449	A	554	441	1	SSPPPQARGEIFF*KNPGEETSOHNKKN EVFPPPPP*KFFSPKAFIF/RGGGGPK RPPPKKKFFPKTFRVFPKPPQKKKKFF FPPPVKFGPPRIFFKSPPLFFFFF FFFFFFFFFFFFFFFFRMCDCRWHGKFWIL RDGF
549	14450	A	555	3	455	NTNSSMYVCIYVFI LRQSL/DSVTQAGV QWRDLSSLQPLP\GSWDHRHLAQ*YL FNVLLEV\FVYERGTIMVPIL*DCNVN CRVFGTRSLSVYCVMGIFYRC/HIESML CDRCFIFFDIGSHSVTQAGVHCNGL\ MKPLPPG*RNFSGLN
550	14451	A	556	1	299	RRMRQENRWNPGGTGCSEPRSHHCTLAW ATEHDSVSKKKKIRSSLGKKT*FYHNI LKAMG/CITGIHKGPEGAWQREGHPTTP QGPKKAPQRGQTYDPD
551	14452	A	557	3	391	PVWNNSFEASSGWLIGFKKRSCINIKV QGETASASVEAGVSYPEDLAKITDEG IKQOIFNVDKIT/Y*KKISRTFIVRE KSMGFKASEDRM*FLGANAASNF*LK PILICHSKI PMTFKSRAS
552	14453	A	558	337	1	TRFPPFLGGFSTKFFYRPLVRFPLL/RE RKIFPLPPVFGGPPALGPFWGFLFPN PSKKRPPGFPWGFPP/CPPKFLPFKPL GFFPSFRGFFFFFETVSLQPS*SAVV Q
553	14454	A	559	117	419	IPPLLLGVGLFFFFFIRKKRGVFSRWR GGGSNFGLETPPLGIDPFSGLTPPKSW ELRAPPPPIKF*KFLKNGF*WVSPG GLEISALLVFP/SASQ
554	14455	A	560	347	1	IYKELRQLCRKKSNIYIKKWKNNRHF SESIQMANRQMKRCS\TPVIREMLIK TTLRYFASPVKMAFI*DR**MF/WQRC GEKGT/H/CWWECKSVQPL*RAVWRFLK KLKILLP
555	14456	A	561	2	375	IPPPLQNGEKIFMII*TGAEKAFYKIPF PPPIK/TLNKVGIGKNFPHIRAL*EKP PAYIFHGEAESFPVRSGLRCLPLLLLF HPVLEVLVRAICPLK/E/IKGTQIGKEE
556	14457	A	562	391	2	ASGSKGKKKYPPLRGSPPLPGNPLFFL EGGEGKFP*P/RNWGPPPKIFPQKGQGN PFFFFFLKGPKGGFPPQGEKGVGFPL PGEKSQRPF*GEKGVPPP*KKKPPPPF FFFFFSETVLLLPKLECS
557	14458	A	563	384	3	ISDSGVHPLGLPKRILLQLSYHVWP*P KCFC/PHLCLEMTLFQPP*GLPSVCAPS KQEEHGCFFPISVARQEC*PLFPKNLDT* HFVGNFLKFFFFFF*DGVS LGHPGWSAI LTHCNLCPLGSSNSLPQ
558	14459	A	564	522	120	SLFLPTLECNGTISAHYNLHLGSSDCP ASASLVAGITGMCNLCPLSSIDPSTSAS *VAIDLK**GARGNCPVS/VLEKGWPE AEMRGESASWDPRLGRPGVAKRICRR HCCPVQPPQVSMESGPASPN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
559	14460	A	565	73	264	KDRHIDQWNRIESPQIKSMTIHLWSFDF FLQGY**KDRHIDQWNRIESPQI\NL*L YIYGHLIFFYKQGE/IQWRKKTLSKWF WDNWIFKCKQ
560	14461	A	566	413	1	EKKKKVPSQVLTTPKPQVLGNFPRFSEBQ *LSLVPVSSLPQLSLSGKNQGP*ARRVA LCFGKSPGSQQIWF/RLP/EDIVTTVQA SYSKKRLFLSLLDQYVLRREGAVNSA NLSLAPW
561	14462	A	567	397	1	FLGQDLTVAWARVQWCSHSGSLKPRPLGL KGSSRSATG/SASPYLVPMFLSNLFWHV YIL*LYKTMGTI*MEM*FTPSCPMYSVV RDV*IFFSFETEACPVQAQGLQWRSGLL PQPPPPGPKRFSCLSLLTSWD
562	14463	A	568	437	1	KFSEDPAKLIGEDGYSKQVNLNAN/ETA LYWKNMSSSTFLARKETSMPSKLQGTG* LLLGANAAGDFQLKSMLTCHFKNPRALK NYATSPPLVLHKWNNKAWMTVHMLTALL TEYPKPTIKTYTYHNTTGSLLTPHASAH ASAHAS
563	14464	A	569	234	1	FFPPPPFKASSPPQGTSSSRGVF/PPFF PPPKKGFFPKIPGSSSSPPFF*EKTYFR FFPFFLAPPGVFFR
564	14465	A	570	2	396	FS*AFYHFGIALTPQLGGDWSAGITQV KSLQVPVVNT\SGLLASGERIT*ADHNV IQNNRRRIQALLITVLGLYFTLLQAS ENFKIPFTISDGIYGSTFFECAGLHGLH VIIGSALLTICFIPQLTDC
565	14466	A	571	3	403	HASGLPSSWDYRRPPPRANFFVFLVEM GFHHLNKAIKSFACNEIQPLSAVSVAG LVGCV*VCKCLFPVL*Q*LPQF*/S/HS IANWMREWPLRLSLF*LIC*GERMSGFA TQSRDPCLPGFLYQVLSLAKFR
566	14467	A	572	100	371	YKSNDFYVYGILHPLTTI\FFFFFPKKK KFPFVFQVGGQGNLS*LNPLPLGLKGF SCLKLPRSWNNRGAPPPFPNGFTSKNG VSPCNPG
567	14468	A	573	371	1	REGARES/TWSSSHTPVQKGLRYGIIIF ITSEVFFPAGFF*AFYHSSLAPTQLCG HWPPGTITPLNPLEVPLNTSVLLASGV SIT*AHSLIEN
568	14469	A	574	353	103	SLQLQPPGLN*SSHLSLSSWIYRHKFP CPANVRFFVFFCRDGVLLVAQAGLRA/S ASQSAGITGVSHLAQLVNPLLFYFSRAG D
569	14470	A	575	1	206	FCIKKIIGFIPGK*GWFNISQPV*SLTN RIKEKIHISMTAEPIISIITEKVFDKIQ HPLILQKPPGQK*EYKPLNLKIGICEKN /PIPNIIYNGEILKQGCLLSPPLFNIVL EDIVIQSVKIKEGINIETQELR*SLTNR IKEKIHISMTAEPIISIITEKVFDKIQH PLILQKPPGQK
570	14471	A	576	157	255	YISPTPPFPDLFF*NYLPNPKLTSPAP NFQIY
571	14472	A	577	365	3	PPHPSVFFF*KSPPPPPPLFFFPFPPL FRGGPLYYSPP/SPPLFFSRRGKDTNPP PYSGLSVAGTTPPPPPRTPPLVSPPPP PFFFF*RGPKNKKAKQTITFKSPPGT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion
						NKPKHKNDRI
572	14473	A	578	2	323	VGSWEPDEKVSHRELLSFLFYPPFSHI SS*ETLIDFALTSTDIWALWHAENQTV VKYINFE/HVWVT*FCHPTSPQAISC*E DERPGAVSHACNPNTLRGRGRQIT
573	14474	A	579	369	1	AHLKGTGGGFPDFFPINLEFRGGLTSCP NPLNNWE*R/RPPPPPGKIFGAFFFFF FKVETGFHRVDLLVLIS*PCDLPASASQ SAGITGVSHRARPTPG*FKKKIMTF/CL *KWSHYVAQIG
574	14475	A	580	394	125	AAEGEGREGWRNRPRGRERASDRERER VR/ERGEERERGEERAPQ*SERWR/E/R SRERERVRELWSDSDRALEREALLR
575	14476	A	581	416	1	KGQDLYGEV*KVLLKVIQVLNKNWDM CS\KINILISFPPIALKFFF/ELDEI/ CSFV*NKC*RIAEVLKRRQ*CLGGHL /TSPHIRRSYNTTFSOSIWCCYRTKQID *WTRTONPEKDLRI*GDLYDLRCCSS RA
576	14477	A	582	3	403	NCFSQFNVIIMEIPAKFFIDINKLILKC FCKGRSILKKR*EDS/QRRNFLVIKT VYWQRECHIDQWDRINNPEINLHKYSL ILDKGAKAIR*TKES/I/YSK*C*NWKF CM*EK/IDPKLNPLYK
577	14478	A	583	402	121	QSLTHSKALTLFNSMKAEEAAEGKVEAS RGWFMRF*ERNHLENIKVQVEATSAGVE AAASSPQD*GKTTDE/GGYTTQIFNVD ETAFYWKTMPS
578	14479	A	584	255	517	IYIFGFI FRGRVLL/CTHPS*SVVLQS* LTAALNFWAQVS/LPSSNDYRCTPPCLA FFFFFCRGGSTLCPRLVGNNSNPKFFP LGTPCF
579	14480	A	585	1	414	SSHSCCSKA*SSMGSPAPYKLVPLFLC LFIWDGVWLCHPGWSAVVQSLTAASTS Q\VHPSS\CLSLRNSW/EYRYVP
580	14481	A	586	392	43	CWDYRCEPPCLA\TETGSSYISQAGLEL LASSNPPMVCHPKCWDYSHETMHAQNF FLKGIS*F*LCCSHFIHNHLLWLKGVH TYTHAHTGLEKYKTQCLDVKCIYSDLLD GAIK
581	14482	A	587	1	394	GTR/YGINLFITSEVFFAGIF*AFYHS SLAPTQLGCHWPPGTGITEPLEGPLL NTSELLASGVLIT*AHPSLIENNRNQGI QALLITIVLGLYPTLLQASEDFEDPFTI CDGIYG*TFFVVTGLEGLHV
582	14483	A	588	190	3	DGINLKIPGGIFFFLKARSHSVTEAGMR W/P/NYGSLOPRPPLK*SSHL SLLSSW DHRHAPPSC
583	14484	A	589	157	387	TKRGRVGVVWIKILGINLTKEIKDLY SENYKTSLEIKER/DTNKWKNIPCF*T ERVNTVKSILPKAIYRFNVIP
584	14485	A	590	891	0	PPPPFFFLPALIFFPPPPQ/PKTPRK KNPPPPPPPP\PPFSSHIP*QFLSPPPQ HHHFIIHPPPPQPPHPPYNNPFKFFFF* NINVPPPP*K*IYFF*TKFFFFIPNIF F\TKKKIFLSPPPKFPPLLTNLSLPIL IKNLLSKPPPPQI
585	14486	A	591	1	496	GTRAYQIVKPTP*PLTGALSALLMTSGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PMRVHFHSITLLILRLTNTLTYYQRWR DVSRESTYQGHHTPPGQKGLPYGIMLFI TSKGGFFARFL*AFYH\SSLTPTPQLGG HWPPGTGMTPLNTLKDPLLNTCVLLASG/ VSIT*AHHSLENNRNRIIEALMTIV
586	14487	A	592	175	2	PPFFFFLLRHSLLTAQAGVQWCDLCSLQ PPSPGPKRFSRLSLP/H*PGMVANFCIF SK
587	14488	A	593	107	733	AAAAASKVLM*REGQLPGAT\GTGGVQA *APGSVA/ABGASVEGPGFGDTAPAHQG LSPTRSHGQGGAGRAS/SSQQGSPPGGRG DGASEVWSGAL/SPGGGKDASASVPRG PYAEAEKGGWALRGLGGVAAPGPPSRAG QAPSGS/YTGPNARPAPWPIPGQGGGLR RDQAG*VSSWTGSTFPAHTAHRAPGHG GKGGSPQQPHPPQGPQIPT
588	14489	A	594	10	435	FKWLLKSHAICFWTRS*SYCDNVCVPSL WAHLGIRTEIPEFFLSKFLCTSIIPH TYRRQLRLIQGST*EA*EDKLEQK*AL GAAQFTLPGMDVFCVFCF/CLFEMES HSVT*ARVQWCDLGLSLQLPLGFKQFSC LGL
589	14490	A	595	437	3	DEPKKWKTI PCSWIERTNI/VLKMAILP KAIYRINA/VPKLPSTPTEVGTFSQN *KTILKFRWNQ\KRA*IAKATQSRKNK ASSIT/PDVASNYKTTVTARTHWYNNR HVDQWNTIENTEIKLHTYSQ*ILSKAGT SKQWGEHV
590	14491	A	596	2	498	FFPFLGKTKPPTLHFFPPPPPIFFFK IFFGLPKKKNPPK/PPFKRPPSPKPF FFPSPPPPNPLFSKAPPIFFFFFKKI FFFPFPLFKKSPKTP*ILGFPSFP FFPPGFPPFSLF*GGVSLCHPSWNPVVL SRPSSKLASAFRMPPEVG/SPFPSP
591	14492	A	597	1	311	RRVSSESRRSLESRRSLIQRMERP RCQRFRENSCVAPRCKGPGGKLQALF *VPVAQLGEPGAQLGDPGAHGEATVPEV QGE/PAALLPGTAK\PGEGSPGFIPPR HCRGTGEBGSPGFTQGRETSKAQRTGC LLSCRGCLCLSVSGDS
592	14493	A	598	302	2	FLRFFHHKKFTKALNRHFSKDILILLSS NHMKGCSMSLVIRD/MLLKIT/MKYQFI PTRMA/IIKKTDRYWQKN/CEKI*TFIH CW*\NEKMQPSWKAVWQFLRK
593	14494	A	599	3	386	HTWPPPPRSPTAPPARTQPPSLQSALEPA PQPGKKKKALRNEKG*NGSKKG/RGQPR PPPLRGPNGRTRS PAGICKGGGFCPGV SKAQGAPRPGGRETVVPGFFGRPPPLPR GPGPPGVLTWSRHCPRLR
594	14495	A	600	374	53	EGFFFFFRWVGQRALFWSPHFPFPGV KIFFPPPPPGWGLRGLPPPPNFNFFFL KKKGFSPPFCVFSQLPPAGVPPPPPP/ TGLDLRG*PPGPPPPPPPPPP
595	14496	A	601	393	1	VSPPKGCVS ENKIPPHNYFAKTFVHV KLFVAPLFLQILF*GPFLTSIRGLIL\ WIPYSPGY\TLTLIAPRHFLRTIIPV RSVLEKTYLGLSGMPRRYSDDPDAYTT* NIGAFRIARES VVGRKLDL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
596	14497	A	602	1	155	PCFVT*SGVQWRNHDLSLQPLSPGFK*FS/CSSWDCRHAPPHLASFCIFRSTRP
597	14498	A	603	170	455	KPNASLKRVLILCIQLQSSRQKNNPT/VKKWAKDLNLFSTEDL*TVNRYIKKYL TSLVIKKYHFIPTRLSKMKKTEHSCWE SCGEIETLTCSW
598	14499	A	604	3	449	TLLSNLEAAKKKKEDALNETRES*TKLK ELPGVCNETMMALWEECKPCLKQTCMKI YARVCISGSGLVGRQLEEFINQSSPFYF WMNGDRIDSLENDROQTHMLDVMQDHF SRAFSIIDELF\QDRFFTREPQDTYHYL PFSLPHRRP
599	14500	A	605	169	435	KYENTKINRR/VAPN*ISLSPEKKKKKK KKKKKKKKKKKKKSSASSKASPSSR GG
600	14501	A	606	453	29	TSPPPPPPGENFF*KKPP*K/HFFPPPPQF RFFPPPPPLKIFFPPPSLFFFWGVPHF PPPPKKVFFPKSPRGFFPPPLKKKFFF SPPLFFPPPPGFFLSPPPPPPPPPPPP FFFSPFFPPPPFFFTVKNFYLLCYFYKN
601	14502	A	607	170	408	NEYDHFSTIIKERRDFIVCVFFIFSR*S FTVVTQAGLSSLPPLPGYKRFSCLSFL CSWDY/RVVHPQGSANFFVFLVEMG
602	14503	A	608	2	448	SLHPVIYSEGIKSRSQSPCWR**KTVKKK KKNPNQKPKKKKN/RPKNPLGGGKKFF *PEKKPGGKKILKEGKKICPFPPQKK NFKILKKKKGAPLKNP*GAQNFFGMK KINFFP*REVKKNPIGIPKKKPLFWGGP IGANFPENL
603	14504	A	609	441	28	GGTFLKGIKSAPRI*KGFPWGGRFPFPA RDPPQFGG/PKGGGSLSPRLNPPGPPG *TLFFFKKPKLTGGGGPPPLIPALRGVR P*NSLYPQRGGGAQIPPGPPPPGKRAP CFQKKKKPRRKEKKK
604	14505	A	610	445	1	LWLKNTGGGGSPPLFFPLGEPKRD/G FPRGRGFGPPPPPIKNPPFLKNQNNPG GGAQPGIPGFWGG*GGEFFLPP\SPGFH *PRFGPPPPRGTKREPPFQKKKIANC FLLSDKSLLEERAWQVVGPSPLEPTVA PKPNBRGKAQ
605	14506	A	611	253	437	KKKKVQDMFSENPKML/NEIKATLNKWK DISYS*VRRLCVVKMAILPT/IQSYRLN IIPKI
606	14507	A	612	186	2	KKKKVQDMFSENPKML/NEIKENLNKWK DISYS*VRRLCVVKMAIL/P\KQSYRLN IIPKIQ
607	14508	A	613	37	453	KTPPPGENFFLKKPKKNFFPPGNWGVF FPPSPLKFFFP*TFIFGGVWPNFPP KKKFFFKNSPGVFF/SPPP*KKKIFFSP PRYFWPP/HGFFFKGPPP
608	14509	A	614	1234	0	KKPNTPN**WAKDLNRHFIDKSSIKDD QYY*SLGQCKLISQYNTCTRIAIKKT NNNKSW*GCGETGNLIH/WIECKMVQ
609	14510	A	615	327	188	FFSSLLIISIPKFNHVTSLRLNK*AM LGSSHL*LQLLRRLRRDHLSPGVSGCS KL*SH\THCTPVVWVTE*DGRKGLAGDGS HSVTQTGVQ
610	14511	A	616	103	446	KKKKKKKKKKKKKKKKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						DGGGALKKNPGGAQKNRGERKKFFFF*G G\KKKTPGGFWKKNPFLGGGNPAPPPPK KKKPLEKKNF*GGRGEKPSPLPGKEK FSHKKK
611	14512	A	617	3	429	GLLSIIYKELLQINKISNLVGKWKDK/ NKQFLKKEIHLAK\YMKRYSTSLVTIE M*LKTRYFHLPLNKKIKHDNNIHC*GYK EVGILHILLEA*IGKPPWKAITVTVLNA PVFCL*FCFEMEFHSCCPSLKCRAPTSF IGAS
612	14513	A	618	427	6	WGGPPPPPIFFFFPPP\PYFFFFFLQ ALFS*RVFFFLTTPPPKNFPPP*GPPPP PPPPPPFCV\FFFFPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPFLVENCVFINSITSIDIEQKISI SC
613	14514	A	619	68	434	YSKD*PINTKKKKKKKKKKRGGAFKK KPGGGKKNKGGKKKNFF*KGGGKNPRG NFGKTLFPGGGKGEKPPQKKKSLGKK KI*RGKGGKKT*NP/CGKKKFSFGGF* KKFPGGGGKY
614	14515	A	620	454	90	NFPTPEKFGPPQGNL*KAPPPFF*KG I PFFFP*QKRGGFKSPQKPPQKTI FR PHPPKGGPQGPFPFGKIFFLEF\KK KGGFP*PRFFFPFGPKPPRPPKAG IQGTTPRPGP
615	14516	A	621	432	2	PEAFSSLLHPAPGEKFFLKKTPEEKFL TAKKYRVFLPPPLKIFFFP/LRALIPL GRFAQIFPPQKKGFFPKIPRGVFFCPP* KKKNFFFLSG*IFAPPGIFFKGAPPPF FFFFFLDRVWLCYPGWSAVARSRTS
616	14517	A	622	422	2	GGGPPLPPPRGGLPPK**KA/VGGGK PPPPAPL*NPPPPKKKIGGGGKNPP PPLACFFFGFLPPPPSFWGGEKFFFP FLSGPPPPQKKKKKKKKKKKKKK KNKKNQTKKKKKKKRAARDPRVRPRV
617	14518	A	623	176	401	KFSMFIILWKAYTLCVVCVVCVVCV VCVIMYLFISSQ/RRCLFLGEGKICIS LTVLRGSRVCV*SQDLVPC
618	14519	A	624	1	355	HSSGLDNLTAHSHLCCGV/CLCFLVL VCVVCVVCVCLVCVCL/CLYFGPQV PK*SKNSSTSCLLFHFTSARTICP/CC/ CVVFCFCFFA/CYQTC*ILTSCL/AIC TAGVCL*ANKYSM
619	14520	A	625	2	400	HTRLIFCRDGVLLCCPGWLQTPELKSL FSFGFLSLFFFLERDPGSHGP/VGGG PNLG*WKFPLG*KQFSFTLWRRGNT\ RGPPPPPLVFWF*KTGFCEVAQAGL EQRPFGDQPVWASQGAGITGVP
620	14521	A	626	307	3	VFFRLPLTQGPGLFACFPFPPCRFFFS FFPGSNSPFP/L*KLNFWAFPPPPFF FFFFSILFKDRVLLCHEGNAVV*S** P*TPGLN*SSHLTPSGRV
621	14522	A	627	1	391	NPPPLGGAKEGGPFRARGSNPPPYWET PFFF*NPKIFPGGGHPVIPSFFGG*GR KFPLREGGVPL/RPNFPP
622	14523	A	628	191	375	LILIFKTIENFLILNFF*SGGATQAGG QGRNLG*LQPPPWPKRFSCLNLLSSW\

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						DYRGWP
623	14524	A	629	3	382	HHCCQIRLFILLITASEVLFCFVLPFFET GPCSVTEAGVQ*CN/HLQPLSPG/PPTS AA*VAVTADVHHHAWLFVCLLI*DGWS VTQAGVQ*RDPSVQPPPTGLK*ASC/P AFQKCLDYR
624	14525	A	630	396	2	CRIENVLKKKKLEMSNLSEBMLKANIG QKLSLLAPQQVVNAKESLLKEIRBALPL NTQMIRMQNSLSADMEDIL/VVWIR/DP TNFNIPLSQSIIQSNA/L/TLFNEMKP* RGEEAA*EKFDAISG*FTTFKERS
625	14526	A	631	47	392	LHSFFFLFLGKKIFTGGGGGGQKPPF* NPPPPG*RNFFFLPP*KTWFMGPAPPPR KIFGLKKKGFPPLGGL/SIGTPPPRG PPPLPFRGGCYGGGPPPPPIFFFTFK NFSN
626	14527	A	632	39	382	LIFFSEFFFKNFFFFGRFFFWGGVAPIF PPPKKIFFSQFP/LQVFFFSPP*KKKFF FFPP*IFAPPKTFFSIPPPFFFFFFFFFF FFFFFF
627	14528	A	633	2	213	LDKPGKHSKISSLQKI/HNGVCLQS*LL GWLREQDCLSEGS*GCSEL*FYHCTPAW ATK*DPVSKKKKGFLK
628	14529	A	634	2	206	QENGMPNPGGRACS*PRLRYCTSSWATER DSVSKKNE/TNKTLLREI*HFVGGPNG KKGLLKTVMGGLT
629	14530	A	635	205	2	KRSLGLLQI*/VQWGDFTLQPLPPGV KQISRLNLLKKWDY*RGPSGLKFW/IF L*KQGFPPQFFRVFN
630	14531	A	636	3	399	QVQQTASCPDSDLSSEDEDLQAMASM TFPKKKKKKKKKKKRGAP*KKTRGG PKK/IRGKKK
631	14532	A	637	122	373	VSNILWTQSLLLFFFLKGSLLFVQPG GQGLDLG*TKFPPRGLKEFSCLTLRISG NYGLAPP/HPG*FCFFIKKGVFPCCPGW F
632	14533	A	638	390	3	LLVLFLPDGWSPPAFPHEQKLPEVSPK ANAAMLVPQPAKP*AHPTFFFY*FPSFR FFFARMG*SS\YFVFNLTSLSEILKGPI NDMREVFPPIFRLILFFPGDVRLLCGP GWSSVVQ*L*LTAASA
633	14534	A	639	392	42	PSGPGKPGGKTFLRKPPFQEAACKRQGFY PLFPKPLKNPKAPQNRKNLGPICPPPK P/QGPLRISPONSQSGSL*GPNKGNCFP A*TWGPPGAP*RGPPKGPFFFFFEKVM AMGLA
634	14535	A	640	390	1	LSFSEEGMSTAAGQKLGPLCO/TSQVI NAKETFLKEIKSVIPVNIQIRK*NSFI ADKEKILVV*I*DOTSPN/IPL/SQCLI QSNVLTFLSSKKAERGEBAABEKFINFS *RLRKEAASADREAESYPEDL
635	14536	A	641	368	3	KKGGYGVPPFPSPPPGFLGEGSFLPPKI KVQKTL/SWPPPPPPGGKKTFFFKKK RKNFLTGFFFFP*KKGPPFFFF*CPVV* KFWGGGFKPIFFFFFF/RDRSLCCPGW SAVV*SQFTPRV
636	14537	A	642	134	413	QKDQRNRIESLE/IR/PHTHNTLIFDKG VTGFQYKDSLFNKWCWDN*RE/ITQNL

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						SLDPAHTTTNVNLKWTCLKARP/VKTL VENMGENLRD
637	14538	A	643	2	436	GRVESINLPLGCRLEFKKRDNIKCGQ/G* RAGGSLIHCW*EC/EVVQPLWKRIQQFL IKLNIHLPRDSTILLDDIDLDGHPKTS LFIIITHNCCFIHNHP*LEQPKCPSTDVW MHKWPFIHSMRHYSATKSAVVDNFKGI LL
638	14539	A	644	446	75	LDLLTS*SACLGLEPKCWDYRSEPPPAF NF*/STTK*SLWSSHKQDYICRFLLSYT ATQKFSTLTYY*SHLKT*NAQMPRLYL QSLILGSI*KSNI*FQCAAKAENH* *SDLYCQIMLEFSM
639	14540	A	645	318	1	KGVPRCKNSYVGPSPGPIK*ILFF*I F*DRISLCSPGWNARVFS*LPV/T*TTG VKKNWPLSLLNI*GYKGVPPRGIFFFF FFFRDR/SLTMLPRLVTWQVIFQ
640	14541	A	646	3	348	QFSFFVLIYFTLFPVSCF/WCFNL VLFCEIIFFLIFY/YYSVLVSFFYCLLV LFLSKLSFF/C*YLNITVFICSMTSFF* RIL/CCLNFIKTSFNFL**FGMVLESC FFFFFWP
641	14542	A	647	2	553	AILIPDKIDLK\VTGDK*NTMIKGS IHQEDVTTINIASNSR/APKYMOKLK GKERQISP*K/VVGIFNTFFSI/DRAPR QKINQEIENNIIRQIDLKDIYRTFHP TSEYIFFSSAYET/FSKIGHKLKHTSL NKYK*TEIMQSMPSD/HGGMKLENNE/N VGKLTNMWKSDTLVSDWLGAVAH
642	14543	A	648	388	1	GPPR*SPPFGKPRGAVPQ/GGGGLKPPG PQGENPFFFKPKITLGPWGWP/RNPPP LGG*KGKIP*/PPGGGSGNKNFSPSGP PGKQKQNFSSQKKKKKKKKKKPES*C PGTSFPQVTDGSAINASS
643	14544	A	649	387	25	PGMRGGFPFPLKNFFPPGP*/MSGGG GGPNPFPKPKGFFPKNPPGVFFSPPKK KIFFSPPPENLGPDRDLKGPPLFFFL QKNPGVFFRAGQGNPPQKLAKIFPLPPG GGGAVRHI
644	14545	A	650	918	2	LGLKGLTYKILHSTIADHTFFSSSHGT FAMTDHILGHKIHLSFSKE*EIIPSTS FQ/HHSRLN*K*INNKNWVKIP\FWR LNKTLNNT*TKE/GLKRHNILS*TKN ITYQILWDAGAVLRGKFIVLT*IRKE ERSK\TTSFNIRKRNKKLIINIRTEINE IENRKSEKILN\TKSWFFKKKSIKSIK TLARLNKRKRKETQIPKHQK*RRGITG NMANKKIKRNIHQPYTHKLGNDNIGQ FLEKRYLPKLKQGEI*SGWAYIN/SKEM ESIINTLPKRKAQDLKMFQSE*YQTFK EKK
645	14546	A	651	282	265	GVFFLKKRPTVF*KKKI*LGPHPOLKGP PGVFQ/HFPI*NFGISGRGDLFFFFFFF FFFFFFFLRQGVVSAQTGAQWHNQGS LQPPGLK*FS
646	14547	A	652	6	223	LYAHKFNLDMDQFLQRHNTFKLIQEE /HRLTVIK*IKSIVINLPKQKA*GPDGF SGEMYQLKEEIIYNVF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspond- ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine : C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
647	14548	A	653	128	337	FXFFFXFFFXFFXXXFFFXFFFXFF FXXFFFFFPPXFFFPFFFXFFXLI FFKFFLFFFLFF
648	14549	A	654	238	2	MAAASTLLALVIISTTF*LPOVNGYIE KSTPEECGFDP\SPARVPFSIKFLLVGS PIQTHALDIALFLSHTRALPHHTT
649	14550	A	655	325	3	CSEHKKNVF*LRAKKTNNPNLKWKADLN RHFSRENIQVAEKHI*ICASGLGLEM IQTTKC/WHPVWKT/VITLQN/LHTRL PYD/PAILLLGIYQRELKTCCHKMYTS V
650	14551	A	656	3	1655	FPLGMESPSVAQAGVQRCDLCSLQALPP EFK*FSWLTLSSWDYRRLPPCLANFVFL VETGF/TMLSRMVLIS*PCDPPTASQS GGITGVSHRVQPALLFFSLCCLVKMIVH APLVKTCRPSTVGSL/SVPAFWME
651	14552	A	657	519	84	SVRCQSA/QMGASHLGYSGRVDPLEE AVFPFSDLKLHAGITITTLKAVRQGHLS GEAKDF*RPAEQ/GT*YTSKLA/STKON ILHEE*ITFVLLLPKHGEGIMWSPVPPK FLFFS*GMTNSGSGAGILDVPNHPSKD *HYVLTISH
652	14553	A	658	38	383	BXCIFFFFLELRFEGFTFGGPPGGRAQFW NKTPPP/HKKREFPALPPPGGNGLGP PARENLFV*KRGFPLGGKRGLNPRPQG NPPP*PPKGG/GNNGGPPPRQKK
653	14554	A	659	98	394	KEPGKKRETFSQ/NKKKKKKKKKPF PPRGKKNPFKKKRGG*KNPPPRGGGKG NFPPVMG*RGKNLPFRKPLFPFPQGGG KN*KK/RA*KNSPQNF
654	14555	A	660	214	567	GFSVINIGLKMMMIIILRDSLTVTQI GVQWHNLSSLQPPPPGFK*FSCHLHLLS RDY*HAPPCPVNFCILS/BRQFHVGOA GLKLSASSDPPTLAPQAGITVPSHQ
655	14556	A	661	463	392	S*HFHPSSSSSSSSSVINY*/EGLLL C/QVAHFYNIDQQMIQSQRPMMLQSA AFBQIIKVNGLLILL
656	14557	A	662	205	242	GTGWQGGGLDG*QMTLWPGSGVGGSA P*GI/GPGLPGLPAPPASP
657	14558	A	663	63	351	QSETPSQFKKKTQIELLYFAVSLLGIY QKERKSVLKKHYTPMFTAALFTI/VWDQ PR/CPKYMKR*NVMY/HVYTHTHMEYY SATEKNEILF/FATTW
658	14559	A	664	1	358	FFLRQQL/DAAAQAGVQWCNHSSORAPP LGLGRSSH/PASLAGWSAVA*SRLAATS TFRVQVILLSOPPE*LGLQSCSITQVGV QQWRDLGSLQPPPLPGFKRLSCLSLPSN* DYKRLAPP
659	14560	A	665	10	257	GMNERGNITKEIKKIWEYYE*LQTSQ DTL/ELNKPPERKYK/PRTNQSINN RTITS DYISNFKRLPKKSPGLDGTGEF I
660	14561	A	666	360	2	ENKKIPNSAPPPGSPFLFPPLWEIRPEG FLKPRVLNPPWPNN*APPFKPPMPGPPF PLFRGVRVGDPLSPPLGLRLP*PGLPPG PPG*PWGQNPFFSKKKKSWLDSSGFL EPNISVN
661	14562	A	667	328	1	NLFAENYECPENKKKNFQKKKHQIWQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SEFMKVTEYKLNQYQ/SQLYLYMPEKNT *KV/ILEKHPL*PQITKYFGEILKKDVL NLVYTDKYKISLREVKGQNKWNNVSS
662	14563	A	668	405	566	IHCQWECKTEQILWKTWVWFPTKLNILL PGDSAIMLLGIYPKELKMYIHTETCT
663	14564	A	669	218	2	LLMLESIMFVPPPPSPFEKWL*Y/CH GAHANFLPSFFPSPFFSLSFFFFYNRV FLCCPGWSAVVRSQLT
664	14565	A	670	2	210	NFGQEENSEMNSLCSYLNLEKGEQTRP KASRRKEIKI*AEI*K\QVRSNRENK* KKWFFPKINKIDKPLARLTKKWR*ITI VRKETGTITKDPADTKRIMKEY/YKLLY MHSF*NLSRNLKRYREVIKINERSGSL KRSIKLTNL
665	14566	A	671	200	3	SLCHLPHVASKATLET/GLVEHWM*DFP CFPFTESHCIAQSGVQWNCNLGSLQPLPP RFKLFSCLSL
666	14567	A	672	94	374	PKFRPQETTEQTSQFLQINCKGRKRQG KRTYRLGEIQKQSQPMATFELYLD/H*F *LAKETL*LGAVATCNPSTLGGQAGWI TRSGVDQPGQ
667	14568	A	673	312	3	WKMGOQLPGRFQLPQLSQEKILSLNSPNV FKKKKLK***NILPKKKRPDCFTHKFYQ TFKEEIPF/L/HKLT*EFKKEILLKS F/YRGSVV*AAKLNADINKKTH
668	14569	A	674	34	438	QLT*FD*HFIKYSTQQKTFSSTHRVP AKLGHNLVY\KANLNKFKWLQVISNMFL DRDRIALKINNK/PSSPLKYLQTHLLL NDPRIKEGSKREIKDFALNDNATY*NL WCL*NGTLRKVYTTKCLFRKEGPOM
669	14570	A	675	3	349	QKDRKSVRPSS*NPPLAVEKIP/LKQN PERFNGPAFFKIAHGLTSSLVFLANSN YERTHSRIIILSQGLQTGFAIKTRKLL ASLANLALPPTINLLGELSI
670	14571	A	676	346	1	KMVKLL*NIVWKLK/GLTEVPHGSAIF PFFIPIFPKEMETNVHIKTCTWAFPAF FPMAKKKQSGNNPTTDE*IQK\W*TH IIDYSAIKRNELLTHATSCNITLSKRS QTKK
671	14572	A	677	357	6	AAGDSELKPMFIYCFQKPMPL*IMLKST LLVLYKWNHKAWMTACLFATWFE/HCK PKLETYFSEKRFLSNIT*LMKASGHPRA LTEMYKEINVVPKPSNTTCTLHPMDQEV ISTFNSY
672	14573	A	678	401	155	YYSVAQAVVQWRDLSSQLQAPPPGFE*FS C/PASWDYRHKLLTSGDLPASASQSAGI TGVSHCAQPLSLFVFFLTNRQFVAALS
673	14574	A	679	292	395	Q*KISFEMLLIITNVPGHPRTPMEMYKE LNFF\MPANTSIP*PMDQGIIVLTFKSYY A/RNVFCKAIAV/DSDFSDFGQSKLET FWKGFTI*DVIKNIDDL/WRGVKIPILT GVWEKLIPTLINNFVFKASLEEI
674	14575	A	680	275	3	WPRQASLALNT*SIHIYIHTDMRTHAHT YIFGMKSVTOAGVQWHNHGSLEP*SPGL RRSSHPSLPTSGEHRRTPPR/LADFLHC L*R*GFTML
675	14576	A	681	330	507	GSV*FVNLRNCQPFVQSGCA/SLHSHQ E\WMCSPHPRHYLVASVIFILAILFFP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LRRSL
676	14577	A	682	390	43	HHLPYRYICLSISSILCLSPFIMYLS/IYLSIYLSIYLSIYLCQRCQIPLVFLCLLLS*LS*IILILNFSCTFFVORTIVLS
677	14578	A	683	396	63	ADPTEIQRIISDYDQRTNKLNL*EMDKFLKTYNLPRLN*EEVETLIRFIANHEIALI IKSLPIKRSPLVGGFSGVF*HIDKEELTPVLGLFQK\IKKEBILANSFYBSR
678	14579	A	684	1	396	EETLPLFADDMILYIIKKKQKTKTKSTKRY*N**M\NVFGKVAGYKVNTQKSI N*QYTI*KVKLAS\FSSSPQKNKIGINLTKEIQNVYSENYKTLKEIKDLNK*ESIPCSQIRRFNIVKMTVLLKLIYR
679	14580	A	685	283	3	NCVSSNTHLWEPKQKPLSSVSLTDVCP PMLSAALFAIA\RSYTLPTRSSIDE*IK KMWYIHTMEYYSAPFKKRIMSFLMPRME LKIFRVNKIR
680	14581	A	686	53	324	HCFCDRIRAAFCFYILDCTFFISYTHKL I*IFFFFFLERESI FVPGVGGGGPNFGS LNPLPPRLRRFSCSLTLPBGDGYLGPPT PT/NFCVF
681	14582	A	687	39	208	NIFFCREGFAMRLRLVSN*NWPGKVTH IHNP/STLGGGGRITQTQEFETSLVDA GA
682	14583	A	688	47	341	SSGRVFLVLCFFETGSHS/VLFRLAYSG GISAYCSCHLLSSGDSPISTR/GTTGM CCSAQLGFCVCVCVF/IFVF*VKIGFC HVAQAGLELLDSSNPPTS
683	14584	A	689	229	1	GRVDGRQIACQEFKARLASQAGITGVS HRAQFFFCFC/LLFVVFMGSHSVTQAG VQWCAPGSLQPLPLRF*FSC
684	14585	A	690	339	1	KKGPPGPGPTKPEGGRFPRGPPGGGKEVF PPPPPGGKGEKKRGAPPPFFFLKKKKR SGKGG\N*FFPPGGGKGGQKIKKRVFF PKKKKKKKKKALSLSLSLSLSLSLSLG
685	14586	A	691	372	0	YDLYIKKL*N/LREKIDKFLDTYNLSR LNQEIEENLNTPTITSNKIETVIKSPPT\ KQKSPGPE
686	14587	A	692	117	297	APLLESSASYLHFSN*DLQMAH/KHTK RCSTSLAFREM*IKTTRHHFTPTKMAT SKRHT
687	14588	A	693	122	322	EQTNSWSIDFFQRCNSNANGKXNCLFN KW*WDNYVAI\AKMKLSLFPKYIKTNS K/WIKDLNIRAKT
688	14589	A	694	21	342	RSHERHLNEYATQOGNSDVHPLLHSN ISTAI IWQLQRQERRKEKRLKEVKNEKA LKEIFFLRGWVLLCHLGWSPVVG*S FIV TLN\FGLRQSSHLSLPSSWDYRPV
689	14590	A	695	2	343	KFVPLHSGLGNRSQKQTLRQKKGKGV FVAWAKVQWHNHG*QGP*TLRQSSCLS L*GGWVKL/PGRHANGFHHVKVGLLE LLTSDDAPSSASQKAGITGMSHTAPGPK NLV
690	14591	A	696	336	3	IPPVKSPKFPILLKKKKFSLFCFSGAPF PCYSPPAQKKGW*KIFSPPPK\QKKEG ALFFSPKPAFFPPPPFKKKKKKAKEGH YLMIKGLIQEKI ILNIYASNIGARRRG
691	14592	A	697	374	2	AFY*KKMVSRTFIAREKSMRPFKASKDR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LTFLGAGNFKLKPVLVYHSENTALKN YAKSTLSVLYQRTTKAWMTSHLFTWFT EFFEP\TVETYCSEKKIPSKILLTDYA PRHPRTLMEYSC
692	14593	A	698	361	3	PQMCPPPPR*QGIIPL*L*THCFCTVK ARLFLFPFF/S*RKGGFFFE*RKFFKY FGWELFQIRFKVFFCDRVSLCCSGWSA GART*LTAASTSPAQASLLPLTLSSWD YSHVLPRLV
693	14594	A	699	75	362	KDCAYGICSKKQKGFCLTQTGANQQYEE I*GLET/GFSRSVHSMGQRRYWDYRHAL THPANFVFLVETRFHLHVQAGIELPP/S SSQSGGITGVSQ
694	14595	A	700	2	277	FFLYTSNEQSEKKI/RETNWFIITSK** NRNVNKEI*DLYNENSKTFLKEIKEDLN KWKILSS*TEKLNIIK/PTAI**FNAI LIK/IPMVFDK
695	14596	A	701	1	407	GTRKHFSKEDRQYHKSRLKQIKT/TVSY CFTPTKLTIVGKTANSK/CWAGCKVIGT LIHCQ*ECMVLLWT/SVQQFL/RNVK LYETAISLLGICTREIKTFLHII\IIA KKWQQLRCLSTDEWINNM*YIHTMEYYS A
696	14597	A	702	209	3	SLNRRLSFFFY*ROGLALLI/EPGWGAV ARSWLTPASN\FELQRSSCLSLRSSWDY RRVPLHRVSLRFSC
697	14598	A	703	308	3	TTGLKRFAVRGPPKCDWYRCEPPGLATS SVLKAQPIGSPVPPRLSRILSFM*NQ* YRMLITSTKYFPRMVISIRPCDLPALAS QSAGITGMSHHAELVPLV
698	14599	A	704	603	2	PLPP\GLQVESF/CVSLPSSWDYRHAPP RPANFSVF**RRGFTMLAKM/VLIS*PC DPLASASQAGISGVSHAWPKQT*LLD TDKTEGIFLTNHLRIPPPMFYQYILIK VLESVKETKDKRKSVSSTLYRCL*ILF IS*AYIKFTTFFFF\ETDSRSATQAGVQ WHGLSSLQPPPPGFK*FSCLSLSSWDY RSMPPRPA
699	14600	A	705	3	366	ARVTYYSKGKKEPFGYLGMA*AMISIGFL GVIV*AHHIFTVGIDADTRAYPTSATII MAIPTGVKIFS*LATLHGSNMK*SAAVL *ALRFIFLFTVGGTLTGICLSNSSLDIVL H/DITYVGAHF
700	14601	A	706	358	3	GFHHVGQAGLKLITS*SARLRLPKCWDY KREPPHLAPDRKYFSPLVFARDNFVPQG P*\HVWINICLSQVKAATGIYPGEAGAL RNRLHPH*RIFWPQRPRVPIKSPWTLRV ISTLCSC
701	14602	A	707	358	67	QLSSTIY**KN/RIDQWNKIAQNTSVH RKLISDKVTKPIQWSKDSLPNKECWN* TSICKK/LSLDSALTLPFKTINSK*ITEP GSVAHTCNPTTLGG
702	14603	A	708	34	363	RTVFFFFFFFPPKTPFFFPGRGG *IPPEKKIFPPVFRGKFKPRHLDPGG GNFPRKPPFFFLGP\SFFLGKTLGGGG WIPFPPPPWPNLFKKIFWGAGGSPSF
703	14604	A	709	1	380	STCKRMTLDSYFTPYTKINSKWNKDLTV RGRTIKLIEENIGVNLHDLGFGSGFSDM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TPKAQAKRKIN/WDFIKYLFKCA*EDSERV/N/RRSTEWKIFANHIQ*GN*NIQRILKLSKL*ARLKWAEDL
704	14605	A	710	382	30	PGTTGVHHHTRLTFVF/CGRAKISICWL VVNS*AQSACLSLPCWD*BPQHPARFV SFNTRSGIPIISTNPSSLSSAFPSQGFV FLFPHPASHPETALAEFFLGTFSLSP GPPTPAS
705	14606	A	711	1	377	LLVICGMQMKITVRCN*TLNKIATIEKK TAKCC*HYGGLKTLHQWCKSNMVQPLC KTV*QF*KCLNIQLLYLLK*KKAYTHPS NCTQMFI/ALFVSLAPNWKQSA
706	14607	A	712	1	390	LKYKIMLGMAAWACNPNSYSGGPNITA* TW*AYMALTRLEPGRGDHTAALQPGRQS TTPF*KKKAVPFRA/RPVKMRERI*KP FSPE\RTYSCAQEGPGRTFGSAQDLEAA GGRGHHRMGAUVQEPHRLIG
707	14608	A	713	2	393	KVRRQIINVDATDSIGIKWIIWKHYV* LYANKFNylaEMDTYVERYKLP\KEIDV MNSLVPABEIIIVVVKILLTKTPDPIHT NEVYQTFKEYY/PVLYKLFQKIEDERTF LSSFCAGINLISICKRFFF
708	14609	A	714	219	1	PRGAVAHACNPSTLGGGGRI*TOSSI IKACCLIHDLAIQTQKQMT/WPGAVAHA CNPSTLGGGGRIITRSGARDQPSQHSKT PSLKIQKKLASVVAGACNPGYFENYIQ KLRGPGT
709	14610	A	715	381	126	I IAGGGGVCT*SQLFKRLRQEDHLSPGV RGYKEL*SYPCITLAWTE*DPVF*KKNY /TLNTSPKETNKK*GVRCIKTGKVLIFV AAG
710	14611	A	716	417	1	CYCCWGATNKILLITDNASGRQIVLMDM YKKNNVVFVPVNTSRFVQLMDQGIILNF KSYLRN/TF/HKCIAVINSNSS*ESGQS KLKALWKGFTVLYAIQNICDSGQVKMPT LTEV/WKEVILPLMGDFVRNRTSEKQNY KLS
711	14612	A	717	406	122	MFSRDAVSLCCLGWS*TPELKLSLSSLSL PKCWDYRGEPPCSAAKDF*IIRKR/HSC RNIIRNSDAWQR*TTLVSYDRNPP*FPS PPPNSPLCPAA
712	14613	A	718	535	1	HNLNKIV*NLHVENYKMLVKDKKT*ISC LWVRR/LVKIPVLPKLFYSVIVFPIRSL VRYFIEVCTFTLKCIPKEKDLKQPNRF* KKKKKVHLFFIKVYY/KLQ*YIATVIKT VWY/W/YSKIDKAKWYKTEKAEV*PHEY DQLILAEVQINH\NLFNKCY*SN*TTIG KNMNLNLSFTSYT
713	14614	A	719	255	1	GKLQPNKGLISLIY/NL*KLVKSNPKE KWAKGMNR*LTEKGIQIAFRHMKRCSPR FIMKAMHIIITTSYHFSKRKTRIQRLT
714	14615	A	720	381	0	KPIAVNEYIKSIDLPINNLTLYLKL/ EREELTLCKASRAEVI\KIRAKIIRELT PIRKTDNQSWFFLKIHKIGQ/PFKLD*L QKKKRVREKVPITKLYENRVITTNFTE /IKRIIREYYDH
715	14616	A	721	3	381	IYREWDLTRDGTQGGHAPPGEKG/VC RYGIILFITSEGGFFAGFF*PFNHCSLA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PTPQLGGFWPPTGITPLNPLKVPILLDT VLLASGESIT*AHHS\LIENNRNQLIQA LLITILGLYFTLLQA
716	14617	A	722	56	455	KTIINIKPPAI IQYQTPLFV*SVLITAE \LVLLSLPGLAVGITILLTDRNLNTFL DPAGGGDPILYQHLF*FFGHPEVYILIL PGFGIISHIVAYYSGKKEPFGYIGMV*A MISIGPLGFIG*AHHIFTGGIA
717	14618	A	723	398	3	HQLPVFWQYNKKAWTTRPLFVDWLH*CL VFEVSKYPASKGLPFKVVLMNDAPD/H PTQNSMSS/DSKGIEVIYLPNTMSLI* FLDQGVIRTYR/RHYQYSMQRSIRPMQ EISNKENI IKVWKNSTDDAIVA
718	14619	A	724	318	14	TPPFFLNIPNLFFLKFPSPPPFWLTKS LEFFPLKLPKVPFGK*SLSKF/CPFPKFN PKPQKKNFFPPPPPPPPPPFFFLRHN/ VCHPAWSALAPSQLTATSAS
719	14620	A	725	2	371	APRCKRFSCLSLPSGWDYRCMPRPVNF F/SIFSRAGGLES*PPMIPPA*A/FPK/ CWDYRHE
720	14621	A	726	430	97	PKKNPFWKRA*NGGAQKDVPLSLP/SGW AGGSPWGPFG*PPLGPKGGPPFSKKPPG GVGPFLMPPTPEGGGKLA*DWPPGFNP PVSIFLPRPPRAGGKKGTPFPKKKKEK
721	14622	A	727	406	1	GGAPPPPPPPPPFFIKKGVFPF*QEGFF PGLKN/LPP*PPKKVGVKGGSPPPGGFF FFFKKKVFFPPGLRTRAQIKVPSTLVG QG*KILPPQVSQEGGVKREGPQAQLFFF FFFFEMESHFTQAGLOWRDIGSP
722	14623	A	728	98	368	KPHKNAKCPIRVAIVADMENNKYW*GYG EMGTL/LHY*WEGNIEQPWE/T/VWQLL EKLNTLPCDPATPLLGIYPKTLESRDS NRFFIFFFSF
723	14624	A	729	19	404	VCVISICLATEILFFLHTRPCVCICYCVC VCVCLAVWGTL CVYVCIESCVCVCFHLT GVLC/V*VCVISICLATEILFFLHTRPC VCICYCVCVCCLAVWGTL CVYVCIESCV CVCFHLTGVCVCVCIESSVVCVPPT CGTVCVCVRPFGVLCVCVCVCQAAWVAV SMCLTP/CPC/VCVCVCVCV
724	14625	A	730	432	12	FFHKPNFPAARKGRLEFFIYPSKCLISP KAL*F\FGGVGPPFPFPKKGFFPKVPR* CFFRPLIRKKQILFLPPLNLAPPGVI*M /PPPPIVFFFFFKRDRVSLYCPGWSAV A*S*L/TAVRTRGLK*SSCLSLPKWEY KCEP
725	14626	A	731	332	7	NKTRKEKFLTRSISR/CFPPFFLKIIF FPLRA*FFWGGLPQIFPPPKVVF/PKI PKVFFKWPPLRKKIFFFFSPLILGPPRV LLKGPPLFFFW*VFFF*DRALLCHPY
726	14627	A	732	70	294	FLRCVETAINKIAIILANF*NFL*RWG \FTMPRLVSKL*DSSDPPTSVSQSVGI TVVSHHARLNFFYYQNSRR
727	14628	A	733	1	355	FLLRHILLCHPGFCSVATAYCSRDPGSS D/PLPPQAPLEDQ*PRLQA/WHRLAPPH SANFF**RQGFTVLARMVSI SQCDPPH SGPQGA
728	14629	A	734	50	395	IPGLTRQWLLDPCASPSTPPYT/P*VQP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond- ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						STPQNSSPSPKTHNQKGLPMLPSPTPKP STAWKKAILEHTSSSSSSSSSSSTCRNR NGYTYTVPEHRPARGHTASQTRKQVLAA THKP
729	14630	A	735	451	0	GPSSSPTNIPTPVSWNSFK*SSQVAGAT GTCYHAWLIFVFSVEMDFY/HPVA*ASQ SAQLCQYFMIFLRQGVSLCPPGWSAVAW SKLTT/CLCLPGSWDHRCALAHAPANFLY FWWR/HSC
730	14631	A	736	2	477	PSHVS NKRLISKIYKELIHLNSKKVSNP I*K*QSLNRD FSKASFLPP*KC/QMVN RYIKRCSTSLIIKEMQIKTMTMRCHLTPV RLAIMKKS KDNKPSLVWDC*IRVLHLF/ CK/WICQYVQL/FNLLSNFLVRQPF/Q LPAPNSPTLG
731	14632	A	737	3	2344	AAGGPTAQSPAQLAGRALRLARWRVAV GACRPGAGSPCSVQGAASELSRPQOTW IGSLKP*TFGAAAG*AHRCGGSALLN* ATPRPAPGLPASPTSSQALPAPLGAWGH SDHQPRAFP*SPQASTAIRKEKKQRAQP GRASVCPASNPFISSRALPVLQHGPPI SGAGSAVASQAPGSS/GSHAESGSPALA HTP*GS*EPHSLIVESTRKS\ELPSSSQ GRLLPLLLTPGVA/PVGTKLPGATAAT AGALHQPLRLSSLQGVGGAKNKQTGCC CLQLPTTGLPQAPGALRPLGRIGPAAAP GEHRQRTSPQGTVPYGGIRQGWEPQRL RAYGTALPPEHTPPGSSGP/ROAPGCRG SGAGEAAGIRD TGGGGPGRRAPCSQASP GRGQWQAQVGCETCRGCAQSS/GGGAVQ PGLPRKPYPHS/AR*ENLVVPFPCSPRT RAQBPQTQGE/GVEGPQGS PCAPGAVR GRGIQLSSEFGKLARQG/PASGDGP*EG TGQEPSQAFSSARHPWPSEARMPTAIC RNQAQ*LQLTSSQPSMGPLRLKSLPATP QPNSYWDGNSATLGRITNTRRHCGMSN FGARGDLLGTVP T*QPLMQRRKEKPRVG GEPVQSHTVCG*\PAGVSRGWPLRPMLP ERWRPLSASSGSQGRPGLHPPSLA\CGP SSSPHRTCSF/GLDPGLPDAGSIKPPSL VGAGQGAGST/GLD/GPGLSLLSPGKSL LPPSSPATGLSGLGWAQSAF*SLLTVA* WLNVPVNGPSDTADCTPAQAPTAPAMLE NQANKSDFFFH
732	14633	A	738	37	450	NQKKWPPRSSSKPARPLFFFL*QKYIKD P*KTYQGCFFFSPPPKKNPPPKGGGF FFFF*KKKGGGPPP/QAKKRGGGPPQK GGAKNPPRGFTRVFKGPFKKRGPP
733	14634	A	739	2	426	QEFVLGSAPGCGCWVGEGRVSSPWGDR KVGGPSNSRHWNGAGPSCPPGPSLAAG LPGRRAGSWAPVLW\PGPP*GLAQLPSP LW/PPSPQEREPLPD
734	14635	A	740	21	392	AQEFKSSSLGNMERPLPYQKKKKKKRPGG GA/RPLETQPFGGPGGGEKKGGKKKTSR P/IRGKPPFL*KKKN\CLAWGGGPAL*P QFFGGVGEKKTFFNPGGGGLGPKPPPT PTRGKNQTPQKKKKK
735	14636	A	741	1	408	PSSQGG*EAGG*LEPRSSRPAAWAI* RDP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1. 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						/GSPKGGKKKKKKKKKKKKGGGGFKK TPGGAKIKGGGKKNFFPKGGKKNLGG ILEKKLFFGGGKNGEKPPKKKKGLREKK KF*RGKGGKKAENPGGKKIFQKKKK
736	14637	A	742	394	1	RDPLEAVCFPSDLQLRAGRTTALFKAV RQGHLSLQRLRLRFVCLCPAPRGAYRS RQASLNRRGFHPVRAYLLCLPKQASEM AGAPSPA*LPPCSLISDCCASNQ*DSVG /VGPSEPGEGYNLVVRRFLS
737	14638	A	743	384	1	FTGPYLKNGYSFLFLYPPPSVLGNWQP PHPGRVFPF*DVNFNQWIFVSL/ISSLK DEPAFSSSTLYSF*QHFFITYLPPP/CF FLIESCSVAQGGVQWCNFGSLQPPPPGY KRFSVCGLPSSWDYRCV
738	14639	A	744	2	410	TPLNPLEVPLLNTSVLLASGVSM*ADH SLIENNRNQIIQALVITILLGLYFTLLQ ASEYFESPTISDGIYGSTFFVATGFHG LHVIIGSTFLTICIRQLIPHTSKHHF GFEAAV*YWHFVN/VRGLFLYSGSIY
739	14640	A	745	393	1	PPPPPRGRGSPPPPSRKGKPKGKPPFP GNFFFFPKRVFPF\CPGGFKS*V*GVP PPFPFKIFKFKGGTFFPGLWSPLSKKS QFFWVPKPGERKLPFPFFFFFLRPCL SLSPRLECSGAISAHRNL
740	14641	A	746	2	290	KNLCRENYKYE*KKLKTMKDLCKEYYKV *MKIKENM*KDKLMNPK\NNIKISTLI KVYKFNAPIKIPMTFFAE\LK*ILKC V*NYKRP*IVKAI
741	14642	A	747	59	364	CRFFFFGLGGGGGGGGGPPPPF*KNP PNPPKKIPNWGFPPRGPGFAPKKKGPP LGEPPPWGAPLYNPPPPGGGAKFPPI FFPRAGGPQKRVG/RPPPPPPPPPRPK KKKNLH*LECVGTEEPTRPPTRP
742	14643	A	748	2	371	SSCLDLPCWDYRHELLHLAHLVLGIF LLLLFCFVLRW/RSCSVVQTGV*WSDLT SLQSLLP
743	14644	A	749	339	198	IADMEKV*AF*TEHKTNHSILNQ*N*I*S KVLTLFNSMKAERD*EGPEEKFGASTGW FMRFQEISQLYN/IDV*GEAASADGEAA ATCAEDPAKIPDEGGSPK*YIFNVD*AT FIRDLSWIFCTSCCSFISTCCFTLHVM L
744	14645	A	750	249	2	KIFKPPAFVPSFPPFL*DS SSPPEP*I SGGRVGPPI\FPPPKKGFPPKNPPGVFFS PPLRKKILLVPPPLNLGPPKGPLKRPP
745	14646	A	751	1	288	VVNHMTDEGLVSRYY*QPLQL\KRKTEN PVQKWTCPNRRFSEEDQMARKHKQGW PASRAIRGTQSKIIMRCHFTTHRMARIK KEKEAGPGGSCL
746	14647	A	752	494	2	ETGSWFGPQRLEVQVWIKSSLQP*PPW APVILPPQ/LSSG*DRHVPSRPG*LKK KFFL*RWGLTMLPRLNLNNLPTSASQNA AITGVSHCARSASVFLILRQGLWVWEE/ GAQW*SALSHLPV*/LSR*WCQP*PLG* DSGSGSPLWRRLAYLPLCALNKEVTMCS
747	14648	A	753	1	533	YLSRLECSGGITAHN/LRPPGLK*SS QLSLQ\SSWDCRPAPPAPARLIFFCRF EGRSRSHYVAQACLKLPKS\SNPPTVA/

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FPKCWGYRCEPHTGLCS/GLSEFGFCL WWGACSRSSHKNPGCGTA/CPAVFLHSV GYASHPSSSTRTAFTLGWVLVVFVRDKG LTVFSQAGSTVGVILG
748	14649	A	754	1	346	ELSKSTLPALCGNDKAWMTAHRFLAWF TDYLKPTVENYW*EKKIRLKVLLIDNA PGHPKALLEMYTEIHVVFMPADTTSIL* PTHQGVISTLKFCYL*NTFHKVQ\CYID SDSS
749	14650	A	755	1	323	EDQTSNVLLSLNLIQSKALMLFNSMBA E/R/SSEAVEEEKFEASRE*FMRLKERS LQNIKVGEEASADGEPACDPEDLABI TDEGDCIK*QIFIVDKTAFYSKMPS
750	14651	A	756	1	344	ARQQPGDPARGGGRGRRL/QPRQAASFC TGTARARHTCEGAGVLRPPADKLASLN *HFSQKKKKKKKKKKKKKKKASSSS KKKKDSSYSSSSSRGGSSSSSSSPPPP PPP
751	14652	A	757	119	317	NRYFFFLRVKKFPWVEGPFFFLR*SLTL LTLVAQAGLQWRNLSSLKSPGFKPFS /PSA/LSRWYRR
752	14653	A	758	2	363	CILAIKSAINRIAN*YI*KCSMSITK RQA/IKRKNKTRRYQLIPVRMTLIKKKK RW*RCEEKGRLAHCWF\ECK*ROPL*KT K*RFLKKLKL\P\FITAIALLDIYPKQIK SE/CKKH/CAILEIALPTIAK
753	14654	A	759	358	1	KADFCFPPTFSRVRKKIFPPFPKKWG* KGP/LPPPGENCVFPPFKKRGFSPLGG GFFYFFPPGFPFPWPPFKLGFGLTPPP GPPQKILVFFPPPPPPFE/DGVLLCRP GWSAVAQS
754	14655	A	760	316	2	KATRSQDIRRIQVKLKEIEPQKPLQKTN KRSRYFF*KH**NRTLTRVMENKREK/N EIDPIQNHKEDITTDPTBIQTIRKYKH LYAHKKKLEEDVKLLDTNTL
755	14656	A	761	3	321	FPLGLWGLGAKPEGQAPLYPPTLSKRV VPLC/DKGRSAVTFTNTYSSGSSRVFP PPCM*YRLCIKGRSSDPEQKKKKKKK KKKKKASKKKKAPKSSSPKT
756	14657	A	762	315	2	KTERW/VFEKINKMGQS*DLTKIKNREN /V/QINKIQNERGGLSTGSTEIQRVIRG PCEPL*AQILDNLBKMD*FLQPFHLPRQ NYKKKKII*KKPISKVIELVIKNL
757	14658	A	763	226	329	NPTTLEGQGGRIKSGPEF/CSRDEVSPC WPGWFQTPDLWRSVRLGLPKWDF/RR* APPPGLNLFFRMLSTHGSW/CQHPCFKF PTSAFYIYIYIF/SFLSRSPFFVAQAV VQWHDLSPPPPPGFKQ
758	14659	A	764	335	1	QSQERPDSFQVMNLTLPAPSMFLVSPR TELSKSP*\PPAFLCPCVWPHSTLLSQT LKY*IKYP*SPTPPPSFVLF*RDRVLLF HPGWSTLAGS*LTAASNSWAQVTLL
759	14660	A	765	100	310	HFGRPKRENCISP*V*DTLHTHTHT HTHTHTHSRSENGMRLTPHIPRVRW\ GIIC
760	14661	A	766	315	3	YFPNPPRIFIQNPFLFGFFPKKKEGE KNWAMETPRFSPPLGGKKAPTGFPPPP IGF*GPKPLIKGRGP*/PP*KNTKIFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFF*DRVLLCHPG*SAVARW
761	14662	A	767	1	309	KEPYKLTTELHNEIRVACGHLSSKKKITW VSDS*ASCPKTRGNFIGPSAGSRAPSE KLEAHFHGCGSVNRVHLT/CK*HKRRPL GVAHLEVSDQKSGRTSLALD
762	14663	A	769	1	316	GRAPPPPPPPPTPRVHTSSKSESEPER /DGRE*EPTSLERL/LFFASYFCLEAR QSTALPPLPLSPRSGPT/VLLCPSPL PGERPPNPPTKLSREKQTKQTHRAR
763	14664	A	770	2	366	AREIILTF*QMITFLNTKGR*SLILA SLIIFIATTN/LLGLLPYSFTPTTQLFI NLTMALPL*AGAVVIGFRSKIKNALGHF LPQGTPTPLKPIPIETIILLIQLPIAL AVRLTANITA
764	14665	A	771	2	364	NAPFVISGAWTEYPLSHFIQRCRQKKE/ LNLQIGKEBEIFLFDKAML*IESPKES VQKRLDVIYKFSRIAACKINIOKSNIVV YVWNTQFENEVKTI*DPQ/DIKHWGIIL SQRKKE
765	14666	A	772	3	376	HEPLGKLKLSLLFILATYSLTVYSIL*S G*ATNSNYALIGALRAVAQTISYEVTLLA IILLSTLLRRGCFNLSTLMTTQEHL*LL LPS*PLAIT*FICTLAETNRTPPDLAER ESELLSC/FNIEYA
766	14667	A	773	3	350	HEFFFFILKMYLGQAQYFICFLFFFLGF HLK/HKSCSVTQAKVQRRHLGSMQPPPP GFMQFSVAEIKDVHHAQLIFYIFRIFI F*P/NFLRHSLALVAQDGVQWRDLGTLQ PLPPPG
767	14668	A	774	1	359	GTRYAAMLSALGFI FLTARGLTGIVLA NSSLDIVLHDTDYGAHFHYVLSIGAVF ALIP\GFH*PPLFSGYTLDQTYAKIH\ FTIIFIGANLTLPPQHFFGLSGMPRQYS DYPDAYTTW
768	14669	A	775	2	369	ARGSICLRQTELKTVIAYSSIRHIGLVV TAILIQT*SLTGAVILIIAHLTYSL CCLANSNYERTHS\RIIILSQGLTLLP LITF**LLARLANLALPPTINLLGELSV LVTTFS*ANIT
769	14670	A	776	2	353	ARGTGA*VDS*LTLHGSMNK*CAA\LL \WTLRCKILFTVRGLTGMAITNSTLDIA LHDTYYVVAHFHYVLSIGAGFAIRGFI H*FPLFSGYTLDQTYAKIHFTIIFIGVK ITFFPQ
770	14671	A	777	3	353	HEGLHL*LPKAHVETPMDG*IALDAGLL RLRGYGIHVTILNPLRKHILHPFLVL SI*GIIITSSICLRQTLKSLIAYSSIS HI\SLEVTAILIRTP\SFTGADILIIS HGLTCS
771	14672	A	778	367	2	FCPI/CPNQKFMGVGAVGFPALYPNPPGG LGGLV/TPGAGVLNPPGPPG*TPPPPKN PNLGGCPALFFPPLKGLGWKIALTPEAK GSINPSPPALPGGPNQTFPSKKKRRK LMLVYSIELTSRA
772	14673	A	779	3	432	HEPLHWLSSCVCPACVCVCVCQ/CLWLQ VGQV*CNYSWQHEPLH*VHTRVYVCVC LCHSVAQAGVQ*CNYS/CTAACNSW
773	14674	A	780	213	466	DDILEVWNYSISFLFFFNRAFLPPGW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GAGTQL*LPASN*GPKGPSRLTLL*W/DNRHGPPC/LDNFIFLQKKNLTLPLRLALN
774	14675	A	781	304	373	R*VFFFFFLKKEFHFFPQAGGQNGEMG*LHPLPPGAG/RF*CLTPPHSWDNGEGPPRPPNFCFFRGKNSPCGP
775	14676	A	782	389	1	PFPKN*CRVNSRPNVKHKT/OLLEGNLGASVDDLEFGDDFLDTIPKVQSMKERS/WDFIKIKNVCFADNVKRRGPATNWKISVKDLNSKGLLPKIYEELKLNNTET*R
776	14677	A	783	1	383	LT*KWSKVLNRQLTRETRA GTSP*PLTGALSYLLMTCLGLAM**HFHSITLLILGLLANTLTITPGRGDVSRQSAYQGHHTPPVQKGLLYRIILFITSEAFFFA
777	14678	A	784	1	389	GFF*SF\YHSSLSPTPQLGGRWSPTGIA PLNSL*VPLLNTWRLL GTSIVIPTGVKVFN*LATLHGSNMK*SA AEL*ALGFIFLFTGSGLTGIVLANSSLN IVLHDTYYGEAHFYVLSIGAVFAIIGG FIH*FPLFSGYTLDTQYAKIHLT\IIFI GVNLTFFPQHFGLGSGNA
778	14679	A	785	374	1	ELNAYWNVMNLQNLINNAQPLSIMQIFQ ILIKSQIQNTLVVVISDGTGYPGIDKWN CI*LKILCIVKVTINRAMPVIDWENTF STYTNDKGLIPKYKELKHS\KQTNNLIK KWAGLHSHSRA
779	14680	A	786	1	363	GTRLYHANTN*KKLRAVAILISEK\TDFT VKKIRNKEGHYIMIKRSIL*EGITILYV GTPSNRVVNYIRQKLIKLPGEIDESTII LRDFNTPLSVIDASTRKKISKNIVESNN IISQLDLID
780	14681	A	787	1	361	GTLPSSERKNPTWVSLNQKLEMIKLIEE GMLKAETGHKLRLLOQ/TSQVNAKEKF LKEIKSATPVNTRKTRK*DSLLADTGKV LVACIED*TSHNVLF*SLIQSKALTLL NCMKPERGE
781	14682	A	788	1	352	GTRNYAKSTKSKLYRWNYKAWMTAYLFT AWCTEYFKPTVETCYSEGL/SLKILLI DNASSH*RALMEMYKQINVVFMNDNRIS LLQPVQD*VILTFKSYLRNTFHKALAAR DNDSSD
782	14683	A	789	365	128	PLDQHGETPLLLKIQKLARRNGAHLYSQ LLGRLRHENLLHPGGRGC/SHCTPAWVI E*DCLKNQTKTKAPRRVSISHSA
783	14684	A	790	217	257	WGGVAHPVIPATQEAEEELSLGGRDC SELRSCHS\CTPA*VTOAGVQ
784	14685	A	791	2	363	LAILHQTVS*FVHAKKFWKDLL\KSAT PVAI*MIRNLNSLYNIMETV*VV*KED QTHLIPLS*SLTQSKALIFFKAMKTD R GKGAVE*KFEATRGWVMRLKEKFCLS/H HIKVQG
785	14686	A	792	2	362	GQKLGLLHQTVSFVNAKEKFWKELL\K SATPVDI*MIRNRTS\LISDMETV*VV* KEDQTSPLIPIR*SLTQSKAVNLFAMK PVRGKGAVE*KYBASRGWFMQYKESK/ RMCNIQIQ
786	14687	A	793	2	360	ARAGSTMAFKNYAKSTLPVLYKWNKKA* MTAHLFAARVTKYVKS/YCLNKKIPFKI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						*VFIDIVPSHPRALIGIYKE/INVFMPA NTTSTLHPTDQEVISTFKCYYPKNRFRK AIQLPYSNSY
787	14688	A	794	2	359	AREKLYLSILTPLQRSIVIAFAATELTR YYILFETTLIPSLAISTR*GD\QPERLN AGTYLLFYTLVGSPLLLIALIYTHNTLG SLGILLTLTGQELSNS*ANNLI*LAYT IAFIVKIP
788	14689	A	795	157	365	GIIEBKGYLPEQIFNAKCSGMISAHCSP RLPGSSYSTSA*TDF*QVQWYDLSSLQ PPPPRFKLFYLSDPSTWDYILAPP/RPS **FVFFVEMGFRQTPE
789	14690	A	796	224	372	IPFIFIFIYLPTEWRQSFALVA\QAGVQ WRNLGSL*PTHPPPRVKRLSCL
790	14691	A	797	482	1	NSFFFFFLFPEAKDHKDPSPFPVFK KLKGFC*APF*VQKPVFYLKSF/CLKDY MLSFPESKVNFPSPFFL/SPSPLMVGD PPLPPETYFSFCF*DPHSINFFLPPGPF LFHFFFFLRWVLLCHPG*STAV*SLLT TS\VK*FFHLSLPSWVYRCTSC
791	14692	A	798	1	415	NLGGGGCSELRSYHCSPAWATE*DSISK QTKTL/NKDHTRAGWERA
792	14693	A	799	2	401	VQTGFHHVQAGL*LLTSGNPPASAS/Q SAGITGMSHRARPQ
793	14694	A	800	73	307	PMALBHHGCGMCLDFLPTFGKSHCFVLR CAEMETRSFLPSWSAGA*Y\CLLQPPPP RFS*LRLPSRWDRHLLPCPAN
794	14695	A	801	87	401	SLIEIWLKKTCHNLNVVLS*HSLKA IVLARHS/VESLTHVLMCLV*NFVFAF S*RLCFFLKISRPPVVVAHVCNPSTLRG *GGHITRSRDRDHPHQGEIPS
795	14696	A	802	3	354	LRHYTF\PG*QSETLPFKKKKKKKKKK KLSFFPPPKFLKKKKGLFKNPFKKKGKI FFNPPPPKKKGFLIVNPPPKKNPPPL GGGGPPKKIYF*KTFFFAPPPFPENPPF FFSPRF
796	14697	A	803	1	830	VETGFLHVRQAGLKLTSGLPTLAYQS AGITGVSHCAWLFFFF*CLAVTQTEVA PS*LTIASN\PGLKLSSFTLPHHARLI FKIFSRNEVLLFSR\PSQTPNLMQSSCL SLPKCDYRCEPLYPABSLF\FIKLSC MLKCLEVKCNDVCNLL*NTLIKWINEWI EGWIGRLTCVKQIEKNVICRI*VMLKAT QPVGTEPS*ESRSTNSGEAMW*SKDNTF FPVFSVFLVLRQ/LCFVAQAGVQWHL SSLQPLSPRLK*SSCLSLSSWDLRARA
797	14698	A	804	389	3	FIWPFKGAPENSFFVFMWIKGHKCPKKG FGRKKNQLGPKIPF*KKKKGAFPLWLK RFQGPFFFFFEMEFS\IAQAGVQWCDL SSLQPLPPRFKRFSCSLSPSSWDYRHAF PRPANF\CVFSRDEVSPCW
798	14699	A	805	161	21	RGGGCLQSQFR/RLRHRNRLNPGGGGC TEPRSYRCTPAWARE*DSVSK
799	14700	A	806	405	82	FFLRWTL/DTVTRGGIQCWNLGSPQPP/ PPRFKRFSCLSLSSWDYRRPPPCPANF LYF**RRGFTMLARLVLP*PRDPPASA SQSAGITGVGHRWPMPIFENRFDL
800	14701	A	807	938	2415	KITFWETFWITTVHPLCKERRAIGIL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine; S=Serine, T=Threonine, V=Valine; W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						RRWS*NNW/MIHTHTKNLNPYLTPDTKA TFK*IIGLT*RAKTMQL/LESFCQKENT GENLSDLGVGKDFLRHKKHGSIKGEKLA KLDPIQVKNF*SLKDTFKMKKYLALGWE KIFABRVSDRGCVSRRYKEL*L/IELKD NPIRKGGNNLNKVHQRI*MANKHMKRCP KS*VIREI*I*TIMRYHCILPRMAVMN/ SD*SHGDKNGSSGTLIH/CR*ECEMDQ LLWKTIGQFLSK*M*RCHTDSSIPFLII QEK*NCISTKKTCTQTFTAA/MYLLVIA KNWKQLPYPSVWI/QIWCYIT\MEYY SAIKRTVDTLNN\QMDLKIIRFNE*S/H NLRRVHCHMY
801	14702	A	808	414	1	KPKAKLFVFPVRQVNAKEKFLKEAKSAA PLN\RMIRKQTSLTADTEQV*VIWIEY* TSHSIPLSQSLIQSRVLT\SMKAETGE KAAZENLEDSRG*FTRLKEKSHLHNKIV QGEAVSADGEAAAGYPEDLAKIIDER
802	14703	A	809	399	1	TGPPPRNQPFNKPAGNFWLFLFFFL*F /CNFFFFFTGAFSLSGI\LV*CLML VWGNFSP*PFKYCFTFSFSLFIFLIFL WLLNTCLYICYTFCSYLTVL*CSFLFS SIFFLLYF*FWRLLLIHPPPTRP
803	14704	A	810	1	392	ILLAGATEDAEPGSG*TGYPITLGSYSH PGAYVYLTILSLHLAGDSSILRAINCI\ TTLINIKPPAVARYLTPLFV*PVLDTAM LLILSLPVLADGVITILLTDNLYSTFFD PAGRGDPILYQHLL*LLRH
804	14705	A	811	66	411	RETRAGAQGLSRFSPWGNPSQKIFLGP GFKKNPGPQKGNFFFFF*KKFPLVSPG GRGGGNFRSLQGGPPPKVPPFCFNPFRK GG*/MGAPP
805	14706	A	812	3	392	LSVPQFPFFFLKKTFRNCPFFCFSPNPI LGFPLKGSKK*GSFFFFPPPNYSFVWF PSYSF*NQPCLTRGPF*NQKFPRL*KGV PILRL*SPLFFGPPPHSF/IFFFDRVS LCHPGYSAVAQS/LLTAASS
806	14707	A	813	690	153	IISIDAKAFYEIPPPSVISSSSPTDSL YYNLGFLKNFKKGREVKYLNIIKIYIEK PTANIIIFISGKLKAFSLRSGTRQICPLS PLQFNKVLVLARATWQKEIRNIHIEK EEVKLSLFVSNILCIENPLKMP*KNSSN **IQRVAGYKTNI*KIS\AFLYTKNKL CCLSHPIYDIPL
807	14708	A	814	32	376	LFGLARSYITEGGRLPENPTIPHG*REF WELCNKCD\TMREPKPSLHCSRCHGCVTR MDHHCWPINNVCVEDKH*LFLQLCFYTE LLTCYALMISFCHYYFLPLKRTLVRN VYI
808	14709	A	815	2	423	YPLYPFKIFIFPKGFNFCREVGPICPPP KIKVLSKNSQVGFYATPYKEKNNTLPAR VNEGPPKDSLKRPLFFFFF*RDGILL CYPWS*TPGLQSRCLGLLKHWDYIC* PLHPASF*KKHYSRLILP/SLADAW
809	14710	A	816	404	54	SLAHFFPPPKGFFPKIPRGVL*PPP*K KKFLFS/HPPVNLGPPRDFLKGPPSSSS SSSSSSSSSPGG*MIFY*/P**FGPAL VQPMACYCKASCKVKAPFFSTHSGLMVA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PPTTAQS
810	14711	A	817	3	410	DAEVGGSLEPG\SGGCSEP*SCHCTPAW VTG*ETVSKKKKKKKGGFFPPFFKRG FFREIEKKFGKKFFSKKKKKKKKKRGG PFKNFWGGKNLGGKKKKFFFLGGEKK KPRGFFEKKTFWGGKNWATTQK
811	14712	A	818	1	404	IPINSLTSKINKLLKRHLF/HLNQBET DNLTRTIPININ*FYKQNTGPDGSI KFY*TIRKT*Q*FYTSFQIKNEVLN SFYEASTPLASPKKKKKKKKK
812	14713	A	819	421	2	LPPKRRCFSPKPPRGFFFPAPS*GKKN/ CFPPR*NLAPPGVFLKGPPLFFPPFF FRGRVG*SWVPAASPLQGQVFLPPQ/SS *VGGSPGPPEHARVNFFPPFFFP*F** RQSLTMLPSLVNSWA*TILTPQPPKVL GLQ
813	14714	A	820	84	418	ILTCHNARLGEKSQIVTMQASQNNPKLV NICEVFLVFFFWKPIFFGTQVGGQYFNL SSL*VRLPGYTHFFCLTLPKSNDRP PS\PIFFCFNKKGVSPGYPGGCNILVF
814	14715	A	821	290	3	FSPPPENLGPFRNPLKGPFFPPFF FFPPFFMFCVLIY\FIFFCTNLLFLDF CIT**T*NWFISSKAVCLFLFLQPAS QKTKNRCKRSFF
815	14716	A	822	416	2	ITKLTEKKIWSGKRKNKYVYAGASQ YTAVVLRPQSMITLKDSERKAPHWGE NVV\HVHFIWKER*PEV*YIES* GGLASWSGPEKNKIGLGAQV*RRDMK TDPLECTQINIPGFVCLFGDRVSLCW
816	14717	A	823	409	45	PPPPFLFFFF*KKKAPGGSGGPKF*P PPPPKGPFFFKKKKKKGGGGPPNPP PPKGGGQK/QFFPPQGGNFKPKSPPPQ PPRGQKKPPPPQKKKKKKKKRLNVTG PQFLQLESGTY
817	14718	A	824	1	408	IFSEHNGIKL*INTKRNFRNCTNIWELS NMLLNH*VNKEN*NKFIKTNE/NKN ITCQNL*DTTKVVLREIYSKKCLLQKK KKKKKKKKGGGALKNYLGGGQFYGGE GNFIFFWGGAKKPCGWIFRRRPFFW
818	14719	A	825	259	274	YL*VLLLYRRYSA*IP/LGYLKKRKL LYQRDTYTFMFIALLFTIAKMWSRP*SP VV
819	14720	A	826	422	105	FFFSKIPWGNFFPPPKRIFFPPFPKI FFPPPPFFFWGGFSPFPSPPKVFFPK SPPVFFPPPP*KKKFFFP/HPPLIFFPP GFFFKPPPPFFPPPPPPPPPPFW
820	14721	A	827	15	402	IKSLGKNIGINLGDVLNNGF*YTLPKA QATKEKIDN/WDLAKARNICA*KDTIRE VERQPKK*QOTFVNHLFDKGLVSKHV/N EL*LINKKTNH\HL**WAKD*NRACSK DVHMTDKLMKDVPSLVIREI
821	14722	A	828	420	3	KDAHTCPGCKGFGSGHRAKAIKRNQ FLLTTTEFLTHKCLPGQEPWQGHQ* DSPPRVSPAGTWQPPCHRRERACLA VE/GPS*IQEQKSLFFFFSLLRWSL/ NSVAQVGQWRSLSLQPPPPRFKQFSC LS
822	14723	A	829	1	269	IKIKNLARHGDSCL*SPLLLEMLRLEEN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond- ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LSPGSRGCSEL/CQPARQGETLSQTNKQ TNKKPHQVQLPCFEIINFKEFITCLVLR LPGNSW
823	14724	A	830	432	1	GYNNQQIFDQVDTAFY*KKIPSRTSIAR EEKSMLGFKASKDRILLGAKVAGDFK LKPMVLVDPSTPRELNN*ARCTLVPL/V KWN/KAWMTAYLFTV*FIQYFKPTVDTY C/FKILLIDNAPGLPRAVMDR*EESNV FMPVNTTL
824	14725	A	831	1	233	KKLQIKYLGINLMKYTIHVVSICQKLLM KEINEDLNKWRDVLCLWI*RLNNMSILH KLIN/RINLLQLRI
825	14726	A	832	3	477	YQTCEDLTQMLLKIFQKIKGEGII PNS LYDASIAMPKSKDKRTKKF\NYRPISL MSIDAKILNKILPNQIQQHIQKFIFIPE MKG*FNIRK*INLIHLITKMKTKTPMII SIGTEKVFDDIKY/FPFITLTLKLGIDG RSLDAIMVARE
826	14727	A	833	3	402	RYQTPLL*TVLITALLGLSLFVLTG GITIPLTDRLDTPFDPAAGGDPILYH HLF*FQRPFAHILILPGWGIISHIGTY YSGKKEPFGYTGM*AIISIAFLRVIV* AHHIYTV*IDRDTRAYLPSLHN
827	14728	A	834	7	395	DFQRVSCMALSSNSFFFFWERKSLFFP GREGGQIWNVTPTPLQGRNSPASPPG GGGITKKAPKLHPPKKGWGGGLEKPP*N QRGGFGI*SPGKKKGFGAG*KGQKSKG GKKKKGRA\DP*AYIPLK
828	14729	A	835	41	444	DPRVRKKERENLYRSVSIKEIESVI*NF PTKKI*GLDGITSEFIQILPKKKPK\IK KERTFSNPFDKTNITLI/SKPETFTKK EN/VRPVSLMNI/DCKILKVLNACTL\ HI*REIHDS/INFIPAIQISFNIOKTN
829	14730	A	836	3	415	HAYYIVKPSP/WIPKALSALLKTYGLT M*MQFQSIKDLRLGLLNTLTIYQ*WRD VTRKSTYQGRHTPPVQKGL*YGIILFIT SEVFFAGIF*AFYQSSLAPTPQLGGHW PPTGNTPLNPLEDPIINTSGLLGIGVS
830	14731	A	837	378	0	TPPKGPGGKIFLKK/SPGRKIF*PPGNG /PPFSPLSPLKFFFFPKAFNFWGGGPGQ GPPPKKGVFSQNPFPKGRPPQKEKKNF FP/PPGKMGPPQGGFF*RAPPP
831	14732	A	838	383	38	GPGEKIFLKKPREKKLSPPGEKAKFFPP SPLKNFFPPQGVFFLGGGPKRPPPKKK GFFQKTPRGF*IAQKKKKKNFPPRGKF GPPQ/RIF*KGPPPPFFFFFFFFFFF WSL
832	14733	A	839	59	418	TKISSKQKQY\TTPGW*MAEISTTFED AEIIDALIFFNLPILWHKKPDCSWKVS VYCKL*VVSLISATGLDIINT\LLKEM KRVSGTWYIATDLAKTFFYI/PDQKEFA FSWYG*KDIF
833	14734	A	840	5	335	IRHLF*INKFENLDKMDT*KLTYEGIR SLN/RII*NF/PVVKSLGSGSFTSEFYS LFKEBITAIYKPIWRVEKGGI/LPTCFA TRITLIPKPETCIMRKKKNGPVLFMNGH F
834	14735	A	841	1	38	RRLKLEDHLSLY*KINSKWIRELNIR/P

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ETIKLVKKDKGNV\QDTPGKDFMVKTT KTKIDKSDYIKLQSFYTANETVNRVKLQ PIE*GKIFKNYSKGLLSMIYNELKQQ HRNNNLI*KLEDHLSLY
835	14736	A	842	2	424	GRVGSIPLSQSLIQSKALTLSFPMKAET GQEAEEKKVEANRGWTRFKERSGLCNI KVQ/GAGGDTAASSPADPAKINDEGGHS /KQQIFSGNETAFY*KKMSSGTSIAREE KSMPIFKASKDRVTLLIGANAAGNF\KL KPMP
836	14737	A	843	281	3	FFFFFFFFFFFFKTFLPFGYWFSIFFP LLFSISLSSPSGFSVTFAPQPF*VSR YHYQHFNSTF*FL\KL*FIF*IFFLISI LFLFHGYNF
837	14738	A	844	409	1	RCGGTCPWSPVLRRLR*KDHLSLRG*GC SEP*LHCTPAWATE\DSVSKNKKKGI SCROHIVGSFFFHLKMLNGLLSFFTL NVIIYVVEFKFTILLLYSICSLSHLP SFPKSWINSKFESLFVCFNSFS
838	14739	A	845	63	451	KNQEQSEETLPNLFYKASITLIPKLD QK*KKRKKKKRKKK\EN*KPITHRNIY AKILNKILAHQIQYIGKI IHHDQVGC P/GAFDKIQYRCMR/TLOKMGIEGTHL NIIKAIYIRPTDSIIENREKP
839	14740	A	846	60	460	RNNEPFLDQIVTYPEKWILYDNR**/PT QWLDGEGPKHLPKPNLH/QKKVVTVW WSASLTHYSFLNP\ETITSENYSQEI DEMH*KLQSLQLASVNRKQIPLHDNPR LQVAQPVLQKINELGFEVLPHPPYSPE
840	14741	A	847	344	2	NFLKFHPGGGETFLQGYTYGFSPTP*K FFFSKPLNPLGRVGGFFPPPKGFPSK IPQGLISPLRGKVFPPPRNLGPPR VFLKAP/HPFFFFGI\PHGLQPRPMI*K PTRP
841	14742	A	848	439	132	RRVAAPPPSKNIFFPPGSYNGGVWVQK SPPPK*GFFPKP\SGVYKNPPQIEKVFF FPHARIVPPPGDPKTPPPPIFFFCNSI NFSLRGAQLVWDFLGSGC
842	14743	A	849	94	470	LNHFLSFFLSFFLSFFLSGSLSLSLF FFFWKGSPPPP*GTK/QKPLKKKKKK GGGGGQNFPTPPGGKKNPPPGGGGGGS PAQKKK/EGGGPPGSKKNPPGGGFKKK KPPKPRGGGGKPPFP
843	14744	A	850	2	396	FFKKENIQMANKHVKTYYTLLVIREMKI PTSMRYHFTSIRVAKILKTDNTRC*QEG RTIRILMLC*LQNMVLLL/WKNWQFLT KIKIFLF\FDPTISLLGIYPREMKTYVH SSFIHGNSKNRTGNLNVHN
844	14745	A	851	369	36	SKGASDILEKPLF*EVGLPTSPPLGE KMP/FNYKGGPGKGISLLIPKKKFI GGHFFPPFP/PPFFMDRVLLCHPGWSA VAVSQTTSASRL\K*FSCLSYSEG*DG RIS
845	14746	A	852	1	367	PPPPKIKSPSGPGPPSKRSGPCAPPRG KFWFLSQKGWGGP*FPPPPGVKPE/NIP *PPRGRVPL/HLNLAPPPGPPK/PKP PSP
846	14747	A	853	1	378	AMLATLISNS*PQ/CDPPALAPQSAGIT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GMSPCARPTSCSFYP*ILLTVRTFIKIR NFFFFFFDTGSNFVAQPGGEGHDHG***P QPPGPNKSNLNLPSRWYGGAPPCPVI LCIFCKDEVSSCGSG
847	14748	A	854	369	1	SACFGLPKCWDYR/R*ATTPSLEIIYI ER*EKTTSPDNANRFDVTKLHHYDCSV DF*KAL*NGDDFPVLMKMHMQSLNII\ FVFCFLRQGLALSQ/AGVQWRDHGLPQ QLPRLQPSHLSL
848	14749	A	855	380	335	NPGGRGCSELRLCHCTPAWAT\SETLSQ TKIQPKKQEV*LL
849	14750	A	856	373	1	LRILNKKGLANLIP**R*KIHSQVE FIPMQA*PIIRK/TPSIKWPIVTRKKK KKSQMLISIDTEKIFDKIQHLFLVKPVI KLGIEGTFINFIKSIY\KKSTTATIISG LNASPLRLKTRQDF
850	14751	A	857	369	44	KVQNLVFEKLLNKKVDLNKW/NSLCT RFRKLNIANIIMFKLIHRYN/SKVKIPI KIPANCFGEIDKLILKFI*KFKRPQIAK IILKKNKDGYYLPDFKTYIYMQYHLC
851	14752	A	858	1	348	QWHAPAS/LARPPPPRFK*FSCLSLPNS WDYRHAPPRLANFVLCFVG*GGIHL
852	14753	A	859	1	366	CTSPTEFNQKLEMIKL/EEGMLKATG*K LCLLCQKV/QVVNAKEMFLKEI*SASLV NTTMI\RKQSFTADMEKV*VV*LEYQTS HNIPLSQSLIQSKALTLYSSMKAERGEB AAKEK/LEASR
853	14754	A	860	12	366	PSTLGLRRASCLSLLSRWDR*RHMPHPA N*KNFFCRDG/SLTMLLRLVL\NSWPQA IHSPWPPQ
854	14755	A	861	424	78	NPRFLEGQTASFSLAPNF*TTLGKKVNP FF/SLKNPPPPPPPKIWAQPGFPGPPS PGGLNGGFFLPPRVKAPIIHKGAPPPQF PPQKKKGPRVFPKKKKKKKRKEKGMTR AFCYP
855	14756	A	862	327	3	SHWFFAAV\GREISM*AMAPDQTKKICP RSAEDAKEYFLTQATGSILIRAILFNN RLSEQ*STNTTNQYSSLIIMAIKIV GMAFFHF*VPEVTQGSPLTSGLLVL
856	14757	A	863	1	341	YDRNKWKDIPGS*IERLNIVKLSMLPTV IYRFNVILIKIPMTFFAETEKSIKFSR DYE*PKQS*KEQNWKTHTP*FQ/QFFTA TVIKMVWY*NKDRYIY/DQWNRI*SLGI NPCI
857	14758	A	864	32	324	LVWFFFFFFFF*KKKFFFFFF*RRGK NFFFFFFPPPPGLNLFF/CPHPLKWEKR APPPPN*FFFFLKKTGFFFTQKGLNF PPLETPPLTPPKGLN
858	14759	A	865	350	3	RVKNRPFWGF*MVLKPLSFFSKTN*I LFPLKIFSPPKTVPWGKIFLGAL*NPFF CFKNPLWFFGF*KL/SFFFPPLYFF*KP LAPLKRFRSFFFFFFL*DGVSICRPGWS AVARSR
859	14760	A	866	342	118	GSVTQAEVQWCDHGSLOPETPGIK*S/H PPTSSYQVVGTTGVCHPGLAMLRLVLS SWPQAILSPWPPTVQGLQV
860	14761	A	867	1	354	VKPSF*PLTGALSALLMTFGLTM*IHFH SITLLILGLSLNTLTIIY\Q*W\RDVTPE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						STYHGHTTPPVQGLRYGIILFITSEGV FWAGSV*TFYRSSLSPTPQLGGHWPPTG ITPLN
861	14762	A	868	3	344	QIKNPDNISC/WIRCGATGMFLHCWEC KLLQPLWKTT*HQ*SRR*AVPLSGMFP/ NRYSSCTCPASI*KTFLSALFMMTPL/C LSRVEWIK*SWCNQKL*Y*SVMKRSEEF SLKNA
862	14763	A	869	345	1	KQAGLKNVKITG/EGASVNQSR*VS/YL GTIKKITEBKGYLPERVFNAGASAVF*G KKLEPQRTFISK/EEKQAP/GSEVGKDRL TLLFCANMSRFMISTALLYKAADLQSLK GKDKHRL
863	14764	A	870	340	45	FCSECRDRVSLCCLGWSRAPGLK*SSCL SLPKC*DHRC/AA/VPANFQRCILEKKN QIY*CAERIL*SERPHTRHLDSSVTNII PCPLSKVIFWKKKNQIY
864	14765	A	871	209	72	KLWDIHTMEYYSIAIKRNKPLKTTWMD LKDIMLCEKANLKRSHTV
865	14766	A	872	3	353	SFFLGPPPPPPPPPPPPQPLPIFFWRF FCFSPPKKPPP/PFFL*GGSPPPPF*RG FFFF*KKGGVPPPPPPPPSPKVSPPP PKKGGGG/PPPPPPF
866	14767	A	873	3	267	DFTMLARLVNS/WPGVVAHTCDPSTLG G*GGWITRSGVRDQPGQHGEI
867	14768	A	874	1	346	PRRPPPPPPFLIVFIYFKCVYLF*DKV LVCHPGWASVPHHGSLOP*PLRIKQSSH LSLSSS/WDHRHAWLVFVSFYRDEVSPC LANFCIFL*RQDFSMLPRQ/VLKAICLP WPPSL
868	14769	A	875	1	172	KLLSSGSPASASQSAGITGVSHRARG LLNFFC*CAFSVPGPCLGYPDTFTH/LC PPSFHQSVIASLDFSCLS*L*MSP
869	14770	A	876	1	348	LLFCFNNYSFFHGVPKIPAFFVFGPGC LPHEFFPITPAFFFLDRVLLFPFGWRE MGPF*APPTFSPQG*GVFPFPQPQ*LGP RGPPQPQGVFFFCIFGRDSA/LAILPR L
870	14771	A	877	1	203	GFHYAGQASLEVLTS*STCLSLPKSWDY RRGPP/*PGLSYFLYPSLRS*FICAMSI HIPFIKKKASD
871	14772	A	878	343	102	EWEDCPSPGGRCSEPRSHHCTPAWRE TLSEKKYLFQ*KLKNTKIYLSISIP* ELET\ILKILHFKMMNPLHSYNFFF
872	14773	A	879	2	359	RDITKGDMMQETKHM*SFSTSLTSGI\H NSPIRPSKMNIDSTRYWRGCAIRALI HCWWRC*MVQPFGE*ISSFSKLNMYLS YDERPTFRYEK*K/P*VHPKICV*MFMA AFFLISPW
873	14774	A	880	205	1	PFRGVTEGL*EPYVESVI/AGGTTARR PLFFFFFFFPLRWSPALVAQAGVQWR DLGSPRPPPPGFK
874	14775	A	881	150	2	CRARVDGVWRNPGSLKPPSP\GSSDPF TSASQECGITGAHHHTLT*VF
875	14776	A	882	345	1	KGNQPWKTEKRALFC/TLKKKKIFRNSP PRGNF*KFFVKKKIPLKKEGFSPTWGK KKEFFFKKKKKKKKK*AKOLNRNPSRE DVQMAKKHMKRCSTSLIIREM*IKTTIR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						YHF
876	14777	A	883	2	355	DRLLFSASHLDLGLTYLLFGA*SGVLGT SF\SLLRABELGQ\SGCLL*NDHIYNGI ETAHAFVMDLFIVRPPIIGGFGN*LGFP NKKGADMAFPRIINNISF*LLPSSLLLL ASAIVEA
877	14778	A	884	262	2	PTCEQSEREIKKTIQFTTESK*IKFVGI NLAQEAQDLYTETIKYKTLLEIKDNTK *KNIIYV\SWTRRFNNFKMLGWAQWLMP VIPA
878	14779	A	885	16	318	ILRADCADLFFFFFLGKKKGFCFPRKLG RGETLLN*TLIPR\VGKNF*PKLPKIW/ DFKGWPHYH/AENFVFLKKGGLTLLPG LVLNS*IKEFFHLWPPKGVA
879	14780	A	886	298	322	KRRTF*YPPGEPHFPPPPQG*KARGAP PPPPKKGFF\PEKKKKPGVMVQGTQKP PKKTKVRVD
880	14781	A	887	353	3	FPFWGFLKTLFGKALWLFKGFFFAHQK FFFLPSLPPPP\LGFFLRGLT*FKIFSP LF*KGAPQKGISHPLFFFLISPKPPPPF FFFFFPFPPPPFFFFFPPFFS\RDRVLL YCPGWGA
881	14782	A	888	22	341	IPCTCLKLHGKVDHDSQSLWPKPQEE MRTLENNLAVLQSIQWLDIELPYDRAI ICAREIKTYV\QQNCT*TFMLALCITAK KW/KQLKCPSTDEWVSRMWTCTR
882	14783	A	889	51	338	ERSQLQWLMPTIIPSLFFFFETQFLCCP GGRAWAIFKIFEFLA\PK*KQFSCLTQ TI*VYGLNPPPRKNFVFLKERGLFHVQ SGRDLPPSGDPP
883	14784	A	890	1	225	GRLRPENHLNPGGRGCGELRLCYCTPAW VTERDTIS/RHTHT*NYFY*GSI*QLAN SCCCNMLNKFNVICILRW
884	14785	A	891	357	164	GKGCSDSRLCHCTPAWAT\TKTLSQKKL ILKKQNKFRS*LDD*INMRCTVWPCFHV FLFIRAAPLESWLYNK*MNRNT
885	14786	A	892	207	302	EPFSGTIINESIHQEGTIVLNVTSSNR PSKYMQLTIELKGEKVKSTIIVGD/FY THLLVIDRTSR*KR
886	14787	A	893	86	332	VMRVSCCLKD*ISLCHPTWSAVVQS*L TVASNSW\VKQSSFLGLPALWEAELGGS LEVRSRLRPVWAT*TP\FCKNKKL
887	14788	A	894	2	336	FFFWPPQTFLKNPGGPGPKREEGPGGS PRGQKQGGPGLHLTGFGGQPGG*KNPEP GPGGRAPKGETRGEggGPTRPQIP/QLI NGKSGKPPKVTLNGAWGTIKIFLIKTPV G
888	14789	A	895	1	214	ARESLASFLPPSLPFLGLRFLPSFLP FYFSFLPSFLGFGSFLPST*VPSFLPSF LLFFPSFLPWLWFLPS/FLPSFLPSFLP SW
889	14790	A	896	131	352	TLHESDSSESVPDFKISDALAVEDDQRS PGTLNAAELS/SSVRERKKEK/KPEPG L*DQSIKESDSYMSGGRIQ
890	14791	A	897	3	184	CSVAPAGVQCHDLTSLQSPFP/SSSNPP TSSNPPTSAP*VAGTTGMCHAWLIFVP LVDA
891	14792	A	898	327	264	NRAVSLMNLDAKVL\KLISASQIYVYIK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond- ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KMIH/HNQIRFTMRM*GQPII*TAINIY HKLIK*GRKHMIPLIYAVKIFEKI*YHN IMIKTLHKL*IKEPPGSPFIYSL
892	14793	A	899	3	313	TKAASHSQ\LANLQFLVGRH*HLKSRT ISPGRVGATAAVNSTAILEYLTAEVLEL ARNASKDFTVKHTTPHYLQLAIRGDKEL GSLFKSTIAGKGVIPHIHKS
893	14794	A	900	340	1	HLCPHKEHLY/LLQTSCPLAII*FISTI AEHTKAPFDMAKVESELVSGFNIEYAAG PFALFFIAEYPNIIINTLTVTIFLGPT YVALSPELNTTYFVPRKIVVVRVFIIM FV
894	14795	A	901	1	252	LTFFPQHLLGLSGMPRRYSDYPDAYAT* NILSSVG/SSFSLPAVILIIFMI*EAPA SKRKVLIVEDPSINLE*LYGCPPSFPSF
895	14796	A	902	326	1	LGPPPLKEPPGVFFIFFF\FWNFGPV GPF*KILIGPLILDPPQFFFGVSVQIVF PPF*GKIPFF*KNTPPFF*GIGGSIPHP PLFFFFFLL*DGVLCHLGSVA
896	14797	A	903	1	352	KGIFPVWSCG*KGTQKKGSLSQGGQGNV PPCGIHFVKEFLGFPGAQLLIS*GGRLI F*KGPKKGFLL*TVFG/RRQFEAPR
897	14798	A	904	325	2	RLEEKLNDYWNEMVKKNTRYPLNLFVE DIQKRPDQTVVQCDACLCKRK*PYGMDQ HLEK\WYWCNNHDSQFRYCMVPKDPEDM DLVHPNYGKPKKPSKETWFSQMP
898	14799	A	905	1	329	IGLAIHGAERIVRGQTAKSLAVHN\VCE QKKIKKKKGPGREFONLKWENPKNPGG SF*RLGPQSNFFYLKQ/RLGFFF*KKP PKI*ILAMEPPNKKIF*KNKNKAHFFF
899	14800	A	906	148	2	DVDKFLFLSLPTL*RPYEGSYMIEGT\ TGQPYGGTMSEFNTLEANMRIR
900	14801	A	907	384	1	ESKRSIFGFPNPPPPGFGFSRHAPLWL RSREPPHKAGVKKGFPRFRPGS*MPIP* SFLQNCPLQRVGFPSPPPGAPFLKISL FLRQESRSVTQAGV*\YGLLQCRPPRLK SFSCLSLPNSWDYNR
901	14802	A	908	3	297	TKIKSL*INHLIRAKTVKLEENMGINL HDLSSGRQQFFRYDTFQ/SMINTAIKEK IMKLSFVKMGSPISQRTPLRKERQLTK* EKIFADVLLIIGRRG
902	14803	A	909	169	373	ASNILSATDISNTFGPPGSGQFSGREAY VEAGTYTTFNSCLGQVKVF*YWMQLIVS IVLL*LL*VTQKL*L/GPRQEKVF*YVP AST*ASLPLKPCDPGGPKVFEMSVADS/ DV*SLWLALIGESKFRCLVF*SKFLPSS AYTYSPLEKKLFILLGCFVMICFCFCFL RRVL
903	14804	A	910	132	368	GRIFLVGQEKGARVSFLFLF*DRVSLC HPGWSAVAQSLTTS/TWTQNNSSHLTP P*VAENHRCA/PHTPNVLELC
904	14805	A	911	2	339	NSWAQE*AGITGSCHHTQLTLEF*AHDR QMMFFLFFLKTNFTFCPPA*RPWPLGL TE\PLLPGLKHFF/CLTLPNSWDKGHL P/HPYQI/CGFLRKGASLISG
905	14806	A	912	3	381	LNFCDTPLTPRPVSIQRCPLVEAGI RWRALISPOLHPPT/YSLSSWDYKHAA PHPANFFFFFKKGSMTMPRPGG*IF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IYLLTYLERESY/AVAQAGGQGPNNFNSG QPLSPRFKQFSYLSLLR
906	14807	A	913	394	1	MSKKGKIG*KLK*KFAQKVSQFVNABEKL LKEIKHFTLMNT*MI*KRNS/LIADLEK ILVWNIENKTGYSIP*TONRIQSKALIL FYSMMTERGEEA\KKFEARRDYFMRPKE RSRLQNMKV*DEAANADGEAA
907	14808	A	914	326	200	HNWLSIWKKVKSNCFLMPHTKINSRWIK DIKI/R/LHRIKILQENVGNHIYKI*RQ KRS*PRHNFHKNCKCLVWHKTNK*NH* KIYL*CI*KTFVAVFM
908	14809	A	915	3	334	LVVRVKGPKFKFWLHHQLGLYC*VISFF INKMKEYVLIHRIK*DHKNIF*MGYKKL *NVNIW*LVLFGFSSKNHL/WSGAVAHT FNPSTLGDRGRRITQGQEFQISLTNMVK
909	14810	A	916	14	299	YQKLPQKKSPPEPNAFTDKFYKIFK*LTA ILQ*LFQKI/E/KETPLPK*SNESNAL I*KPKDKIT/SKNYKPIVSNIHAKILN KI*GYQVQKQLYSK
910	14811	A	917	3	339	SLQPQSCRLKCSSCLSLSSCWYKHKPP CLA/NFF/VFF*EKGICTVKN*NGDYPL GRRVTKRDHERGF*NAGKVLVGV/CGF ETQSRFVPQAGGQGRNLGSLQALFPGLM PFSC
911	14812	A	918	2	321	GIISGIYKELSQPKMTDSSIKK\KDLNR NFTKEYVQMAKHKRCSASLVIREIK\ IKSTMH*H*\TPTRMTKIKD\DKNTKCW *GYGAVGMLIHCQW\NTKMVQPLWKN
912	14813	A	919	51	326	FFVFCFLSLVFIISLNCGLF/PTFRIPS L/PYLQLI*IYLFY*LKPIFLKFFRDR VSLCHPGWSTVA*S*LIEASKYW/VQ*S SHLSLLSS*DY
913	14814	A	920	239	2	DSLILSAVQ*HDLGSLQPPHPLKQ/FL PSNWHYRCMSPCLAYFLFLVETPFCFV TQASLELLGLSNLPASASQSAGI
914	14815	A	921	1	242	PRPRRLLKYFILFNLRQ/RSRSATQA EVO*HDHSSL*PQTPRLK\HPPASET
915	14816	A	922	249	1	ALFCALKKTLGTLMFIAALFIITAE/SR HNQTPTCLSTDEEINKMWHRRHAMGNYS AIKRNEVLIYAKI*MYLENIMLSEII
916	14817	A	923	404	1	SRPQKKLGELKCS*RPKGLNKKNQKPKG TFFFFETKFHSPCQAGVQWVYGC*SHPY LLHIIFP*VF*MFLILITV/PSRNKDL IGNSEKQIHN/WSSLYFYF*LFFLRWSL TLVPSGVRWRNLGSLQPLPRFK
917	14818	A	924	6	358	FFCSLLGHGGETPNNSPLPHPW*ETKS PPKPPHPLKKKKHSLFFKIFILKKKKNG PPFFPPAGPNPRG*NPPPPQ/RPPKGGP PPKEKINPPPPQGNPKGKRPPLGPF PKKGGGY
918	14819	A	925	268	2	HMYAFVKIDLTALHRSAGKKEIPAGKL YF/L*RKNPKNQIGNQKKKKCLPRAGRM VAHAWNPSNLGGQAGTT*SQALETSMG NMGKP
919	14820	A	926	74	338	IAGITGVSH*ESKNSY*KQFL/WPGTVA HSCNSSNLGGQGEWIT*GQEFETSLANM VKP
920	14821	A	927	339	1	LRLFACFPLPKWWDYRGEPPRQIFFSWH

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						FFKKQGFICPIEKGRELSNCCFQKEVLI *KKVILKI*PFFFFFLMBSCSVA*AGVQ WHDLPPLP\NSWDYRCPPSRPAKFCIF
921	14822	A	928	3	416	RCWENKIN/PFWK/S/VWPCVTKNVNIH SPYDLTISLQYLPYRDEYLCYKNLMFL IVLFIITKNYQPKCASVG*WLRILWYL /YMENYSAIKMNK
922	14823	A	929	344	69	YKRSPL\KSA*DGPAWKSIPRS*YKR SPLLIKAKPDQIISGWEASPLII\PRAL LQKLKPAASKF*W/NPKKRALIS/KAI PSKKNKAEGIMPPNFVK*YRDTATKTA* WYKNSSSL
923	14824	A	930	378	1	HGKKIDPRFIPYTKI/NLKWFDLNVKP KTIKLE*NIGE/TIFVIDHKK*NP*KK KLVN/WDFIKIKSFCFVH*KPAVGK*KR /QP*TRRNVTHTSDRGLISRICKELF *LSKVINSIRKWAQSLN
924	14825	A	931	479	83	SRKGLRGLKRGGFPPPPPKGLPGGVA PPGFEGFPGSL*KG/DRG*PFLKGVKGE KGKRI*EGG/EKGGGFLPPPPQKGFSS NFLGFYAGKKNP*GGSPPPLFGPAQK ISLKGGENKVPPPPGNLFLYLFIF
925	14826	A	932	36	440	TTYASLDEAQLPRAKFNALTT*HIK NGPILGKIGRKYMIADQ\GHRMKNHCK LTQVLNTHYVGPKRILLTGTPLOKLP LWALLNFLLEPTIFKSCSTFEQWFNAPFA MTGERVHLVEETILIIRRVHKVL
926	14827	A	933	8	398	CLQKEETLTNNWHLRYFLPPPPFWPK KGARKNGGRPPGSGPKNQAPCPKPFEN PGEKTPQKRGFFPPKPCPGPGPGTGGQ GKPP/HPQRPQILPFVPOAGPQGRKGG* WNPPPPG*KGFPAPTTPRM
927	14828	A	934	1	441	TRSHRALKEVYTEINIVMPANATSIL QPMG*GVILTLKAYYLRSTFCKAIAVP SDS/SSDGSQSGLKTLKGLILDAL* NIGDSWEEVKISTLTEMWKKLNPIMND FEGFKTSVEVTADVVKITEEVQVESD GTEFLQSH
928	14829	A	935	3	383	PGFKASKDRLTFSSGNNAAGNFKLKPVL IYHSENPRVLKNYAKSILSVLYKWNKA WMTAHLFTAWFTE\PYVETICS\EKNI FKILLIDSVPSPHPRALREI*KQMTIVY MP/STTTSILQPMNOG
929	14830	A	936	417	1	CFFSRDEVSPCGPGFSPSPD/HHDPPPP PSQCWDYRRDPLWPPHICFLIHKKRS SHMGSSMYDP*KPPHKWMKSPPPVSVLY GSIPVQVQIAPPETNPVYFFSPPPPFW GGGRVCVCVCSSEVCDFGGDENIV
930	14831	A	937	412	3	KPTRVKKINPPFFKNTKNKGGRVGSLY SPFFGGLGQKNGFTPEAKGSINLKFP PKSWGTOQKSLFKKKKKKKSILKFIWQ KINPKQIKQS*GITLPE/FKLYYEATV TKTAWRYKNRPIDQWNGTDRNKATH
931	14832	A	938	1	416	KNRHIDQCSGIERPEIDSHKYSQLIFDK GAKVI**RNDNLFNKWFNNWMSTC\RK INLDTDLTYLFQNGSQT*P*NIKLENS MGGNLGDL/GMSQ*VSSSSSRRIHDKK LVS/WDFIKIENICSEKGIKRMKSQTT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
932	14833	A	939	4	443	DFDYNHDHDAELGTRPGSVGQGSFDPQ FTPSRMGREGEGTHSIL*CSSLGMGVIA DLSTDPTELEKRALEVAGPDGQASAI ASPRRKAGDGGHRRALPGCTSLTGETTG KSGEAGQDGKPPGD/GPIGPYSLPGSGP SGGESMMG
933	14834	A	940	3	404	LFMFLEFFF*KPRSC*VSQAGMQGCYLK ALQAPPPRFTP/SLSS*DYWSLPPPLA NFLYF*ETRGTGLTRMISIPQTEMPG LASQTAKLIFP*K/HRVLVES/HG*SAR AVHRGDLHILEP*TPGLK*YS/CISL
934	14835	A	941	397	1	FVPNSQVANAKKKFLKEASTTTPVLSGI RKQNTFAADME*V*MVWIKDQPSYSIPL SQSVIQ/SRALTLFDCTKAERNRRGKIQ WEPAV\EGSKGWLMRFKERSHLHNKIQ DEAVSYPELDKMDAVNTKHQI
935	14836	A	942	441	29	SVTLCKHTVHVPTFLRRGKRCPLFGQCC PWPSPG/PHPLSMSFV*PRPQ/PIPLHS APPLALGPFIPMLSMAGLFPFQGSGLR NWKPFPPQPSLLQ*HFFKPLKPIRGLR PFPSTLSIPLPGTRPRAKLGVMRSRL
936	14837	A	943	2	397	ARDAPEPEGEHLLQGLSARHGLRPRDS RPGPD\PP\SPPHPLPLPAVPTFVFSFG DSWLL*SPFFPAPWASEGGACAPNPHAL VPSPSGQASGLRGGAPSWKAGLDTDGQQ AGRQSPGPAPFSPPLPPSQDC
937	14838	A	944	3	449	LRQVWHEGEMPNKTTLIYHYTPI*ITNI KNTDNTKSLWGCARSFTHC/WMRIKM VKPLWETVQ*YLI*KLQLPFNPAVALW \SICPRKVKT/CHRNKTRS*MFIV/A LFVTAQTKN
938	14839	A	945	380	175	RAPAVPATQAEVGG/LH*TWEDRLNPG GEV/CSEPKWCHCPPAWATKPCNCVSKK KKKEKRINHQHDEK
939	14840	A	946	21	331	VAPLKYGPSKETI/IQSVRQSTECKKIF AYYPSDTGLITRIYEEL*RLNRKEKLS SVYKYAKDLI*PFSKEDTQMANRR/H*K KCSTSLIIREMRFKTTMRVDAV
940	14841	A	947	365	1	GGGPFWFFFFFLLGGLFKIGKIWAKKKT GPSFPQKKRGPKKKKPPGFFFFF*K GFVAPGGQWEGFGLQPLPPGVKQFFC PRFLRW/DSRFFFFFLIKSNAEQFPTL YAGVVMRYIK
941	14842	A	948	357	137	ISAHCELRLPGSHHSPALLCSPGLSRTP NLKQSSLFSLPKCWDYR/LATVPGQLLL F*ARHCISIDPSLHNNM
942	14843	A	949	53	352	REDNHKKCI RNKMNRKANEVNRCFSE EIQMVKKHEKLLASPPIRSMQIKRY/L NSLA*KKEKSD\NTKLWQGFGETKSV* RYIIN/PYDPTIPLGIY
943	14844	A	950	937	3	KVSPYKINIHK*VAFLCTNNIQAEKK/M NMVLEFIIATNKKI/SYLVII*IKEVKYL YNKNYK\LLKKNRDNANK*KGTPCS*I* RINIIMSVLPKATYRLSAISLKL*ML FMELEKE\TILKVIWNKTAHLAKATLT \QSNFGGLTLPGLYYKATVIHITW/HCY KNTHVDQ*/NRRESPEISLHFTQLFSD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KVNRSKQ/WKNCLSNKQWESWLIICRR RKLKLYLSPYKKCNSK*IKNLTVKLA KIVEHQKSTVLVTGLWKGFMNTIKVNA TKIKVKV*HLIKLKNFCTPKET/T*QIC RQQRVWNKLFNSF
944	14845	A	951	246	1	AASTKTGVQTKTCT*MLIALVITVKRE KQSKCSEVE\E*TMWYIHTMEYYSVTKR NDVLIRTTWMNLENSMLSKKDSHKG
945	14846	A	952	2	255	QCGEGKGTFLHCWWEYQPLWKTWV*FLK DPETDIPFDQAIPLLGIIYPKEYQSLYYK DT\AKTWNQPKCQLMVDGIKKMWTVD A
946	14847	A	953	343	3	GSITYKEMEPKVNLLQK*KASCTDGL*G EFY*TFENEIPILYNLPQKTEAKGTLTN SRDEASIIILIPKEKCTRRKENDK/P/I SLMSIDAKLLNKILAN*IQSRIYSRET RLIQ
947	14848	A	954	1	349	AQPFILFILHP\IYCFISS*S\R*QKT LKTTFQGFIFCFFFFFK/QAKSCSRIR GRGPIIAKGTPEPLPGLRDPPTSPT*VAG TKGGGPHTQLKFIFIAK*FYISF*HNGK FCRRGR
948	14849	A	955	2	351	GLKNYAKSTLPVLYKWN\KA*MTTHLF TAMSTE*FKPTVETYS/EKKIPFKILQ LMDNAPSHPRALMEMYKEINAVFMPVNT ISILQPMQGVISTFKSYLL/RNTFCKA IGAIDSDS
949	14850	A	956	336	3	PTKENFEPDGF\TG*FVOTFKELIPPQT FLKTSREYFSSSSSSSSSSSSSSSSSS SSPYRPI/SLMNTD/AKILNKILTNQVR LHIKRNTHDLVGFIK\WFNIRKTDQS NN
950	14851	A	957	181	1	RWDLTMLPWLVSNS\GLRRSH/LPKCW DYRFEPCTA*GWFLIGPHWNVSTVGS PRISRQ
951	14852	A	958	3	293	GGLTSPHVKTYYQATVIKTAWNG*RGVC MDQ/YNKTEPETDPCKYSQLMFSVTK AIQ*RKDSLNIENWNN*MSIHKSSSR KHLNQYLYPYTKL
952	14853	A	959	350	3	NKKKGQSLVFRSPTLFFFFFL*ITEMG\F IMLARLV*NS*RRNMTTSGSQSVGITGV SNHARPKRKLFLFSIIITIGWAGV\WWL TLVISALWDYRREPPRAVLLPFHIQRS RMPLSN
953	14854	A	960	349	1	GGFPPPLFFFPF/PPPWGKPPPPFFYQ\ SFPKKKGGPKPPFFFGSPGWVHKQFL VKSPLPFFWKKKKPPPPF*KKFFPP\VF QKQPGRVKKPPYERNWLLGPPTKKSPK KSTGS
954	14855	A	961	379	160	PGPQGEPPFFFLKNPQKLVGGGRFL*AP LLRGVRQKNSLNPGGGALKPGS/HLWP PSWGKKGDFLF*KKKKKKK
955	14856	A	962	184	2	TFFSPKKIFPFFFSKFFPKGTFFSR ENFFFFFFFFFF*DGW*L\CHPGWSAVVPS RLTATS
956	14857	A	963	1	328	ARLVLS*PQ/CPLPASASESSGITGVS HCASASQAGITGMSHHIRPKWISLYLG FWSFNKNVLHFFCASSLEGESMNNELLS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						KKNWEFLDKRLHGSTKLGNGHVCVNF
957	14858	A	964	1	334	HPLGGRVGGVPLGP/VVLNPPPPQ*GTP FFLKFPNNPGRGAKPVPAPRGG*GGKF LLPPRGG/PSMNPNCPPAPPP
958	14859	A	965	206	360	QKSMSLHQ*QDIHSSQAHKNSSW\PGA VAHTCNPSTLGGQGMQITRSGDQD
959	14860	A	966	10	332	NFFSPGAPPPPPFFGGGFFLKGGPPFF* KKKILGGPPPPKKNPPGVFFPSP/AKNL GFPFPPPPPPFF
960	14861	A	967	1	282	RKCAKDLNRHSTKEDIWISTECI*HC*S LRKSTLKPRDMPHIY*ND*LYKKNDIDK CW*GYGVTGAVFHFHWVSRMVQPLNNW TVPRNVKFTL
961	14862	A	968	339	195	FFFCRDGVSPCCPGWSRTPRPKQSTCLS LPKCWDYR/RL*ATVPSLDYLF
962	14863	A	969	3	342	IKKGHPQLKKPPGVFPVFQFKSYFPP PPPLFNNPFFFR\DKASLCHPGWSAVML SYFTAAYTSW\VRSSSHLSLLSS*EWRH TQPCLEFF*F*FL/CRSK
963	14864	A	970	384	6	GRKNVAGFPLSPLYTPPHGHGLGPPQTF GAGPPAHKSHQKVGROKRGEGFVPRPP AFLFFFFFKE*SVLEKKENLYNSLFAY KILNKVQGETQCEGRAHIC\VCVCVCVC VSVCTCVHVCALAIC
964	14865	A	971	427	109	LNSQFELQEKRIISNLEDNEKII*SEKES KNRMARN/E/QSLRETWDTFGYTNIGIM ECPEGBEK/GKRKRKT IKKKMAANFFHL MQNINLHIQKAL*TPTRITCTGPYGG
965	14866	A	972	389	145	SLQP*TPRLMLSSHLSLLSSWDYRCVPP HLANFLYF**R*GFAMLGSSNSSA/SAS QSGGITGVSHAPVVFTFKKKLVADT
966	14867	A	973	170	419	VSFLFFFFFLERQFYFFSPGGEGEGEG LIEFPF\PGFGNFSCLTLW/RRWD*GAP PPLPAYFGFLIK\TGFPVLRGGGLDRP SR
967	14868	A	974	212	3	QNSMIRYSRMSRSLCTTILILSLNRS LKSPP*/WPGVVHACNPSTLGGRGRI TRSED*DHPGQHGETP
968	14869	A	975	28	356	VFETSLFRNKKEIVKGTSLPDFRTYFKP LIIESI*CLHGIGQNNAWNVRVGNLQIDA /ECAENLIYEKGGISIQW/SLFNK*CWS ITIHKEKKIRPLHCIIKIGTKDFKKLS
969	14870	A	976	350	1	LFCKEKVSLCPGRFEPFGMKKSTLLSL PKMRGYR/RLAPPPQLEIFFHFLTSTA TPL/CLGRSLKRLNSQMFSPFFSEGVSL CSQAGIQWRDFGSLQPAWLWK*FSCPS ILSSWN
970	14871	A	977	4	343	PLHSSIGNIVRPHLLNNSNKNDDTKCW* GCEKPGFLIHCIWEYMMV*LLWKTDWQF LIKPNIHLPYDSAVAHLGIYPR*MKTFL QKL/CP*MFIAAVFLIAKNGKQLRCPV SK
971	14872	A	978	3	424	KRMRRQATDWEKIFAKGISDKELLSKI KELLKLNKKSPKQVACFKMGQT*TAH LH*TIYR/CRRVTHRKDHSTRSWLLREL QILNT
972	14873	A	979	114	325	QQQQNN*IKKLAEDSNRDFS/BDIQMA NK*RCSTSLVIMEMQKVTVRYYYLTLI

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						SIATIKQKKQNPCK
973	14874	A	980	339	2	GPTGFKFNQGGPPPKGSFPL*KISPPS* NPPFFFGPQKGFKPPFPYLPNGKNFF SKKPLFFFF*KKGFFKPPPPPPPPFF* GRVSLCCPGWSAV\A*SRLTVTSTSHVQ T
974	14875	A	981	2	377	QMANKHMKSFSTSSAFMKM*IKNMRSH DTCIRMANINTNDT\CW*GCRSNKILMH SW\WECKMVQLL*TMV*KFLIKY/DTYH DPAISLLGSIKKSKFCT*/T/CKILYL NVLFIMNPNWQSNWYSMG
975	14876	A	982	1	457	INEIEARNTEKFNKTELTSSSSSSSSS PLVGLTKRKKSQ\NEGDITTDIEII/ TIIDYSE*IYA/NKIEQASSSSSSSKT YNLSGPHHEGTESLNRPIIMSEEIESLSQ NLPNRSRADSFSGKFL*TSKDELPT LLK\FORTEQERTLR
976	14877	A	983	332	2	TPKAGQMQLFPQYGSKVARAPFSVVAL PPPPFFHFHFCFPQPHCSLPPQIPPPFS RFFLQVKSSQGGPPPSLLGWGEQ/NTLP FFFF*SHSLALLRLECSGAISTAA
977	14878	A	984	365	2	KSSKLFNYPPLFFFLKNFGPKKK/SGPF FCPFKNFFNPRVPGNPNFKGFFFLKKG PTVF*IKKFWGGLPPLK*PSGVFRFFH FLIWDPRPPPPPPPPFFFLVERGFHVH QASLELLTS
978	14879	A	985	1	153	GVQWCNYSNL*PRPPG\SGDFPTSAFQV AGITGVHHHTLRFPPFGVGFNF
979	14880	A	986	225	1	LYTYRERERERDRDRDRVSHTHLYIHT RTHLDNLFCHPGWNAVA*SWFTVALNS WV\KSSSRPSLPSSSDSS
980	14881	A	987	2	375	GTDEYILIALIVMVSVWCLFPPFEKKA PPCPPAGKTGANFGLRAPPPGIKEIFW PP*PSEEG\EPRGPNPSRGNFVFKKRG GSPL*PRLFG/HPRP*GNRPP*/PPQRG GNNKGDPPPPPGGIFF
981	14882	A	988	55	335	HIYIDVFVSGSWLLTV/ISLLELTVFCY NVGAL*ASG\QASENRSVSDFLPSFY LPKAGL*SFPAFMMMGHKILPEKVIPH MLEEB\TCTERP
982	14883	A	989	295	369	ILVTRNSEL*VLPEQRTFLEKAMALRS IPLLR/NGRPGTVAHACNPNTLGGQGG RIKRSKV*DDP
983	14884	A	990	2	240	KKISMNLEHFMLSERSQS*KTTYMIIF T*KLQNRQIYK\TERIYIYIYIYIYL FFFFFLERKFLFLFPRGEGGGPF
984	14885	A	991	463	0	GFRQLSCLS\LPSSWYRHMSPHLANFF \TF*VERGFRHVGOAGLELLTPNDSPSS ASQSAAIH/GMSHCTQP
985	14886	A	992	82	365	EICHQLYRSFLCSLFC/DHPSNKS*DT MNCVHFIIIRLLNFSFFFFEKKFRFVQV EGQGSNLG*LKVLPPRLKPPFSCLTLLRS WGYRGPPPPPVN
986	14887	A	993	3	317	GLKQSSCLGLPKCDYRHKPPCPHTIIF NTH*IIKVLNVFSFCI/PLCWSIALSD HVQ/PV*LYNMLVSSFLLLLFIEIEVV ILACLCVPGSPILFF*YILTF
987	14888	A	994	350	139	LFRRLRWEQHLS\QGGQCCSEP*SHHCT

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						PAWATE*DPVSKIQQNKNDTFSHTFILL ECRTSKGVSAFLAL
988	14889	A	995	219	1	RPRRFLIQTKAKNHHFTPTMPVIKDN NKC*QGCGEV/WN/CRMVQPLWKT/IQF LKMLNTELP*DRAIPLTGGKE
989	14890	A	996	3	498	CLPWAARQPPSAHPFPQGP*LRTLA PDTATAVNQALQRQES*TCG*SPSGWPA VPTPVAPG/PPSAG*GVDPRAWPRHNG PPGQHPKEKTYQVPAP*VQLSPTRQTP APMACSSLLLPALPPPAPARPPCPAPP FLPSRTSTLPPRRLSSTIKSKTFFGP
990	14891	A	997	2	419	ADTEAAASYPDNL\ANDESSYTKQIIFN VDKTALYWKKTPTSRTSIAREGKSKPGFK TSKDKLTLLLGANAADDFKLKPLMTYHS KNSRAHKNYAKSTLCFRN*NKAWEHLF IAWF/EYFKVTVTNCPKPK/VLLLTHN APG
991	14892	A	998	388	405	G*FFPLSASKFFFCP*ALKLWMEGCHIR PPPQVRFPLOSSQA/GFISASLKGKGF ASMPANIGPPKGYL*PAPPPFFSFLRQ SHSVTQAGVQWRNSSLQPPPG/LRRSS HLSLPGSDWH/MPPCPANFCIFCTGG
992	14893	A	999	1	423	WILHD/NLRQPAQWLDQEAAPKHFPKEN SH/QKKVMVTVCSAAGLIHYSFLNPG TSTLEKYVQOIDEHM*KLQCLQPALINR RGPILPQDNARPRVTQPMQLRLNKLCD VLPHPYSPDFLPTDYHFFKHFDNFLQG KHF
993	14894	A	1000	2	406	SDLFRAI*ETTSVIVYDVSMIDYLEIDSE MIRDLLNTFPV\HLELQDSSGVIQAG ITEASTINAKEIMHLLMKGNRQRTQEP AANQTSSRSHAVLQVTVRQSRVKNIQ EVRQGRLFMDLAGSERASQTQ
994	14895	A	1001	290	3	VTQLPETVPHFLRDRVSFCCSGS/DHSS LQPTPGLK\YPPTSAT*VGGTCHHAQL IFIPLRDGVS\SAQAGVQWEDLSLL*P PPPGFKRLSCLNR
995	14896	A	1002	143	408	IKKKIKREI*KYLDISKNK/DTYQNLWN ATKAVL*GKFIGINVYIFKNRN*NK*F NSTSGKLKLEKKEQTKLISRKETIKI RAKINE
996	14897	A	1003	84	409	DKLAALPSSWTLHPGSLGVTRAPPPPP PPPPPPPPRVLEPVPSLYPGLAVPVV PRALH*PPHPSLPACAPAGLLGGTRQC S\QTILPKKPPPLDADPANEP
997	14898	A	1004	392	2	EKNAVHFDQKNLVSINWELQVPTQVCIQ NKTNSWGIAGYFFHFLKRNQRFNALKV PGPFSS*TIHLVNLKNLFFF*DRVSFCC PSWAVVKS*FTAASL\IKOSSCLNH PSS*DCRHTPLFFVRMS
998	14899	A	1005	2	421	FVSLLLITSAIVAAGAPTGRVYPPPLS GNYFHPGAFVHLTIFCLHLEGVSSILRA INFIASIIISIIIPAITQYQTLFG*SGL ITAGLLLSVPVLAAGITI\LLTEPSLF TTFFDPGGGGDPIYQHLF*FFGHPEVY
999	14900	A	1006	1	428	DIHYG*IIRYLHADGASIFCICLLHIG RGLYGSFLYSET*SMGIILLATIATA IIGYVLP*GQISF*GATEITYLLSAIPY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid- residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						IGTDLVQ*I*GGYSVDSPTLTRCFTCYF ILPVI IARLPALHL\LFLELTGSNKPIG LAS
1000	14901	A	1007	1	419	SPIVPIVMAMACMLTERIILGYIQLRP GPNVGGPYRLQPPADAIKPLSKEP\LK PATSTITLYISGPTLTITIGLV*TPLP IPNPLVNLNLGLLFILATSSLAGYSIL* SG*ASNSNYTLIGALRAVAQTISYEVTL
1001	14902	A	1008	411	27	GQPGQHRKTPSPLSIFYF/ELAGGGDAS T*FQLLRRLR*EARLSLGT*GCSEL*LP PCPPAWVT*DPVFGGRKKKERLSQLRK LRPREVKSLVQHYVAHKGGNWDPNPGPM ATQGRSCTTLCVPLCHR
1002	14903	A	1009	21	377	MSLGGQDSAQTTSPQFAGFFGORSIP DRTGLGFHLCVCKCVCACVQSVCKCVH MCACACMCTRTPMCCECVQCECVQVCVR VSMCVQVCACVRVCACVCSGACG/CTCV T*MSLACG
1003	14904	A	1010	1	412	HKANTSTYLLTLVNTFSG*VRACPTTHK TAEVVASTLIEQIIIPRF/GPAFISKIVK QVTTLDVNWKLHTPYHPQSSGKVERAN SLVKQHLIKALKTRQSWTLLPFALAW LWAAPOSPGTGINPFELLY/SAPLPLSN
1004	14905	A	1011	1	410	FRVAGASRQENGA\TVILRDIARAREN IHKSLAGSSGPGGASSGTSGDHGELVURI ASLEVENQSLRGVVQELEQAISKLEARL NELENSSPVHRSTAPHTQQVSPAPVEP PAEKPATPT*DDVDDIDLFGDRND
1005	14906	A	1012	269	32	NISRIYKELLQLNNKKT\STSKRAQYLN RNFTKDI*MAKKPMKRCPTLLVIREMQI KTTMYRYFTPARMATIKKTDNNEY
1006	14907	A	1013	21	443	RIRKNSYPHYVKSIVAYTFIIRLFPTT IFMCLDQEVILSN*H*ATETTTQLSLSF KLDYLSIILIPVALVATWAIQFSL*YM \NSDPNIKQCLKDLMLFMTILVLSTAN NLCQLLIG*EGA*MISFLLIS**YARAD A
1007	14908	A	1014	1	309	SSRAAAIHGGACLWLQILHLRLRWEG*LS VGGQGCSP*LHH*TLAWATERDFVSQK KKKKPQKANP\HLETSCKKKKKPKMLGP PKSQRKEGPKAPQGRTLWP
1008	14909	A	1015	3	256	EKNQILKWTMDLSRHFSKK\NMQVGNRH MKKC*TSIIIREIQIKTTMKYHFTPVKM AIIWPGAGITGMSHRTQPSPTLLTHVV A
1009	14910	A	1016	397	3	LFSSPPPKWGFFFFPPPRFFAPPPFFFF PPPPFFFFCEKPPFFFFPPGGGAPPL SPPPPPPPPPPPPPPPPPFFK/SPPPP PKK*KKK*KKKKKTPNTPKKPKPKPK KKKKRAARDLELVGRVGGRV
1010	14911	A	1017	2	164	EKERRE*KREE*KERK\RKEGEREGGRE RERERKKKRERKKDRCMFIVHFR
1011	14912	A	1018	1	406	NSSPPKNKN*NK*KQHT**EKNFANYIS DIELVFRTYNELLQLNKTGNPIKNSF*K NQFKNKGK*PNFYITQSP*RNKPI*KP/ AKDLNKRFSKEDM*IANKRIKTCITPLA IRKRQIKTTVKSSFKA/IYMVVKET
1012	14913	A	1019	302	2	IVEPLFLGWLCLFLQNPRVKGPGPYFSK

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						GKANPVVFPV\SKQPFKKPAPVYQKQ LPLP/PALVDKKVL/RFFFF*DRVLL \CCPGWSAMVQSWLTSTTS
1013	14914	A	1020	47	382	AKIALHSSSLGDRVSHTHIHTKRSNEI ELVIKSSPKKKSSGLNGFPPIEFYCSFK* ELIPIFLKLFQQ\VEAVGILPNLF*EVS ITLIPK/PRQEQNSNKTIYRPISLMNIG GK
1014	14915	A	1021	273	1	QSKERRQRTQEEMGKTFHNNRENTLFG FSQSCLKDEIIIIIFETGFRSISQAGVQ W/P/NHGSLOPRFPRLKQSSCFLSPSSW DYMC*LPH
1015	14916	A	1022	327	1	KFLKGWPIYLKKGFFVVPQGGGWANYR SLVPQIYGVK\YPSAFASKINSTMGMC PAWTFPGMAQLINGD*IF/IFFLRQSEA LVAQAGVQWHDLRSPQPPPGFKRFS
1016	14917	A	1023	3	407	THLTQR*/HNIQTFP/WV*TGTLSTVLM NFYLWM*FHFQSITLFIILRLTTLTMY QGWLDVTQQRYSQGHHTPPVQKGLRYRI ILFITINTFFLEGLF*ALYHSSLFPTLH *RGDWT/PTGIPLKPLEDPLNTFE
1017	14918	A	1024	3	425	LPPQKKRGFPKIPREF*KTPPKKKKII FPPPGKNWPPTK/RFLKGPPPSRFIPFP FFPLSSPSPP
1018	14919	A	1025	430	1	GGFPFPPPKNFFFLSP*IFG/RGVCBK FPPPKKRFFSKNPQRGFNPPQKKKKIS SPPPVNFAPPRDLLKRPPIPPPPPPPP FFFFFLFMHPSFPTSVQWQITSLCLL LILQCCVCLIGMVGDQSESSPSHHLQ PRWL
1019	14920	A	1026	463	494	RKTGFPRLT*HLDLDDFFFFFWKGI APRAGGRGRNLG*LKPPPLGWAPFSGLT PPKSWN*GAPPPPPFNF/CVF*RTGFP RLTR
1020	14921	A	1027	606	1	AGGPGPPKVPVPGAFGWG/SLNG*S*LKG KSGKGAPIQSGPTVFPGGIIPKESPLR PPGGMQGRRGPRWPGASGC/VG*DSVLR QP/GVTGRAPCPGASSPQASQAARRGSM GKGGAFHSVWGGCVLSAANPGWQPPGSH G*/PGRRGQSGCSCPKG*AWWRPCLAG SHSSAKHKMSSEGPAPRGRISPVSAG SIGPIAARGF
1021	14922	A	1028	436	1	GGAPQGVLRAPPPFFFWKQNFNFVARI IKGKGVLSPROFPPLGFKKFWGPTPL/ SRWGFKEGLKPPGSFWFPKKRWGFSMW RWV*\IPGKEL\PPPFQORGGIQQGT/ HRPPIPPSLF/CFEMETHSVAQAGVR WRDLGSLQPL
1022	14923	A	1029	1	436	PPKKIIFSPKP*IFWGGGGPNFPKKKS FFSQNPFGVFFSPP*KKKIFPPPPENW GPPKIF/YKRPPPPPPF
1023	14924	A	1030	28	366	EDHLSPGGWGCNEL*LCHCTPA\WRQNK TLSPKEKDHK
1024	14925	A	1031	3	142	FDCSALQEFGTRLYCPSWSQIPELKRCT HLSLPKCWDYR/R*ATTPGLRIVLELQK KLRR*CRELLYTPRSVTPNINDI*HWGG TFVTINEIISIH*YIALAGLRFLLSSDV LTSASQNVGITGMSHTWP

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1025	14926	A	1032	7	361	PALRPSARGQQYYDETCKNKLRCNAQND SYLPDPNPFSTRFSTL/DHSHWQLEAPDA *KAPFGLYWNCGARVCR/QGISAK*TEA CGLGTIKPSFFLIPLKQGELLGYPAYNE NLKKKKKK
1026	14927	A	1033	472	3	TKQQMLNVDRTAFYKKMSRTFIANA SMFGFRASKEG*LLGANTTGNF/LKAML IYHSKNPRTPKNEAKSTLLVP*K*NNKA LVAHLFTA*FTEYFKPPIEIQIITADN APGHPR/MYKEMNVFMSAN/TSIL*PMY QGIISCRIPAARIEVKGA
1027	14928	A	1034	488	0	PLR*ILAQRSGIHSMTK*SGEAAA*KS EARSSWFLRFKEKSHLHNKAQDKAAS DGKAAESYLED/TD*DGNTK*ICNGDKT AFY*KEMPSRMFPAREELMPGFKASKDM LTLRLANAVGDVNLKPMIYYTENPRA LKNYDKTQLC/PVLYKW
1028	14929	A	1035	114	491	NYFKNFTFSNKLTL/CLL*LFL*KLFN F*TF*LLC/I*HLA*NTNTLYSCTKIFS FFIFLFYKHFLKFIYFFYFLDFII*GAY *SLCYY*VVYFSCQFCQVLFHVFWGLCC HVLVRLLYFQTDEPFY
1029	14930	A	1036	114	496	LLRAILTYLKYKISAMNLVSA*FIYLHL TYHCVF/DHPVQGR*LLNK*INELFCYR SFGF*WVFSYSHLSED*ALEEKYLRERS RWVK/DLNVTSSTVKILBEILGKTLDDI GLGKEFMMKTSQANITKP
1030	14931	A	1037	381	45	KNRGRKKN*LGGP/SDRFYKTF*KLIQ IIYKLFQKNEKEGTL/*NSRPISLINIE ANIQN/RAVLAMIIQKHKKIIRHNQVV F/IPGR*G*STCKSI/NVIHKKQRR KSIEF
1031	14932	A	1038	134	394	SFCDKFTNCISESLCQ/SYSPTYIKIF VLFKIRSGSITQPGVQWHDHSSQP*TH SWAQTIFLLSSQVVGTKGMCHHTWL/IF LFLFVF
1032	14933	A	1039	483	30	YDGGSEIINYVLESRLIGTEKFHKVTND NLLSRKYTVKGLKEGDTYEYRVSAVNIV GQGKPSFCTKPITCKDEL/AYVSTTIYT SETCTFVDL**DINKNDLPL*LQILAPP

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						AHIISQEKEIKKIQI*YKEEKLPLFTSS SLFT*VKNLMEFAKKLELINEYNKVER YKINIKNILLAKNTWTLLKF
1036	14937	A	1043	50	457	TKYQLANKNMKICSTLPIIRE/MQIRPH EISLTPIMMALSEEQKNNKYWGCGREVE TLVHCWW*CKTVQSLRKTVHRFPK*LKT ELP*ELPPK/PGSQRDICTPMFIAALFT IAKRFWKHPKCPSTDE*IKEMWYIQS
1037	14938	A	1044	2	469	LKQSSCLGLPKCRDYR/R*ATVPG*FIL *NTTEDPNLTKN*ILNTNH/WCYSVQLI LGESNSTIKTSLSFQASSHQNTTVQFL STSPSPKNCQWLAILPRK*GLTSLFCFA FERQGL/NSVAQAGAQLHHGSLKAQPP RLKQ/FLPNCPTLMCEYRLQP
1038	14939	A	1045	42	200	LICT*MLIVALLVIARNWQIRC/SST/ DEWLNKLW*IPMEYY*AIKEPTIGTC
1039	14940	A	1046	475	36	LNVN*LNHPIKRQKLAG/YVRKHDPTIC CLS\QSRFIFKDTNRLNIGWRK\TFH ANSNQIA/GVAVVSNKTN\FTRNKE* NYILIKGSIH**CIIINICATNS*NLK I*NLKTEMKEEIHCSKITVED/YNTLF* TMDRQKEFHRMQ
1040	14941	A	1047	3	326	FFFFIIIIIFETERDSVSKIIIIKNNK DLF*FLVTQVTPEITNQYISTLPLQSKT KWDRPGTVAHSCNPSTLGGRRRI/TLR SGVRDQPDQHG
1041	14942	A	1048	403	15	EVKNSSFSYRLMTEIMPPGYVSKLYNCD SGS*LS*SFNVCKMNR*Y/LEERGNTS FKSLLLLMWKLHSAIFTS*TPRGL*I YFIYMYVLETWSHVAQAGMQWHNQSSL QPSPPLKEFHRTDIVYAR
1042	14943	A	1049	25	457	YMWVNSHSCMFTLLEDSFPPPLCFI LRSFLLYAELPLAFLLVKDSFILFV*I MSVFHLILKLQ*NIHNIYFTILTIFKCT VQWH*VYSHFSVAKTAT\ISRTCLIPSS WDYRHMPLCLANFFL*ROGLALLPRLVL TSWLQ
1043	14944	A	1050	14	478	PEPYCRH*TTRWN/CWGWVBLVQSLWKA TEQYVLKPDICVF/LEPGVSLGMYSK LCTLC\YQKTRMFIALFLVKS**LPK SS*MVE*ITKL*YFHTMEYTTAM/KNE* ITI*TTIWMNI/TIILNERSQTOK
1044	14945	A	1051	2	465	GIDQPSKPIPL/TQSFTQTKA/LTFFNS VKAERGEAAE/ER/VEASSD*FMRFKQ RSHLHNKVEGEAATADGETAGS\SYPE DPAITDEGSHTKQQIFSVDETACCWKIS SRTFAAKEKSMSVSKASKDRLTLLLRAS AAGDLKEFPRLV
1045	14946	A	1052	392	24	DFAPRRKKRETRRSKINSLTS**KELEN QVKTNQKGSRKQEI*TKIKVELREIETLK TFPKKKVNKSRSWFYEK\INKLDGTLAR QINKKRKENQ/DTIRNNKGDIIITDPEI *TTIRGIPLWR
1046	14947	A	1053	204	488	CAVCYTQISLTEWVDL*SLDPGFETVSH LFDRVNQP*DCRRVTDMLMV*NLHFVI LFFLWF/DFVFLVLRQSFPVVTQAGVQW RDLGSLQPLPPG
1047	14948	A	1054	498	2	SVVVCLFLSPGITSHTYVPMIFKIGAKK

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						VHWWKSILFNKSCWRNLSTCTRMKVDP M/LTPGKTINTNWKDLTPSAESTICLK ENIG/THFDIRLGNFWDMPKA*ATK EN*IPWITSK*QT\FCAKNTVN*VKR* PMD*E/RIFAKHISEKRLICVIYKEQLE LN
1048	14949	A	1055	28	209	IDGRSRGLWW\CVVLASQLLWEABAGGS LEPKSLRLQ*AMIM\DCPPW
1049	14950	A	1056	163	479	TSFLGSQSAGITSVSHCPSEVFFLKL HWRQGGQVALLVATPHSPCCPQYRLAPI PRARHDFACASLI\FVCILLVHLLMPRS VAGRGVGSLLG/CQAGR*L*TC
1050	14951	A	1057	2	1258	ELFPWHFQPSRAASLVVAKATRDKVP RRWPVPTDGRPEGFALSEPHHSCILHGRH QGPERRCHMAASP*EAGNK*PKDKDGHF GERTETAAGVHTGCGGKGPAAAGGR*AQ GSGEAGAAAGGAGAAVGGAGAAVGGSA GGRWPAGLLGQHGAG*GEGPCRQHGPPP GVSAGQAASPAKAGQPGGT*GAAGQP GRG*GPAGPRGGAAERAGAGAMPACGP AGAAEPAEGEARPGAGDYGPAANHPGA RTGAGGAEAGAGAAAGGLPRPAQHR\AQ IHGPVPLGTGGRSSS/GGIPDNMSHRLW QRHRSHGEASAGQRHPHPGPTGGER/GL QSMLSKIREVAQQGGLKVLGRALGDQ EEAPIQQQVFRLLCPGNLWR/RPPHMRP *AVLL*NIFHISRRREDVMDMPSSPIC PL
1051	14952	A	1058	2	437	ERSVRTACCKQSRGLSSLLCPPAPRLS *TGSFVTGSSALEPRSPHPQP\PSLRFR SPGPQPLHPLGPRSPSPSEPTVPSHPA RLPSLSPERTQG\PKAQ*SQLPPSLAL AQPAVAVGGREEVASPACPSWKDKSRLR AVPGSA
1052	14953	A	1059	47	456	TRCYGTLRLDAPGKLWTRKM*VVASTY ARTDRKSSASFRLLPLPRGFQSLHFS LTSPSCLAFSANTHRGLRGENTHITK/C DMAEKV/HN*TAQVQNHDFGSPRPPPP GFRSSCLGLPSCWDYSPLWHHEQIL
1053	14954	A	1060	484	13	FPTSASQNTGTTGVSQHAQPIIF/LFVE MGSPQV/GPASLKLPTSRDLTPASRAA ESVSAHHH*FLNFL*RNASGFVAPSW* TFLL\KQSSCLSLPVC*DCRCYNHAWP HSVFSSQFLSLFFFNFSFLFSLFSFFK DRISLCRPGWEFHQTVQWSR
1054	14955	A	1061	1	494	GSPGHFVCGRRRSALENPGQPCSLQPGV VSGATGAIVRVQRTSSAWATAAMGAYV E/TRFRYT*KAGVGCDRLWGAWLKADG LGETKAENTLHDG/PPEDALYGLIEGDD TNFTIQGEVVHCWYTGTLPDGTVFDTNI QTSAQKMM\NAKPLSFKV/GIGKVSH/G WDE
1055	14956	A	1062	3	395	SDPSPCGGIRFDEMEKPLENYNLPKLKE /DKINDPTFVK*IGSMKIFHTVEP/PS HKCFTSEFY*TFKE*IAPISHKLF*SRG IMGTATPVMFHLQENVIPK\PEKK*T YRPVSLMNIN\KILNKILTYK
1056	14957	A	1063	402	260	WYCPFKV/LLRFSVYSSPPEVWAVGSIK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AELYMLRPLFPRTREVD*TF*ICPV/LK GSPKNKDFCP*GAKTFEYFYPATLGLNL KI*IFRQRW
1057	14958	A	1064	66	379	EFGRGCGEPKLRQCTPAWVTEEDPVSGG KKRKRKEREKT*REPSVSRPESH/PPSQ EAFWVQALSRPVLENFISGRSASGLGK SEAIKSLFLYLAVCSTTEEQA
1058	14959	A	1065	223	437	KSCMSCDSNKIFFLRQGLSCSLTQAGVQ WHYLGSLQPLPQGP**SHLSLLSNWDY RR\PPR
1059	14960	A	1066	414	65	NKSPDRNELAS*KCTQ*THTSIARDFPA KTIQWGNKSLFNINWC*DNWISTSKRIKL DPYIIPYTK\TNSKWARDLHVKARTIKL LEKNGPGAVVPCPNPSYSGGLEARS LR PAWAT
1060	14961	A	1067	418	1	LWVFFFSRQSL/DSVAQAGVQRCDLGSL QPPPPRFKRFSCSLSLRSWDYRCRPPHV ANFVFLVET\GFTMLARMVLNS*PCDLP AAASQSAGITGVSHHARL*FCGF*YIHR VAQPSSQSI*DDHPICKFCIL*QPTPPR S
1061	14962	A	1068	24	440	EV*NLISENYKMLLKEMRGDLNWKKSIP *S/WI*RLNIVKMAVLPKLIYRFLIPI RIPDEFFVKSTS*L/CKFIWNCKRLRIA KTIF*K*RTK/SGDLILTDFTYKTMV IRTI*Y*QKDCID*WDRIES/PEMNPY IY
1062	14963	A	1069	442	26	LRNQVSTPSSKTPRFFFFFLKRQTGAQ RHNHSSL*PRTPLGKQPSTASGVSR TI GASHHTPLIFFYFFN*GKEGWGGCSCFV AQAGLQL\RLQMLPQPPLKCN*RHK PPSLTYPILKRT*SCFSKEKATRIIP
1063	14964	A	1070	294	46	KNLKRKRERKENNKKKAKINDINKSML EKIHKDKN*FFERNKIDKLLATN/RIT KKTQIVIFMNKIRDITTYPTDIKNVKR
1064	14965	A	1071	141	469	PKKQGVQLTQNAPLPFRVGGKRGCLPKK KKERERDREIISIIIIKLPKTKTPG DGFTDELYQTYK*LTSILLKVFLKKRRE CFL/PYSMDPAVPAIALNPPP
1065	14966	A	1072	49	472	EFQIKK*NSFFADTEKALVWIENQNSH NMPLSQSLIQSKALTFLNSMNAERVGKD AEEKLEASRGFWPMRFKKPSP*HKVQGE AANLDVEATASYPEDLPETIDEGGHGKQ /QIFNMDEIVFYWKMPSTRTPAREERSM PG
1066	14967	A	1073	82	419	LTVGFRRETRSSSWVCSSSPKRALHALRF TPALKF*FFFWSFSLRFFFLLDRVLLC CPGWSPTLGLK*SSCLGLPKCN\YRYE PP
1067	14968	A	1074	1	407	LEDGFFKITQSDKKEKKRI\KKCK*NLQ EVW\DYVKHSNLQVIEIPE*EVKLENL FEEVIEANI/PHLASYLDIQIQAQVQRTQ RGYIARQTSKPHIVVRLSKVNMQEKILN LPKEKHLITYKGNISIRLTAKPSPKPT
1068	14969	A	1075	3	396	LHAYHIVKLSP*ELTGALSE\LMTSGL TM*FHFHSITLLILSLTNTLIYQ*WR DVTRESTYQGHHTPPVQKGLRYGIILFI TSEVFLFAGFF*AFYHSSLAPTPKLGHH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WEPTGITPLNPLEVPLNTS
1069	14970	A	1076	250	47	VAACQNAFCTFSCYWL*NLCCRK\MDLD ISLLP*TKVNSRWIAGFNVRALTIKILE ENIGSAFGNRHSQ
1070	14971	A	1077	2	393	PLTGALSNLLNSGLAMRDDLHSITILLI LGLLTSTLTIYQG\WREVTQESTYQGHHTPPGQEGRLRYGTMLFITSEGFLYTGF*AFYHSSLAFTTQLGGHWPSPGITTPLYPV ESPLLNTSALLA*GVSTIT
1071	14972	A	1078	2	500	LHVIGVSEGEEN\GMKQNKIFEEIMGNP F/PNLVKYINA*/IQEMQ*TPNGIHLKK TVHRYIIFQLVRTNNKERLIVAREKWH GIFGGTML*MNDDFSSEFIKARKIEMMF LKYKRGISSSAKHC*SRILCVAQISFVS KG/EITTFSDKRKLRAFIISRPAHRNAK GK
1072	14973	A	1079	419	1	LRWSFALAAQAIVRWRNLGSLQPLPSS SNSPGSWRLQ*ANTAPLRSSLGNKNETL SQKKRK*KDNSEWEKIFANHASDKGLVS K*IKNSYNSITKN\DI*KWTKYLNHRHFS KKD IKMANKHMKRCSTS
1073	14974	A	1080	468	2	KLPPPRGAGSSAP/PLFFPPTKKGFFSP PPP*KFFFSNPLIFLGGFFPIFFPPKK NFFLNPKGFFFSPP*KKKKIFFFFP*I FAPPKFFFKSPPPLFFFFFFFFFFFFF FFFFFFFLRTGRTRGRTRGRTRG
1074	14975	A	1081	467	1	PTYKFNAIPKIQ**FFKKIENCILKFL /WNLKEPQLAKTVLK*NKVEGFTLDFK \LTVTKTVWS*HKDRHRDE/WK*TESLK IKPKYDQFFFFFF*FSFL/HFF*YLTYSQHKLIFNRMPKPFNKERLFNK*CWEN WISICKIKLDHYLTPYTK
1075	14976	A	1082	387	3	LKQPPPHKSFVKNNKNGVSLCCPG*F*TP GLKRSS\HFDLPKCWDFRCEAPVLSLLN NIKL*L/CGRGLIKPQFP/SVK*K**AP SWSAHLAETFFFFRQGLTLLPMPGVQWH DPGTVQPQTGCHK*SSHFSL
1076	14977	A	1083	2	435	FHPPTNWGGFSPPPP*KFFFSPKALNFG GGVGPNFPPPKRFFPKNPRGGFIYPPL KKKNFSFPPPLKLAPPRV/SFKRPPFF FF
1077	14978	A	1084	447	47	PSRKFFFLAPPKRGFFPPFLKNFFFP L GGLFFG/RGVFQFFPPPKGFFFKPRG VF*PPPKKKNFFFPRENLGPPGVFLK RPPPPFFFFFFFFFFFFFGRRFVK
1078	14979	A	1085	438	2	AKNHPKGFSPFKFSPPFGGGGIFIRGO L*KSFFFFKPKFLV*KPPFKIFF/I FFFKQRLAL/CPPGGNKGVPQGFPIF FSRVGKPLFNPPKNWGNPPPTPGKI FFFFCSFLL*ROGLTTSRLVLNSWA*A ILPLQPPK
1079	14980	A	1086	43	265	IKHKLEYIKIKNFCA SNR/TERQME WEK\MFANLISDKGLIPRIHKQLL*LN/ TKQONSPI*KWVKDQLQWPYL
1080	14981	A	1087	11	412	IASGLHDFNKKKKKKKKGGGPKKTP GGPKNRGGKKKIPSKGGEKKTPGGFL EKNPFLGGGKMGQNP KKKKPFGEKKNF *GERGEKKKFPGGKKMSPSPQE/NKAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						RDDPRPPE
1081	14982	A	1088	2	292	RSLPASADSSSLVAASLAGVRDRVSTCW PGWS/AV/VQTL*SARLGLPKCWDYRCE PPCLAEAPSFMRSGKASCTLETWEDKH KYEEAERRFYEHAT
1082	14983	A	1089	376	3	HIGLYIASCKTLLKEIKGS*IDILCSWI ERLNTVKKAILLKLIVGFNTIAI/KILS GLFIETERMILKITGKCNRSQTANTILK PNKVGRLLALPNFKTYKATVIQTVWSWH KDRWYGFFCVPTQI
1083	14984	A	1090	277	407	QIKAERSHHKQITSMRNVKHCSSENYDS *RKPAPGYIIK\F*K*LIKRKILNSGR LKNRPIKEE*RYAYQDISETIKVR*EN DIPKVL\KEKKSQPRLLYPLKIS*IEV KYFFDKSKLKEVITNRSVP*EMLNIVLQ /INYDSPYEP
1084	14985	A	1091	421	2	GHPGVLFKG**A*NEKSL*NCSFFNY*S SFSNMQTRIKNV/WPSTVAHACKPSTLG GRGGQIT*GQEFETSLANTVKP
1085	14986	A	1092	369	3	FLKEIRSVTPVNT*ENLIAD/IGEKVLV VWIENQTSNIPLGQSLIQSKVL/TFNS MKTER*/EKLQKFEASRGWFMRFKERSH LH/NIKVGGAESADVEAGVYDPDAKT IVKGGYTQ*QIFNVDV
1086	14987	A	1093	71	306	FAEDNGL*LHPCSKRHDLAIFYGCTSF VLTFGL*PWFLTQS/FLNPLEFS
1087	14988	A	1094	118	385	SDLGKDFMAKTSKAQAATK\IYTWDYI KLRSFSAQ*TKQSTE*RRQSTE/WKEK IFADYSSNRGLISSRQETQTQWLKIN KNALCTL
1088	14989	A	1095	419	1	DAKIPGQMVAR/RIPRPIKKIFCPDQVW FIPGMQGGFHIGKSNVAPHIQMG*KSF NNIQHPFMI*KKNLSTGTTHEGDITQH /R*MLHEHTTNAILNREKLKAPPLRTGI RQGCIL*PLLFSAVKT*P*AMRQEKEI N
1089	14990	A	1096	34	464	NSSKKEKRKIPHDGLRFLDMTPKT*ST NGMMD/KDFIKIK/FCASKDTINKVKRE *EKLQIIYL/DKRLVPRIYKDSYPIRQ LKKWVNNLNKHCFKEDTQIANKHKECS T\SIRE*QTKTR*RSHFISTRVTKIKMS G/N/NKYWQGC
1090	14991	A	1097	458	28	RIIKVDLKMCTHNFDSLEEMNQFFKSR WPR*NR*FE*SYNH*RN*IHNLVSKSS GPDAFTGEFYQTCEEELAPILQNLFOKM ESIRSNSFYKVRITLIP*GDNGS/TKKE NYSVVSFPMNLDAKVLKILAN*I*VFIK REFH
1091	14992	A	1098	41	500	FWIRHFLSRHKQRKNR*MDFIKIKNLYA SKDTVKEVKR*ST*WENYQI/RMFDTG LVPRVYKEFI*LSNK\DNHI*QWKKAV SRGFSKGNTQMAKKHMQRCSMFFVIRKM *I\KPKMRYHFTPSMT*EKNKDNTCFK SDGBYGILIIYYWGI
1092	14993	A	1099	1	484	RRAPFFFFFKRSFFFWARAP/LQWAF GLVQNPFPRIQPPPLHFP/SCPNPPKK WGYKGPPPTPGKILGF**KGGGPRLNKK IFISRPCDPPAPT\QKVGIQGGTPPPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PPFFFEFEMVSCSVAQAGVQSCDLRSLOAL PPGFEQFSCRGMP LKWIGSHPSHP
1093	14994	A	1100	144	260	ILILDSALGHPEPHEFNTKGIEVVYLPL NTMYIIQPLDQ
1094	14995	A	1101	265	457	DPAAPLLVTTYTREI*MYITKRYTAALF IKTKNWK\RPKCPKGE*INKLWYICTM EYCSAIKNE
1095	14996	A	1102	387	40	RLRADILRLVYNNFLQRLKKQRYLFTG PQYRFLFLELWLCVCVCVCVCVCVRANF *IISRDKVLLCCPV\CFCLNPPCVCVC VCVCVCVRACAIINKLLVETRSCSVAQS GLR
1096	14997	A	1103	465	208	QNMTKTFQDYRPISLMKIYARKQQYRYR Y*RMLHNYQMGTGLRGWFNI*K/SII IHIN*EKKIMIIIESEAFDKC*QSL II
1097	14998	A	1104	57	250	MTCSRMQ/RNIKLLRYKSEKL*EENSTS RNEITILSEEDSFNTVKLEN*MKTVKQK KKTSKKTGVYKMAIKKQISEFGKTSNF Y*EQINT*EKKNFKENWSL
1098	14999	A	1105	2	378	YVDPQCGGILKGV LKGEFTISNEKANP GRGSPSSVSKD/L*CQNIKTIESKKTCL IQKLIKVKAEIYERESRKTMEINETK/ SQPFKEI/NKID*/PLARLTKKKKKTQV LKSEK\GNITTNHTEIKRV
1099	15000	A	1106	291	1	VSIYVSYNLDSCCKQIRIKSCDDQYIFK RLYFFEITFLKPLN*K*VLKKIRDNVLL C/YPGWPQTGPLKQSSCLSLPSSWDYRH VPLHLAPINYFLW
1100	15001	A	1107	24	397	DIDHVEFETVFYHVGQAGLKLTSDDP TALASQSAGITGVSHRTRPSSGHFNTP EPPEASSLSHPK LHKSPVT*NGAGL/Y GSSKLLSCVLNGPISLVHSTLRLRKGFP QGNISQISLMAPP
1101	15002	A	1108	64	414	AQLTPTQPGRAALHKGHV*RKTAPTCL FMAEKNAASFFLFPFSPICINKE/HFK KKKKKKKKKKKKKKKKTRQKKKKGPEKPR KQPGGGLLISKILVVAPPFGFFLTRGFP PIIFF
1102	15003	A	1109	62	475	FEPLFYLMCLLNLFP LQLPRHPFLFLTV DLVNTWGCPLPSSPQ*EWLLAAPHRSTP PPLSSGFPARRQLEPGAGARGP/HHTQA LHLSFFFVFLRRSL/DSVAQAGVQWRGL GSLQPLPPGFV\ILSSPLSLPSLTY
1103	15004	A	1110	76	477	EEWKLYRWRENISNLISDKBLIC*IN/ NQTFNIQPLKTKNPTKDNDLKTFTNED TQKYTYIHQ*R*SHMKR*SP*LFI*KMQ MSTALRFLYPPITMDRIQIPENIKFWRG CGILHSW*TRKMFHSL*KAFWPF
1104	15005	A	1111	1105	3	KEERSETLAKGLIAAGA/YN*KEERSQ INNLT LHLKGGKKTNDKPSKR/QE/I*Q IRAEISRIRPRKKKEKNEFVFLKINKN FKTHSYIKKKREISNTKIINKRGDSTTD ATEMKKITRD*CEQSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSPPKKKIPGPDNFTGEFYQTFQEEL MPALCKIFQ\NVQKPEGDI/PNPFYQVN IYLVPEPDE/QPFVIKTLKELVIYGN/Y

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						L/K*TKIHEKLTANIILNGEKLKSPPL GSGIR*QHLFLPLLFTVLEFLLRISQ EKVIKRMQIGKEKV\KILFTDNRM*WV/ ENP/VNSQNGIKIMKFNKVSQSGYSNTHKS VAFP*TNNEQSANKILK
1105	15006	A	1112	37	466	DRAAEFPTENPLELISKASKVEEPNVS QRPIVFLCISNKQLENEILKIQPH*/PI SVASKNSKYGGINLRKYL*DMHIDNK/P LNKNRGGLCSWSATSVLPLKIDNPSAIS GNYSRFFFFGBIEKLNLPKWYK*VRV AKTVSY
1106	15007	A	1113	33	436	PGLN**CWKNRISTCKRMKLDPNLAPYT KITSKWIDINIRPVTIKLKENRGKGL QH*MQQ*FF*I*PQKQE*TNRTKSDFIK TAQQRKQNERQSVWEKI/FANQISNK ELLSKIKFRLPLDNNKQLT*KWA
1107	15008	A	1114	2	391	PLTHSRMAIKKETK\NYKCWQ*SGGIGN LGNCW*ECKMF*PLWKIVLQFLEKKRN TELP*NPLIPILGIH/YKRVCIQMPT ALFIITK/SWKQPR
1108	15009	A	1115	3	458	IRDPLEEAVCPFADLKLHAGRTTTLFRA VRQGFLSL*KLLLPVQLSHVPRGGVYR GSQASLSCGGLHPVQAS*LLCLPTQASA MADAP\PPASLPPCSSISDCCASSERGS VGMGPSEPGMGYNLLVCRLLRPLEKPSI RVGVSLFSRYHM
1109	15010	A	1116	204	13	PKMKTDSRWILGLFF*FLRQSL/SSVIQ AGVEWRNPGSLQPPPRFKQFSLENQGI PPHGLVVS
1110	15011	A	1117	34	454	IHISVVEFLTSLYGTLSQYNKKTNIL IK*MGKRFAHFT*EGI*IVNKHMKRLP TSSVIREMQTKTVGFRSVLTREAGIKQ TDS/NOAWVRKWSNSTLLCCWVKHRLQ PTWN\TAWQLLIYKMIWQLHFYAQKDIY VN
1111	15012	A	1118	83	451	CFLKFFLYRELISPFL*Q\FVRPSPAF RRKPPPWVAFFSDPS/FSFLVFPKGI VFFLGDAKKVLT*KKNFFFGGRD*VLL CCPGWSRTPALKHSSCLGLSKCWNSTTR P
1112	15013	A	1119	316	441	FIFFFFLKTNFNFFAQVGGHNRNLG*LK LPLPGLKQFSCLT
1113	15014	A	1120	67	312	RQIDQWTRIES*ETDPREYSQIFDKGA NPQWRK\LFNKWFHWNWISTCKQIKKN LDIVLASFTKTSTSHRLRENLYRIHI
1114	15015	A	1121	27	490	GTQLHSREKKNSEFNK*YWEN*ILTCKR MKLDSYFIAYTKINSKWKIDLVNVLGL LAKIK*SPKCKIQNY*TSRRK*KGKDLG Q*FLGYDTCKKATE*KNK/LNKWDYIKL KNPCIA\NKTINRMKROPTVWEEIIANI ISDKVLISRICKKTR
1115	15016	A	1122	490	48	EHTNNKRDTLTVDIGKVLVI*TEDQTS N/IPSNSQLIQSKALTLFNSI*AERGE ATE/EKLEASKGWFMR*KERSHLYNIKV QGEAASADEEATASYQEDLAEI IDENG\ KQQIFNSDKIALHQKKM/PREKSMPPHK VSKDRLTLREF
1116	15017	A	1123	2	259	IYQLIFNKGVKTIQ*RKNSVFNRCYWD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						N*ISIWKRM\GLDPYLTPTTKINSKWIK DLNIRTKTLICSSWRKKKRENFLKKRK KL
1117	15018	A	1124	206	24	CSIFFCIYLFYLYFYLYLQSL/DS VTQAGVQWHYFSSLQPLPPGT\GLF*RT SYSWDF
1118	15019	A	1125	3	351	RRGRGFTILVWAQTPDLM/HPPALASQS AGITGVSHCARPICLFKKRQGF/NSVAQ ARVQWWDHGSLLQPLTLR*YHLS\SW DYRRM/PAMLGFFVYAYPGITLLPRWP WISGLNELP
1119	15020	A	1126	2	349	STNHKDIGTLYLLFGA*AGVLGTDLSLL IRAEIGQPGNLLGNDHTYNVIVTAHAFV IIFIVIPILIGGL\GIWILP
1120	15021	A	1127	362	2	RVSLHCPGWSQTPELKLSCLSLPKC*D YRCBPPHPAYLTSFITEDSKNFYVTTL F*NNIY*TMFIEIPP*VHYGAHLF*DQ LSTFF*SF*N*FFVCLFFRQSHSVAQAG \VQ*CDLGS
1121	15022	A	1128	1	349	IYFLTRSHSVSRAGVQWHSSGSLQP*PP RFKRSSPPLSLLSSWDHRTWG/HMPP/H SSSFSSSLFLRSGWGKGVLWS
1122	15023	A	1129	367	24	INCVFYPCKGVTKKPWT/HF*RGKFII INIFHGPFKLTFCPEGKNSSETLYPFC FLPLSLAIKSRPLGVFLV*KGPLSPPL QGNYGVGWVGFFFSFAFVIFIKKLVLSP YYKN
1123	15024	A	1130	61	299	IPRVDNYCGYVREHLFSFLFFFKRSLV/ SVTQAGA*WRDLSLLQPLPPGFQF\SC FNLLKNHCYRDVPLLNTLCIIPKT
1124	15025	A	1131	2	261	FFFFLVFSFLLRLFLSPSSPPPSVF PFLPSSFSL/CLVSRDLTLSTQTKVQWR DLGSLQPLPSRFKRFSCLSLPSS*DYGR TPLW
1125	15026	A	1132	2	381	EFYFFF*SSQMESPSIAQAGVHWRDLG/ SIAPYASWVQVILPQPPPGFBSFSC RFPSTWDRHAPPRLAKRNXI
1126	15027	A	1133	2	221	PSLLKKLARHSGRCL*SQLLRNLRNENR /CVPAAVTK/GETPPSKKKKNPPKGP GAQTFETPGFGKPKGKIKV
1127	15028	A	1134	331	2	RGPPPLKEPSGVFRIFQKNLESRGGG ERKGQSPPLGPPIRRGLSPKPPPEKGL TVFFFFFFRCKDGVSFCCPG/WISRTPG LK*SSCLGLPKCWDYRHEPPHPAPAL
1128	15029	A	1135	3	391	AVNTQMMRK*KSLIADVEEV*VWIEDQ TSHNIPLRQSLVQSKAL/T*RAKPSMKA ERGKEAAKGLEASRG*FMRPKENN\RL HNIKVGDTASADVEAAASYS*DOAKIT GGCGYTKQQIFNTDEAFY
1129	15030	A	1136	107	350	TYSIVAIVMRFYFFIIFYFLRWSLAVVI QACCHPGNWHGSLQPLPPGFHKFSC SLLSS*GYRCPPPCQA\IFIFLVEMG
1130	15031	A	1137	35	297	TLMHYTNRVKEKNIISIEAEKAFDRIQ HPHM/IKYLNLIKAVYNRPTASIIISG* NLKAFPLKSVTQQGCPLSPLLFNILEV LSTRP
1131	15032	A	1138	378	1	PFTKINLKWIIDLNKHKTIKLEEDIIG ENLDNLGHDYDILDPTPKA*AMKILIN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VALC*NHESFCSENDTVIRMRK*ATDRK KIFAGDMIKDCYSKC/NEKAEVNNMKKN NPIYKWKDLNMLL
1132	15033	A	1139	271	361	KW/YWNPPIHIIISQVCL*GPEIYQHVVYQG MTKQRCQGNM/WAKDSLFNKWC*NKWI FF/C/RI*NLNSYLTPYRKIK*KWIRDQ NITVTTKLLLENMRFSFAFGIGKD
1133	15034	A	1140	28	340	LLYF*YKRGFTMLSRVSNRPQ/CDPP TSASHTAGIADGSHHARLLFFLEK/EPA FGPPAGRKGANFG*REPSPPGFRGIPP/ LPPPGNWD/YGGPPPPKPNFGFF
1134	15035	A	1141	94	128	GSQMPRHLVD*MTRHLATLRES/CYSR/ VYPRFIEFLHFDIQSTGQKSHR
1135	15036	A	1142	85	492	VWVGLLSLEGSPSKFGNFIEFGVLLSSG GFSAWRLFFVYFLRQSL/NSVAQAGVQ QWRDLSSLQPLPPGFK*VLKQRGVCLFV CFETESHIAQAGTQWCDLGSQPLSPPE FKRFSCLRNSRSLRRDIEPSEGNQC
1136	15037	A	1143	372	3	KMNR*PISIKBIDFIVKNLPK/KFGPDG FTGILY\RHPKKEIIQTVCNLFQKTEKE GMLS\IYKASIAQIPKPEKDKQTKATD/ YKPSGIEAKIINRI LANGIQQYI\HDQV RFTPGMQGWSNIQI
1137	15038	A	1144	56	482	TMKTLLYWQKNG*VDQWNGIESPEIDPY K/YIQLVFDPRKAKTCNV/RKDSL VNKC TYAKKKKTLNLFPTPTKITSKTYLKNW N/SVNFLNTPGKTLGDLGFPDRDFKFLN TPKAKSLEKH/MDTLNFFKGKICS*KNM VKKNKKT
1138	15039	A	1145	190	482	RQGLALSPRLCSGVIIAYRSLKLVGSS DPPTLASQIAGITGIRHCPWPKTLFLAS VIMPAHNS*PSLSPVPSP\SLSPPLLA SQSRRSQ
1139	15040	A	1146	138	485	IFFPSV*TIFFLLALFFS**MYLIFVKS SLSIYSVYQF/SFLCFWSPISDPKSQRF SLLSFIVCFVFPNRVLLCHPGWSAVV *S*LTAVSNS\LLKQSS
1140	15041	A	1147	101	426	GDWKKFYIYKHSESKSPLILFEKKKGVL EEYSSFDI**AIKVIYHISRKRK\KNQL ANLTD AEKALNKI*HPFMRKTTQQFSNR SFLHLRKG IYKPTANMIIKEQIIF
1141	15042	A	1148	458	15	VFVCLKICKHRKGTAKKWNYNFMGLPLY MRSVVDQNGTM*KMTIYAPNIGAPKYIE QILMGANREVNSNTILLGDFSIPLSTL/ DKELPELNFT*NKTDLTDIYRTFHPMAA KYTYFAGTHGTFSKMCVPGFDIRVILVE FRRTYGLDW
1142	15043	A	1149	1	507	KGPPAPPPYKPKKFGGPKKFFP*SHPF KRPRGEDP/YKPRNLKPPWAKKNPPFP KKKQRGKGPKNPPPWVKPEKSF*PSPK KTKIWPPPPPGGQKKKKPPPPKKKKK KSVSSSPKNI/YRSLFCTNLKKSFT*F *NLMP/TKLPV*BFPPPPNF*SAP
1143	15044	A	1150	436	32	NLCMYVVMYLIYVRYVCIYSIYVSIYL IDLSLYHHYLSICMCVSIYPIYLSLY LCISLIYHFNLCIYISYLIYLS/YVC M/SSI*SMYVCIYLIYVCIFSIYLYLY IYLSIITIYLYLCMYCLFYLSIEF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1144	15045	A	1151	3	657	QDCKIQNEHKIQNTLFLYTRNAHIKIKF HLHSKKILAVNLTKHV*NFYAENYTTLM KEKI*IERNKDLHRKQ\NLNPCIWIVKL NIVKIPVI\PHR*RSLTPIIIPAK\FE GDKEKIIILKFIWKGKGR*LRP*KIRIK GGLNLPN\LRLTVVTVIKIV*YWWKERD RYLNQ\WNKIENS/EKLKPRKYVQLISF VFDTSG
1145	15046	A	1152	430	438	TFWVKKFFLLNLFPK*INPGFKKKKNRG G*KRP/SGSQVLKKLRGKIALTPEGKKG IRDCFPPPPPLRKKKKPPIRP*KKKKK KRKRDPFPGNHYSNSYRHTSCYFTLLHL TLQIFFTSRSPVAMSCRINL
1146	15047	A	1153	104	478	ELLLEGSPCLRAESKAGPAGRLVPTLLS WRVQSPGVLCWEECEEPSTGEDAPS LAIRETQIKFITRNHLSPLSMALFQTNV DN\RTKRK*CWGCGEIG/T/LHGWWE /CKLTFP
1147	15048	A	1154	171	476	NSSDYFFFYFLRQSFLLVQAGVQWHDLG SLQVTSDDPDLR*FARLSLPKCWDYRRE P/RMSDSNYFLK*VPVN*KARA*LLFIP SSCQAG/ASAGQTLVS
1148	15049	A	1155	3	562	PDYQTARRRQAPADRCQGPAAATICPR* PKARSSSMNRSNPTVTRTAGP*PSWKTG AASKSQTDGDRKELIPNRTNN*VST AAIK*QVRPYLTQKVPAG*TFCPHQKLQ GVRPLCRGPP\RPFGSPAVTDNRQAKLK TPTQ/HPADPPEQKRPPARPPVGRHAEV KQPGPPFPAGPRPAPSTDGL
1149	15050	A	1156	67	417	TLSCETQPGQHGEAPS/PTKNA*IALPL SWARPLYFPAPARFTARGGPVFTSKRVF SPPNRRGWRPPP\QFCHAWNPSPKFLAP KIPPT/GPLPPNKEPSKENVNPG/PLCF L
1150	15051	A	1157	446	87	PDCINVISCFLLTKIYHVFLL*ROGLTK LPRLVNS*QAAILPP/SASQAGITGV SLHTRPIMYFSSYYIIFGDTVLF\ETQS HPAAQAGVQ*CNLGSLLQPPPGFKRFSC LGLPSRMA
1151	15052	A	1158	1	938	FFFFIFATYLFNKGK\LTGKRQSD*SLC KHLKGYIYKKDILTASKH/V/KKCPTSL AIREMQILTGIKCC*RCENGIFTHYW *ARALAQLLWKNV*QHILKLSMCITYNP TILFLGISNRKVYM/CCPK/DPCSRMSR AAQFVI
1152	15053	A	1159	370	3	AFKAAAEGAAMSVTGGQPVLSWVVLGG VTTTT/CPTTFIMPNDTV\RGDILELTR \PLGAQVAMAVHOWLDIPEK*NKHK/LV VTEEDVELMYQKALNMVQNNKKAAGIM YTFNAHAIDEFHR
1153	15054	A	1160	55	471	SPPPGLPKKIFFWPLSFYVWP*PQRFCP LFAPFKQESNPLKVWPPFGALQNKRSKG CSPSM/SARQES*PLFPKNLETPPFGGK FLKFFFFFF*DGVS LGHPGWSAI/IDSL QPLPPGFKQ/SLCLSLPAS
1154	15055	A	1161	3	467	GVTNQQIFPVDTAFY*KMPSTFMARE KMSGFKPSK/DRAGDFKLRLMIYHSE NPRALKNYPKSTLFLV\KNKAWMKHFL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN: 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QPPVETVCSGKKIPFKILLVIDNVPCHP GALMEMYEEINVNTATNTTSIL*P/VT SGVIS
1155	15056	A	1162	216	464	SSEPGSPGELPYGAQEPVMKAPQGILV IR*T*FFETESHVAEAGVQWCDLSLLQ LPPLRFNQFCLSLP\SWDYRRPERHPAN
1156	15057	A	1163	29	433	AVEFGGDCSPQHPLNPPLGSPQHSFPF LIGICT/REE*GWGGGLPVPCPPALPYP STPSWGGICVCYGRGGVAPPP*HPPLT* LGGGSTPTSALPAPGAPRHPGHPLMVLQ TLPWGPHTPARKPYINKVLSCVDF
1157	15058	A	1164	486	11	STCLGLPKCWDYRREPPRALRCFFFLN ILLFLKFTLSEINIPTPAFF*LVFAWYI FFSLFSF*P/DLEHYI*SGICVDTM*VG SSCFNPT/WSISSF*LVCLDHLFFFLF FFFLRQSL/DSVAQAGVQGDLSLQPP PPWFKRFSCLSRIPAHFEWSRA
1158	15059	A	1165	467	131	NRSLEWAKMYKTYDEIKLVNTLPT/RKS PGLCKITAKFYHIYKDGVLVLLNLQEI QVGFHPNS*YQ\IILIPRYSEGTTKGN CRPIFLVNIETKILHEIRAI*VHKQIRT LE
1159	15060	A	1166	455	32	EEGVLKAKRGCKSGLLHQTIVNQVN/AN LEKFLKEIKSDTPVNI*MIRK*NNLTAD KERVA*IQDQTSNNIPTQSLIQSRALT LFNSMKTERGEEAGEEKFEASRG*FMGF KEKSHPHKHSASKAASADVEAVASYLN S
1160	15061	A	1167	26	418	KIWDYVKQTNL*ITGIPERGGEKVNNE NIFEAIQ/ESVPSIFKEVDTOEQEIQR ASSSSSS
1161	15062	A	1168	64	313	KWCKGNSYISKDLKELKYLGV/QLK*VQ /DL*SENYQILLKEIKEDLNKWDIPCS *IRRLNIKMVIPSKLIYRFNAIPKILA A
1162	15063	A	1169	464	36	QQAEEAAESL\DPGGRGCSELRSCHCTPA WATEQSINK*SINQSIK*KSKLC/CWEN TLVKHIFHKRLTSRIYKEL\QQLNKKTN NSL*K*EKDVNRYFIKKIYEDI*MANEN IL\IKLVIREIQINLKEWLSWFCCCCC FVLFPF
1163	15064	A	1170	290	487	GSLPHHTPKR*PFLF/CVFETGSRSVT* AGVQWHNHGSLQP*PPGLKRSHLSLPV LIFLFSVEMGV
1164	15065	A	1171	2	413	GKVEI*FSTLH/GCNMK*SRSYLL*ALR FIFLFTARGLTGIVLANSSLHITLHDTY YMGTHFHVLYIGAFAIIGGFH*LPL FSGYTLQQTYSKIHYTIILIDINLTFPP HHSGLSGRPRRY*DYPDAYTRYILS
1165	15066	A	1172	381	2	PPKLQKNFFFSSTGKFFLGGGRAFSPPP KKGFFSQIPRRFFFLPKKKIYFCPPP CFGPPPTFFLRAPPFFFFFLLLFCSFL VGVKFLEFL/FYLFIFRDTV*LCYPGWS AVVQSWLTAALTRP
1166	15067	A	1173	9	405	NLDKKGRNRTPQSWFQANPMASMTFSKK KKKKKKKKGGGALKKKPWGAQKKPGKK KKNFFLKGK\EKKTFRGILEKKPFGGG KKGNPPKKKKPLREKKF*GEKGEKKP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1. 26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						*KFFFKKKFPPPSKKT
1167	15068	A	1174	410	0	FSYYPPTTRGGCPSPSQIFLPPPLLGVP FFPFSFLKIFFFPRGKFFGGVVPFFSP PKKKVFFKNPRSVYKPPKKEKK*SLQP PG*VWAPPGIFKR/PEPPFFFIYS
1168	15069	A	1176	319	3	KEARSVFRVEGRG*KNFSASGPPGGGNP GGGRPGRGNFVFLIKKGGPPPGPKG/SP FFDF/GGPPPPPPSGGSGVNPFPFPF FFPFEMESRSVSQSGVDPDAWADAW
1169	15070	A	1177	385	1	SASFGLPKCWDYRHEPTRPASVSVTVTS SRLSGA*ARSGKGLVFWAQMVFK/RIP LTKYSDHSREPSLQLCMQSTPSKAEFT VAKADKRLCCTAKSSTAKSIAQIKQND AGRSPQESLHVSGRV
1170	15071	A	1178	147	808	KLKEIKKLEENAGINLYDLRLGSGFLD MTPKAKQKKENLKWVIRMKNCSKASKD TITFYN/YRSDKGLV/SKIKELNSITE RQPNF*KDLNKDFSK/EQMAKST*KTTE RLFIREMKTKT/ME/YHFLSTRMAKI* KDSNR/RLCRKTGTLIHCW*GTAPANLL KNCQPLFPF*GTWQFLKRLNLELPDDP AIPPLVICPKEMKT/C/CYTEICTQMFT AA*III
1171	15072	A	1179	1	398	SRSRHCTPAWVRVTLVLKKKEKEKEKEE KKRCPCYIVSHQSL*KPAWQFL/RNVK/ LELPYDPAI/PLLGKCLKBI*KYAYTKT CM*MFIALFIIAKKYKQLKRLSTDEWIN KMWYIHAI
1172	15073	A	1180	3	389	GYDRVIPNP*PLTGA/LRALLLTCGLAM *FYLQSMWVLIILGLLTDLTIIYHRWSDV ARKSTYQGHHSPPAQKGLRYGIMLYMTS EVLLGGLF*AFYHS/SLCPTPQLGGHW APTGMTPLDPVEVPLNT
1173	15074	A	1181	354	2	ANSSDACILDGHRALPLQLPCCGYSTSP AAQSSTVPMPLLLIPPHCNRTPSLWHY SPASNPTNPSPY*TAPEPPPIPRNNP FS*KFPYYVWVYTSLTTCQPPVSSPNF TOPSVL
1174	15075	A	1182	3	384	GANVSG/DL/KLKPVIYSSNPR/ALK NYARSILPMLCKQEKKEKKK\ANMTAH LFTAWFT*YFKSTGET/CAKEKIPPKIL VLIDSACSHPRALMEMCKEINVVFMPVN *HSI/LFCMQPMDQALSTYKS
1175	15076	A	1183	1	410	PPLF*KFFSPGGVQS*KGGRFWPPP*VG VLPSSSP/IIFFTPGNWGCFSPPSP*KF FFSPKGFIFCGGVGPFPPPKKRFFSKI PPLVFFSPPKKKIFFPPPVNFGPPRV FFKRPPSIFFF
1176	15077	A	1184	406	62	PPIINMLCSLAPFFSPPLRGVLPFPF LKNFFFP*GVYFWGGGPHF/SPPPKKG FFPKFPWPVNPPPLRKK/YHNPFPKG FGPRVFFKAPP
1177	15078	A	1185	337	383	RSYISFQK*VKDLNKHFSKDDTQMAN/K HIKRYSTLVIREMKIKPMTRYHFTPTRM AVPF
1178	15079	A	1186	3	471	LAPSDK*ENRLFGNRPL*EVRSFSARQP PHLRSEEPLRPAATPSGK*GASPPSSHA VREGGGQPPPGQPPRPGGGRCLCPAAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TGK*GAPLP/EPPPLGLG
1179	15080	A	1187	2	406	FLVETEFYVQAGLELLTSRDPPASAS KGAGMTGVSHQVQPO**S*LWT*/PSSV EAGTSFGLSFLSSSWALS AQEGCLAVPS /SGSRGLLVGALLLWTKPSPQLSPVPAS QRLSSLSLMPPLPQPQHLTHTSIET
1180	15081	A	1188	160	459	NFMTIDMLCSAVVIHFCSSGLDFQL*KL FKSQ*ENNLINKWAKDLNSFTIFS YG*K LAHEKMLNI IREIYFTAIMS*YTLTRTV KVKKTDTKCW*GCTATGNLIHCKKNV*P LRNTAWQ\FHKILNIYLPYHPAIPLSDM NSRE*KNI/CHAKMCAWIFI
1181	15082	A	1189	232	2	KAPPPFFFFFFFFFFFSGSHSVSWA GI*W/PGV*WHHGS LQPSRLK*SSC LSLSSWDYRYVPPHLANLKK
1182	15083	A	1190	2	402	PRVRHAGSFPSPPPPEGL\SHTSFSQ* VFSWPSY*TPCLSLTLASVLSLL*QRS PRTLFTITNC/DF/PASHSSCRIPAGL* ALGRQGLFSCFFCFETESH SFAQAEVQ WYNLSSAQPSSEPK*FS/CLSLPSS
1183	15084	A	1191	19	390	WCVPAVPATWEAEPRRSR\RSKPLTGRQ SKLSY/NKKKKKKKKKKKKKTGGGP *KLLGGPKYKGGKKKFFFFKGEKKKS LGGILKKKTFWGGKKWPTPPKRNKALK GKKKFLGGRGNNP
1184	15085	A	1192	485	112	QRDPDR\SAEAAIKYFLTQATASIILLI AILENNILSGQ*TIITNTNOYSSLIIM AIAIKLGIAPFHF*VPEVTQGTPLTSGL LLLT*QKLAPISIIYQISPSLNV
1185	15086	A	1193	55	385	THAFADAWADAWGLFKGILTENFPNLQR YINIQVQGG*RTSSRFNTKKTNSRDLII ILPKVKDKLSKKKKK\AENKKILKYRG GPF**KPGGAQFYGGGRKSFFFFFGG
1186	15087	A	1194	408	3	CQSA\LLGGASQLG\SRGSGVRDPLBEA VCPFSDLQLHAERTTALLKAVRQGHLSL PRLLSF\VCLCPAPRGGACRGRQASLS CGGLHPVRASRLCLRKRAWAMASVPPP ASLP*PCSLISDCCVSQ* DSTGRV
1187	15088	A	1195	5	371	LFSTNHGDFGPLYLFP\A*AGVLGTDLS LLIRAE LGQPGNLLGNHMYNGIVTAHA FVIIFFIVIPIIIGGFGN*LVPLIIGAP DVAIPRISNISF*LLPPSLLLLLACAIT EAGAGTG*TVY
1188	15089	A	1196	76	404	PTPLRTHDQSSKVSRYKVN IQVGAFLY MLSTRITGI*\IKSTSFPFASPKVKYLT INLTCKVQ/DLWKEKKL/NEIKEDQNK* /NVPFSWIKGPNIIVN
1189	15090	A	1197	50	334	ILHMVSIPISTIY*HLLPAG*AGTHIG* LPPA*FFWVMG/RDRVLLCHPGWNAVQ S*LVVASNSW\VK*SSHLGLSKY*D*RH EPSYPASGTKLN
1190	15091	A	1198	250	1	QYYLVSSNT*SIIDFLQLPQKCIFTVGF SK**CICGFIFKNI*LFF\FCLFSESC SVAQAGVQWQDLSS*QPLPPVFKQFS
1191	15092	A	1199	2	402	TDARHHTWLI FVFLLEMGFHHVGRAGLG LLTSSDPPRP AKLNFL*R*GHAVM\CPG WPHE\TCLGLPKCWDYRCE/HTAPKPH FLFFFFSEKNFIPVPRGGG/WKNLN*

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						MEPPPPG*KGFFCPGPPKYWN*KAP
1192	15093	A	1200	50	437	STLYLEREQISLSVIVSSPLPSTSTG PTAAQSSISGPSLPLPPHNGAGDAPAG LG/YGQGPSGPPWGPS/SGPSPR*ALVC PTDPSGAARGGRG\SRGSCCAPAGPAG LGDHRPGMGEGPAAPPKSS
1193	15094	A	1201	86	313	PPPPGGYPHFSFXXXXXXXXXXXXKSL PPGKGNPPKVGLPPFXXXXXVSPKXXXX XXXXX*NPHSPPRAPGGFP
1194	15095	A	1202	105	485	VQQTMMARIYVCNKPARSTPRFTKQILL DVLK/YIDTQTIILRDFNTPLNSVMSW RQKTNDKNDLNLMLGQLDLIDISRIHL VSTR/YIFSSLHEIYSKSGHMLSHKAC HNNF*KIEIILIIILLYHC
1195	15096	A	1203	1	476	PHFGPPPPQDPRF*G/GPSTRKGFFPQ PPGFFPQAWPRAGQPPPGGT/EPVFPFP KHP*RRNPYPKFGSPPLPGKIHQGSFGP SGQFR\PPRWGKKRAQPTFWAHPPIFF FF*GVLLCHPDWGTVARSR/PPQPPPPG
1196	15097	A	1204	1	269	VVEFETYNLGIK/WSKDMKRNFTKEDLM MADEHPRRC*HHLTPRTAQVKLELEP NE/WQCGEAGPATPCWGDAAPVQPLLQ IGRRFLKK
1197	15098	A	1205	459	42	KLKPMLIYHSENPRAFQDYAKSMLSVLY K*KNEAGLRAHLFTAGFTENFKPAVETY CSE*BISLQI*LLI/GHPR/SLMEMYKE MNVVFPANTTSILQSMDDQGVALTYYEH YISNILEAIDNTENPLIDLKANAWVG PG
1198	15099	A	1206	408	1	EMKTLTEMSSPGMPTEKVSLED/DIN/ EMHRKLQCREKR/IKRN/EINVQEL*YH YKRCNHHVMRMPKEQKKEIFKVMAB NFPNLATNNKSKVKEAQRTPERIKTIYI YIYIS*LQAKEKESILKETCQKTSRPK
1199	15100	A	1207	7	383	LDIGCFWEDKYSSCYFSLATSGKLYF SFSCLIHCFLVVCVRAHK/CI*SRAS* CVCVK\CI*SSAS*CVCVCARTNGI*/ CQCFLVCAQV/CI*SSAS*CVCVCTS GI*/CQCFLVVCVVCV
1200	15101	A	1208	405	214	AEAGRSCLPGGGGCNEL*SPPCPSAWVT \SETLSQKQNPHHKKKTGQVRGQSSYL PLWEVNR
1201	15102	A	1209	384	2	GVTHH/ARARFFC/LLDTGFHVSFQAAV Q*A\NHGSLQPQPPGLPSSCLSLPSSR DNK
1202	15103	A	1210	403	2	VPSIQTNKSLTYDFDFKQLFKTKLKL DASFVNVCNVVEPFRFALSQTQSLCL SLFLLI*F*TINCFCFLRQN/LRSVAQA GVQWRDVGLLQPLPPEFKQFC
1203	15104	A	1211	156	405	ESQMLIQCKSQMLYC*RI*TV/CLCVC VCVCVCVCVCLTCGTRKVCIVFLFIVVL NCK/PLCEPCC*CNRQGWAPWLLPVIST RW
1204	15105	A	1212	70	408	KAFSLLPPGVSPGPLCNRRPNFIFGGP KKKPPPPQVRVTQGFNPPPPFFLWG G*QGD/PPVAQG*MDPPPRPK\GRGP RHEPPPPAF
1205	15106	A	1213	410	3	KKSMFGFKASKDRMTLLLEAQAAGDF\N

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LKPVFI\YHSENPRILKNYAKYT/PVLY KWSNKAWMIANLFIA*FIKYFKPTVETC YSDKKIPFKILLIENAPDHLRALMEMY KEIHAVFMPANTTSILQPMDOGVILT
1206	15107	A	1214	3	340	KIRVEVNKMYNRKLEBEIKKIKSLFFEN INKIDQFLPRLRKTQKMQINKIRNEQG GISINIMEIKYSYKEML*AIICKLNNL HEMNKFL/EHRVPKLTQVEIENLNYIYK K
1207	15108	A	1215	1	57	RGLKIQNVNEIKS*CFEKIKIDKFLARQ NFKRKRFRD*RGDIMADITEI*GII RAYY*QL*GNYLENLEEMGKFLVTYNLP KLNH/DIENLKPPVT/REFKSVIKSLP LKKSPLHDSFTAQFYQTFFEE*VSVLKR
1208	15109	A	1216	350	1	QSSFFSIYPNFHLLSFLFCFKDPLFFVA SVLATNSLPLFFPQISRYFF/PFERERE RERENVVL\CCLGWSAVMQS*LTPALNY W\VRQSSLLSLQAS*SYRCGPPHPANIF HFIFCR
1209	15110	A	1217	139	358	KNTFFVVVEAKRLFVPQAGGQGGNLSFK FPAPP/NLRG*SASSPSSGDYRPTPPCP ANFFFFKKNRISPWGSGW
1210	15111	A	1218	361	50	WGDHGSILKPQPLRSKNPPPLASLVTGT Q*LG/HPVAPFPIQLIFFFFFLRRSL/D SIAQAGAQCWDLSSLQAPPRFTPLSCL SLKKKGPNPVFVITWMNLEDIMLS
1211	15112	A	1219	1	361	LKQHSVNVKTAIFYWKTQSKTFVARE*K GEILSSNRGECLLQSFKGQPLLLGANAA GDFVK\PMLLDSEN/PKALKNYTTS
1212	15113	A	1220	292	362	HIPVVP AIQQA EVGGSLEPRRSRP*PPR LK*SSHLSLLNSWDYRNVL/RLANFCI FLCVPR\FKLGSNHQNASVSQSARITG VSHAWPILKLLKLFVCLFEMGSHYVAR AGLK/PPGLK*SSRLSLQNCWESRREPP HPDTH
1213	15114	A	1221	372	3	RLFFLLPPRPKGDFPPTLLIW*RHGFSP PHVFKPPPLNLILGALKKKFFLPS/LPY VKFYFFKRAPLFFF/IFFRDRVSLCWS *PPGLKQYTHLGLPKHWDYRHESACLAN NHNNNTNFFFETE
1214	15115	A	1222	3	291	RSGDQDCPGQHGETLSLLSLTFVNLSLI CNL*TLSLIFVKIQKLAWHGGVRL*SQL /LRRLRQENHLNQEG/DCIPAWATEKDS VSKKKKKKKGGPF
1215	15116	A	1223	379	19	HMQILTIMRYTPIRMAKMKKIGYTK/C W*GCAATGYI\WECKMVQSL/WQNTWAD S*KLNTHLSYDIAIQFL/GFYSKKIKAY IHTKPCT*MFTATLIKSQI/MQYKCL STDKWIKQNRGIVI
1216	15117	A	1224	387	40	KKTLSTP\PEKHPTPLFHPPPQKGGKA PPSFKPPPKHPPPKGISPPPP*IPPP PIYPPPPAKPPDFFL*SPPPPPPFSP PPPP*TPPPFFSPPLFFFFFLLIR LLV
1217	15118	A	1225	21	477	IVSRLITVRLQKPRLDPRVRPRVRKEN YSSV/SFINIDRNVLNKL/SSQIQQYI KKLIRHE*FWF/IPGIQWFNILKSVIV TYVN\QKWKHTIISVDEKAFDKIHY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						LALILIKKKKKKKRALPQSFI PGDLFKK PNGGF PGLKMMGRAPGE
1218	15119	A	1226	1	398	ERINHTLFFLAEAQKRLPTGISGRGRPA IPHNT PQRAPDHAYLPAALAAQHRAGGQ QAPPPG\SSPSSPYDEVK DREGDVTASH GLRGNGWGS P*ATSLVLNNLMYMTAKYG DEVPGPEMENAWNALANNEKW
1219	15120	A	1227	3	238	DAWVAGHDG/RTP*SQLLRKL RWEHRFS SGDRVSDP*SCLCTLA WVAE*DSSSKKK KGGPFKGTKFNSRGGRNYFFYGA
1220	15121	A	1228	207	2	NRVSPCCPVQWHDHSSLQ/PRTPLGKGP \SASAF*VAGTTGVHHAQLIFHFFFFY *DRVIQAGVQRNL
1221	15122	A	1229	15	413	RKSVNVIHHS EILKKNYMIISIDTEK SFDKI*YPFMTK LSEN*DSLNLINNIY/ AKP/VANTILH SKRLNAFFIKQGCLQGC \PPFLFNII LEVLASTKGRKEIKSLQIR VBEI/KPLSLFADNM/IVYIENPKES
1222	15123	A	1230	363	1	AADPFACRPVSPHPPLYLVTSSQSLT VSPKKQPPSAGMQLGVGDSL SGWGWGRT KTRLFFFKTRSLSAQTRRQWCEHRSQ P*PPGLIKRSSHLSLPS*NHRHMPPHL AN\LCLFV
1223	15124	A	1231	3	402	QANS CIFS RDPGSVQAGLEPLTPGDPP ASAPRCRDYRC\GPHAQLLLTFC*ISI LILV/CIS*MKDYFITCIYFFNYS*QII FYRRASDFFPFLRQGLALSPMDHGS LQ PHPPRLN\HPPTSAGVVTGT
1224	15125	A	1232	3	396	FLSQHGFLFLFFAGIDKLLKFIWKDN* NNYEKED*RGVITLP/QYKAYS VATVIK MVWHWQSDKHVDQWNREPRNRPNYMSQ *FPL*YVSQRNENLPLHKNPYMN VHN GFCNSRKQSRYPSTGEWVNKL
1225	15126	A	1233	3	395	LPKCWDYRR*PPHPALF/LFF*KHPKFP KMQVK/WRKH*TENRLVMYFSEKFGD*L KDQHKLYYLDMAFQFIPTFTYVMRYSIL FKFNIR*LTLSVKMAVFLVETGF\TML ARMVLIS*LRDLPTSASQNAGI
1226	15127	A	1234	416	2	KIDKLILTFIWKCKRPLLAKIVLKKKNK I*RLPLPSFKTYGKGMV/TK/TKWGWPK NRPIKGTGF*VQKKKTPHIYQGLVFD SG ARTITN/WY*DN*IST*KRMKLDLYLTI YKINSKWKIDLNVRAKTMTFLEENI WVI LD
1227	15128	A	1235	384	22	FFQEI*NAIPVNTQMVRKQNSHPANIEK VL/VVWIEGQTSNNIPLSQSLTQSKALT LFNSMKA/E/RGDKAAEEKMETCRGWF RFRERRHVHNIKV*GEAARSCGSLAAGS PLKHL LLLHNTLIC
1228	15129	A	1236	379	2	SPYTKIHSKCLKGLNVRPLTFKPLEENP G/VMVPDLGPGKKFIS*APKAWATKTKI IQWGYIGLK/AFCPAKEAIPRVKTWPSE SEGI PAGHAFYEGFIFQIFKGLQPFH SK KKKDLILKLDLLSADIS
1229	15130	A	1237	1	407	YRVGQAGLKLTL*SAHLGLPKWCDCGR EPPCLTIIAL*SVFSLVLPVAVLIKLI NF F\CRDGGQTM LPRLVSNWPMIC/LPW PPKVLGLQ

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1230	15131	A	1238	3	380	ELSQRTECCMDIMSYYKAIVITMAWY*FK DKQRVQQNEVESPKTLLYIYRLWIYYEG DTTDKG*TF\NKWYDWSWI/ST/CKNM* FDYHFTQCIKIN/SQWM
1231	15132	A	1239	1	396	FADDMIVYLENLKDSKKLLELVNQFSK VSGYKSKV/NVHKSVALLYANSNOAE/Q IKNPTPFTIAAKKQK/YKQKNNGIY*T KEVKDLYKENYKTSLEIIDDANKWKYI PCSWMGRIDIVKMTILPKAI*RFS
1232	15133	A	1240	392	58	SFSMLARLVNSR/PSRVLPAASQSAE IIGVSHYAWPSKLSF*LTIDQTHLSCNL FIYVFERRSCSVTQAGGQWYGHSSLP *TPGLKQSSCFGLPKCWDYRLEALPRLM
1233	15134	A	1241	500	204	SLSLSPS*DGVLCLGWSSTPGLKRFSC LSLRSSWDYRCVPSSQTNF/VFLVEMGF HHVGQAGLELLTSSDNARLGLPKCWDYR RVPPRPAAFFLFFKG
1234	15135	A	1242	2	397	NFMINNLPPKKALCPVFTGEFYLPPKE ETIP*VIRISLSL/IPSIIQKIETEGI LPNSFYEGCIIILISKPYKDI*\ENYRLT SVMHIDARFLDSILANPIQCIKVIHCS HVAFV/SGTQDWFNTQKSM
1235	15136	A	1243	12	362	AGFYHVGQDGLKLLTSSDPPASASQAG IKA*ATVPGLSPLNFCBVRFMESWSWR P*RTS/VCSALAKCWRNRSQVVDKLPS FPT/RM*SPCLHPAVSAFCBSASVLPGI IVTTSV
1236	15137	A	1244	183	383	KQAGRGGSC*/LPRCWDYRRELLHLAF MEG*LKK/FFCKDGGGLTMWRLVLFNFWP PVILLPRPPKVLG
1237	15138	A	1245	410	2	FSRDRVSSCWPGWS/PNS*PQSDQLALK CWDYRCEPLHPAFC*MNFLKVC*HGTS /DSKY/CQHVSPKNKDILSNYNI IIP KKFNIL*YIWFDFFFFEFEFCSCCW*D LGSLLQPPPPGFK*FSCPSLPSSWVHRHV
1238	15139	A	1246	440	46	KTEGANINKNTTYQ/NLWDADKAVFRRK FRALNAYTRK*ERAQNLSSSTLTKRKKE QNKLKADRR/QIMQI**KLKGVENKQTK TIQQIH*TKSWFFEKISKIYEL*QA**R KKGEKTTITNVRNKRYSGRVG
1239	15140	A	1247	266	340	RKCWPGAVAHTCNLXTLGGGGGRIT
1240	15141	A	1248	3	391	DAWADAWGSRRAVALFFFWGFLGGGG LKTGFYFIPQVERRGLNPD*WNPPPPGL RGSSPPT/LPKQWEPGGGPAPSNFWFF FEKRGFPQVTQAGFKLWN*GDPPAGPSK GVGITGGTPSPHPLFLKKR
1241	15142	A	1249	3	323	MHHHA*LVLVFFCGDKVSLCCPG*S*TP DLKRLSHHGLPKHWDYRC/RATTPGFFS LFFFFFNPPPEFLLPWAPPSYSLKONKI FLKRFLEPLAPPKGLPLKRAKRI
1242	15143	A	1250	3	405	QPDSSYPQGRLSAPPEQEGGPWLILPH ACAPSQICVPHGASILSYQERKGTQVL SCEGHCKLSSPVGLVGQSPCWQQPDAVQ WVPFRRRTQTPGTVAHACNPSTLGG*GR RITS/RPGVRDQPEQH
1243	15144	A	1251	407	2	PFLKKTKELEP*GPAIPALGVPSFFRFF FLPYKRKEIKGIRTPPMRIAALFTIAKI LNQPKYPSVDI*LHKRHTSNTTLLSRMK

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						H*WIKKT*/HTDMMYYSAIEKNGILSF AATGMSPKDIMLSEICQAQKNRY
1244	15145	A	1252	1	253	VADVRESLDPGD*GCSELRICHCTPAWA T\SRSTTSQQQLKKQENNTT*KTYGIQLM NCQIANYSCKLLYFRKMSNLQSNLKKKK K
1245	15146	A	1253	3	372	KKKAQKSGTIVLPCNPSSYSGG*VGENA\ WARSQPLGIS*KQQ*QQNQQTTSKTD PYIYG/YLIHDRGGK\NTQGWDRLLNRW GWGIWLMTQRKIKLELYLTPYTRTNSTW IKDLNVAGCGGSCL
1246	15147	A	1254	2	410	KNLTPIVGLKAATN*ESIPPQT/SRKKK KKKKKKKKRGALKKKKPKGGGGGKKNF FKGGKKKKLGGGVKKRGEGKKPGGKKKK RFGKKSFFSRGGKKKNRSSSSSSSSSS SSSS
1247	15148	A	1255	61	487	GRPGPTHAFVVIDSFFMGNEARFINHSC DPNCEMQKWSVNGVYRIGLYALKDMPAG TELTYDYNFHSFNVEKQQLCKGFEKCR GIIGGKSQRVNGLTSSKNSQPMATHKKS GRSY/RE*KKNKKRGGRFKGSQFSSPG MQG
1248	15149	A	1256	118	5	MFIAELFTIA/RRWK*PKCPLTDEWINK M*YSHTM*HY
1249	15150	A	1257	390	1	TQKNTPTPKPKPTSQOHQKKNKPTPPGF FFFSPPGK\GGFFSPLEFWVPPGFFPPP VFKTRPPEFIFGAP*KKFFFSPPRSLNF FFLRGPPSFFFFFFFFFS*VGKEGSSPSH ENPLFVPTGEW
1250	15151	A	1258	378	3	GAFFFFFFFFPKGFFFTPFEFFGPGFFF SPPFPIPPPIFFFGPKKKKKFLPPPPQ KIFFFLRPPPLFFFFFFFFFFFFFFFFF FFFL\DLD*NVLSGTSAPEKNQELLGMV AYACNPSTLGGRGG
1251	15152	A	1259	462	287	RDG\FHHVGDGLHLLTS*STRLSLPEC WDYRCDLPCPAIPAVTLYQIQYRPLGLE SKA
1252	15153	A	1260	446	34	NVRAET/IKTLEVNTGVNLHDLS*/GKA FLDARPKAQVAKEKSRQPSLHRRLR/FC ASKDPIKEVKRQPT/WEKINHVS DRGL EFKIHKELEKLSNNPI*KWDKDLNGHF SK/ELQIASKHMRRCSASLVIRKCNBIV DPD
1253	15154	A	1261	2	383	GSQRKWFLEMESTPGDNAIDIVEVTTKG FNYYMNLVDKAVAGFERIDSNFERSSSV SKILSNSIACYR*IFCKKKSQMLQ/QTS LWPFYFKKLPOPPQPSAATTLISQQLYTL RQDSPPAKRL*FTDGL
1254	15155	A	1262	476	50	FFFFFFFFSDTGSHSV*AAVOWHDHDSLQF *PPGP\SDPPTKSSTREF
1255	15156	A	1263	143	472	TGAVPIRPSWN/RPPAMIFF*NAQGILF AEFLASQRAILWEFFEKAYHESVLKSA KGLAEKCPGKLHQRVLVQYDNALAHFSH QTRTTKSSTRQFR
1256	15157	A	1264	179	489	YIFFFLSLFFFLWPRPEYRGAITVHC SL NLPGSSDPTASASSVAGTKPH*YIFFFL SLF/CFSVAQA*VQGGNHSSSLQPPGL K\YPTASASSVAGTKPHPLIFFFF*KKK

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						FL\CFVPOAGGQGHDFG*L*PPPSLKQGGGLTLRIGDYRGPP
1257	15158	A	1265	1	536	FRGGWGSVRRAPGTASCYLALAGGPPGQCPPAAISCPSPLPWGS*TE/PYVPRRPGDPSAAP/PSW*VPRPGVPRNVPGRGVGGQDGGCQAQDIQAAASLMADTAPDSPGSA GSVRALPACVPEISGS/SGLPFGAALP*VAA/RPTPGRHVDTHPRQHSFCGGQEGDIRAFPTLYLEVYPGPP
1258	15159	A	1266	403	2	TSLHPRGYMRLLRQGFISAPCGYMRLLPRGSSSLHPRGYMRLLRQGVHRTCPWVHAPSQTGVHLCTPWEHTPS*RFISAPLGAASHVT/GSLSIQHIIYIFVFCLLRQGL/NSVTQAGVQWCNLSLQPKLPQAQVILTK
1259	15160	A	1267	2	401	FVLNPGGRSCSEPRSLHCTPAWATRAYLQLGKKKKKKKERGEENKNQGGPPRPLKREVGTPGQKKPL/WGGSNGAGQKQPA/QKKGKKKKADHKGQRGKN*KRKREGGGSTS KNNSRGTGAKA*NPTIWGGGGKKI
1260	15161	A	1268	49	416	LRGRALDPRLRECGDLGAPPAPPEVALRAGTCWTR/CTL*APPRGA/DRSPWPPRS PMCKAG/DECQDGI PG\MKAWSGLRTRQCPWP*PKLPCGPGHPAWRT*PLPQTA/CGPGPAAPCAG
1261	15162	A	1269	420	47	GPPGWASFRNLNFPKARR*GEWKTPGESGGAFFSPPGKNF\AQQN*GRPPNPPPPPGPGKGGI QTRGGAGLGKNPFRFWGGFPNPGNK*GGGTTKKKEGPPPLFFFFLNTDFCNLIKRDRLGVGAHL
1262	15163	A	1270	404	1	AEILELKNVIDILKNVSESLNSRIDQAEERISELEDRLFENTQSEESK*KRI*KNEARQDLENSFKKANLRVIGLKEEVEREMGVESLFKWIIEENSPNLEKHIHIVQEGYRAP\FNSNKKTSRHSIINSHTK
1263	15164	A	1271	387	2	KKEKKKEV IIFVLLLPLK*FQNIQVWL VRELEKKFTGKYV\FA*RKILPKPTQRCTKNKQKRPRIHAPTAHVAILEDVSVPGEIVGRRIRVKWTQQLTRVHSDKAQQNNVERKVQTFSGIDKKLR
1264	15165	A	1272	1	393	PRMGRPLPGGAPHFSDGVAGQRRSSPHRRSGRAEALLTSQTRGLRGAPHISDDGRPGRDAP\PS*TGWQPGRGAPHPD\GQ PGRGAPHIPDDGRPGRDAPHPFYGVAAGQRLQSRHFGRPRQAAGRWRL
1265	15166	A	1273	3	317	SSYETKGVMIASFSSREADNHTAFIRIKTNASDSTEFILPVEVEVTG*WKTDEIESCFVFSIAYSQKVNKC*LFFFP\APG IYSSTEMLDFTLRTQGGKIF
1266	15167	A	1274	92	368	LCPPGGGRAGQQGNL*GVPSPPGPKGFWGPTYGGGGKRTTRPGGKPEKSFDP/GPPGPPGGTKGNPAPKNFFAQKERGPFPQNGGPGNKL
1267	15168	A	1275	401	3	DMCDWFKKEFSDTTPKA*SIKEQLTSEFIKIKSSCSPS\KNTIKGLTRQEKLGKI FANHMSDKGLVSRIVEELSKLN\K*KLNF*KWAKQ*DHLLKKT*QICKERYSLGKGKITMRYHSTSIIMCIKTIHS
1268	15169	A	1276	298	426	GATMLVLLP*LAFDLRQSL/NCFPQAGV

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						QWRDLGSLQPSPPWFK
1269	15170	A	1277	421	1	VSFKDQKL*INKENHPKWKKICNQPL PQIRYMDANKHIKIFSTSLAARETNMKI TT/RILWKTWVQFFKKVSIYLPLEPAIS SYLFTQEK*KHIDGSCSPSRVATAKLLA LQWRRPSWNCMHQRAGSWKQIGAPFFSK L
1270	15171	A	1278	1	218	TRSGVQDQPNQHGETLSLLKIQLASYG GVCV*SQLRELRLQKNCLNGPRSHHCT PAWAT\EQNSI*KKKKG
1271	15172	A	1279	88	396	TFLFSSSSFFFGGGVPPCPGLRPG\PN FASLHPPPPGFGGFPSTSPRA*NWGPR PPQATLGAFGLEGE*IFPPGRPPPE*L WGPPPPPPQRGGMWPTPL
1272	15173	A	1280	94	399	TDFLFL*TDFLFLCLCSLKNKIWVNEFR YGGFSLGVSNTQALPFSQEVNDAIKQMK KHLKLA/DKISIVRCITKMGMLLGYR SSWQVKRITWQLIVLNMLAYRAVFGI
1273	15174	A	1281	236	2	TQSRLVFFYMTGPAVYLNHHLRTHQGS HLCFFFCFEMESHSTYQAGW\VWWRDLS SSQPPPPRLKRFSCLSFPSS*DY
1274	15175	A	1282	37	410	KKKTLKKIKKLCPPGVKGEFNPFFVLS KVFPKKERGLFFKVTFSVLTFFKKKNF KIGGSGGFPPLWFFFFFY/RDRVLLCH PGWNAVTRS*LTTSDSSDPS/CLRLPS SLDY
1275	15176	A	1283	404	232	LSSWDYRCLPPHPANPLYF**RRGFTVL ARMV/GPRDSPASSQSAGITGMSHCAQ PG
1276	15177	A	1284	3	402	MQIKITMRNYCTPVRMP*KKK\SRTPR C*GGGGTTKILIPCWGDYKIGE/PLW/K SVWQFLIK*NNHLLYDPAILPLIFYTRE MKTVHTITKYCNHNEK/CMQGFTALF /TLPKTE/SQPKHSST
1277	15178	A	1285	1	253	LRGKFMTLHS/SILKRG*SQINN*TATL IK*KKKGKIKPK/RSRRKVIIMNRNK*D *KQNNKFNETRSWFFKNMKKIYKSLVR VT
1278	15179	A	1286	400	105	FNFKKKKKKNREVSE*QY*QAKYLKRN FTKNI*VAEKHMKNQYVIKEMLI*LTM RYYYTPIK\MAKIKLTDNHKCCQLKPSY MVGKEFGKFLIKLNM
1279	15180	A	1287	400	119	TVFHHIGQAGLELLTSSDPPVSASQSAG ITGLSHW\PASSSFHSNHCVPVLEPHQ VAQLDSFGYEKVCFSFN*VPGAQDKNDL SEN
1280	15181	A	1288	157	386	NDLQFHPFYCLF/DLFCQSLKKAGMQWH DLGSLQPLLPFRRLCLSLPSSWDCGH VS/PMGP*FCIYTHIYFLVBMGF
1281	15182	A	1289	400	124	FDAPAKGQGGDFGSPPPPPPG/AQKIFP PHFSQ*IG*KEGAPMGQPIFVSFSKTGA PPPGQGGFQIPTCGGPPQNFQIQQGAP APGPGGGFF
1282	15183	A	1290	419	3	KNFFFLERGGFFFPFGGRAGGGF*FPPP FFFQGGKISGPPPPPKRGGPPGAPKL/R EIFLVLKKKGPPPLWPGGFLNPAPKNFA RANFFKRGGSRVGPPSGGFNLNLGGGW FFRFFFFFPPFLVFETEFRFCPPGWSA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						M
1283	15184	A	1291	397	39	WGQVWAKDWIHGLGPKTKQGCPPPLGVFGCP/SLIPPNLFFYGIPGGLKIFVHKNNPPFIKKEPANWIATFFPPGVFLFFL/CFFETRSHSVTQAGVQ*RDVLSL*PTSGFKRFSCLSLPSSR
1284	15185	A	1292	399	1	LNFFFLHRQKLCNIGSDDKVPASFSTYEPERICVFSLLFEIIFSDFDNKKIRIYK KHSRIYKDLLKFNNDKPNVKKWAKDLN RHFSKDGIOKVWHIRNC*TLAIK/EMQNTTTMR*HLMPNRMAKIRKTI
1285	15186	A	1293	412	1	ARMVSI SRPLGTPIWRSQKGNKRVSFP TRPNPLFLKNPKKCPKSRD*NKPLLKK KKKWSGPCPAQ/SCPGQNP/SPPKQL PPSPSTPPSRPSPTLAFPMAS*LAISPA HTHCCWRELSGTHLSIPCLKPLRGP
1286	15187	A	1294	229	1	FFFETESHVSTQAGVQWNCNPGFKRFSCFGLSSSWDYRYAPPRP\ANF*FLVETGFYYVAQAGLKLSPGDLPALAS
1287	15188	A	1295	401	2	STLPVH*KWTTKAWMTAHL/ETAWFTEYFKPTVQNYCSEEEKIPFKILVLIDNAPGH PQALMGMNKEMS VVFIPIV/NTTSILQP\ADQGVIFTLKSYCIRNLPQHQCPTPAWVTQLDSVSKK*INIFQPGMVAHACN
1288	15189	A	1296	1	336	KKTPRRKTHKEHHNGEK\LRAPFLRSGIKQ/GCAF*P/YILNIVVA/VLAKEYGKEIKASFRKEELKCLFIDMIIFVEIPENS PQKL\IN*FSKVAG**VSTQNSVAELFF FFFF
1289	15190	A	1297	3	384	HTNMQKVLV/VKTEDQPSHNIPLNQILI QNKSLTLFNSIKAERSEAA*EKCDSDRGWFMRFKKKK/RISITKMQGEAASAVVQ AGTSYPKDLAK/DEGSYTKQIILNVNET VLY*KMI/PTEDFVVRKDKSM
1290	15191	A	1298	3	395	SRSVTRAGVQWHDLSLQSPPPGFKQFC LSLLRSDYRLSPPHQMGGIFL/VFLF FFFPGKGVFLGGPQAGGKGNL*WNPP PRGLGEFFGLNPPRGWGFQ/HPPHPQL F/CCFFRGKGSPPRAGRAENP
1291	15192	A	1299	260	4	GFIVSSAVFPLKCLLDILVSSSVLLYC LWNFKIQKSRFRYNLSPLVSSFKNSH*N SNI/WPGAVAHACNPSTLGGRGGRITRS GD
1292	15193	A	1300	91	219	LSRLSAWDY*HVPPTHVFFVEMGFHRVQ ASLELLS*GDPPALA
1293	15194	A	1301	277	441	TVEF*GVQSMKEET\ELCLFEDDMSVYE ENLKELTKN\LLK*ISNYSKVAGYKVN I*KAI AVLHTSNEQ*NFEIGNTILF/TIS TPXYLGINLTXYAQGLYENYSNLMNEI KELNTW/RDILCS
1294	15195	A	1302	256	482	YNVYFKICIGPGTVAHACNPSTLG\G*G GRI/TLRSGVRDQQVQHG
1295	15196	A	1303	182	460	VGREFLDMTGKEFTYKFLYIRKIN*SSS KLKTFVLPKTLRLD*KAKLQTRKYL*I TYPVKGLVSRCLKKLSKLSKKTQQLKK WAKDMNRHF
1296	15197	A	1304	1	468	FKQFSSLSLSSWDYRHPTGNFCELAPY KQNA PCSNVFTDNVPVIST*QGLQALS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond- ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PNVNEQSPWRETKKTAVDLCGVIWKPCQ VFLRKKPKTKTGQ/HEQQIFGF/CFFSE TESHSVTQAGVQ*HHLGSL*PLPPFFKR NSTTRTSDYDGP/HVPP/HPA
1297	15198	A	1305	880	1026	EEHGAGLSGSQDAAGGVPA*GGWAQLW VTRRASLFLDKTHWPVDEQNLSLYTIE ATAYGLMQLELGRYNETHAIAKWLLEK QELGGGFRSTQ/SDGDPRETTVVALEAL TRFREAVPFKGIQDLHVQIRAPKTALNV NWIYDHSNAYQORSKFLAQDDLEIKAS GNGRGTISILTMVHKS PESREDNCNLYH LNATLHSALEENKKGGETFLRMETRFQ NN*EATMTIMEVSLTGFYPNQDDLKQL TSDVERYAFQYKTKTSTSDSTVVLYLEK LSHEKNTLGFVRHMLQAEFLQALVT IYDYYEPSRRCSTFYNLPTQSSSL
1298	15199	A	1306	3	726	RTDHYQFQSLKHCLTGGREALNPDVREKW KRQTGVELYEGYQGSSETVVTYKNWLSYE DANTYIVK*KTL*TKKEG\IICANPKG MKIKSVSMVKESLPYYVHIVDDGENVLP PVEERNVTVRIKPTQLLCILNCLDKCE KTAVS*QGDFYITGDRARMDKGYFWFM GRNDDVINSSSYRIGPVEESALVEHTA VLESTVVSPPYIMGEVGKAYIVLTRAY SSHDT*ALTRVLQEHVIK
1299	15200	A	1307	230	486	NAICPNSGSKSLGLGSCSVTQTGVRW*D HSSLQPRPPGLK\YPPTSAS*VA\GPQA GVQWHGLDSLQTPPPG/FKRFSCLSLPS SWDY
1300	15201	A	1308	463	440	SAIPVHT*RRRKQTSINADMEKV*VWVI EDQISHNIPLNKSLIQKALTFLNGMKA KRSEEAGEGKFEASRGQVMKFKERSHLY NVKVQGEAAGADGEAAASYPEDLAQSTD EGGYTKQQNFSIDV/TFYWKMSRIF IAEPHHTD*GDNGSVP
1301	15202	A	1309	463	59	EVISTLTMMGKILKTKNAK/CWQDCGTK RTFIHCWNGYKLVQPLWKR\YTFPYNL AIPLIGIYP*/NMKIYSHKRTCTKMF/I NSLPIISKWNKHLRYTFTREWIK/M*YS HTKDYYSIAIKRNKLDMFNSNMHESQKHVG
1302	15203	A	1310	438	29	PGGKGGGGPTPAPFPFPPPPKVGVPW* GFPRPFLFKPPPPNKAFFGAPHFF/SL PPFPRVFKKTFPTKKKFPFPGGGGKKK PPPLQGGKMGSAKLFPSGGKKPWGISP QI
1303	15204	A	1311	2	310	HNQKNEFGPYVTSYVKVKEAK*IAKTRK LLEENIGVNIHDIELGSGFLAMMP/EA* AIRLKIEKLDIFIKNKSCASKDTINKVK KTGRPGMVAHAYNPSTLGG
1304	15205	A	1312	19	348	RGQQDVLPG*RGQQDVLPGRGTYSEYGL IFSARNPSMEV*SVNHRPFHHGVP/HQ NCSDSGSYFISKRCGN/WVSACGIH*CC LVPCLPKAADLGE*WNGDFSLSGKEKKK EFLIMTFSQ
1305	15206	A	1313	2	424	ENKLTNHGKTGNGGAQSQ/PPECEPRTH LQRLGEGRGGEPPWQGGPD\PPSNSSL KNPQAGVPPFSSSLKGVKRDERSVSDSG EQREAGTQ*TFVNGKKKKKKKKKAKKA

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1306	15207	A	1314	375	3	AYSPDSKA/FSSKSSPKSS KKRTLLIPLMNDAI/MNKILAN*IQQH IKRIIHNDQVQFVPGMQGWENIQKNINV IPYY*LFY*CYINRIKQDTLIIISIDTE KNDKIQNSFIVKTLRK\IKENFLTILIKR IY*KSSNNKKNID
1307	15208	A	1315	403	3	LEGVSFFFPRVASQGSILGSCNPPLPRF HHFS/CPHLLSKWGYRFPSPPA/FFFF FLKTGFFFFCKNFALCSFP*KQASPPPP LTVFFFS/HHPFFFFFFFLFFLRWSFA LVAQAGVQWHDLGSLQPPSLGFKRF
1308	15209	A	1316	38	427	PEXPAPTRPRPSAQWPPRLRSEEPRLP AAPSEK*GASPPGSHPIWEVRSVSARQ PPRPGGRWGVNPPPGQPPRPGGGRCLC PAAPTGK*GAPLPGQPPRPGGRWGGYPP ARSAASYGR*GAPLSSRP
1309	15210	A	1317	43	399	LTFFFFLGEGARPPPPGWGPGAHQGITA PLFWGGQGNPPP*PPGEGEPS/QGPPPP GGNVFFWKKKGSPPAPGGPWTGGPKGLP RPPPPKGCE*RGNPPPTPKFLGFTTFQ KKGKNSGP
1310	15211	A	1318	437	54	MNEQKGERGLSSSLGLPAR*D*GKGNVKE GR/EGVTFSPREPKEESLRWSTPQKEIV GVINHPRGQRVDRQAGSGCEGFALRAQ TGGPPA*EITRAGEQKAGGSKGAQTLQ RETRPPRGQRGGGRSASL
1311	15212	A	1319	351	133	GGGWAEEVPLTSQVGRSGRGTPLQPDGAA RQRPPPPRRGSWAEAPTSQTGRPGRGA PHLPDDGRPRGRDAPHL
1312	15213	A	1320	474	11	KINSFSQKKKKKQCSSIRKLA*/DQNR HFIEETQIPNKHMKRSSIS/LAIKEMQ IQITKSYCIIIRLCK*LIKNSDSIKCWQ GCREI/GSLIHCWRKLMNSTALQMVK
1313	15214	A	1321	485	33	CPASRVAGITGAHHHAWLI FVFLVEMGF HHVGQAGLE/LPVSNGNGGHL/RLCLLF GYCGQCCYKPS*RRFFCVSFIIRA*K*G FVCLFV*MVSCCVTRLEFVVTHRCNHSK LQP*IPGLKCS\PASGF*VARTTGLYHG VWHVSNSTALTSLGLO
1314	15215	A	1322	451	145	THPFGRPRGGVFKVRKLNPPWLKKNPL FIKKKKKKPGGGGPFITPSEG*/GKK KGFNPEKEASNPKFAPSNPQTGLGKKK KPPSLKKKKKKKVYSLIF
1315	15216	A	1323	470	151	GKAEERHDPGRACSEPRSCHWTPAWAT \SETPFKKKKKKLCISWPGTVESCFVR T**I*LRQVLYLFLFQPKNVIYLFICL HDKANMVMFLDFKYFCFLFLD
1316	15217	A	1324	64	367	TWEGEGSWLTSQDRTTAPLHPSLDNRVK LRLKKKKS VGFLSPSILLAKNQIKKPAP FTMA/SK/RIKYLGINLT KDVKDLYNEN Y*TLMKNLKGGAMCSFTSL
1317	15218	A	1325	193	381	AQLFKTSMGNSETLSLQKKKKEKS*LT PSSWDYRHPPRPVNF*FLGEMGFRRV AQAGLEL
1318	15219	A	1326	410	7	GFFFPY*LPK/SLRC*GKDFYNQSGGQA RWLPFVIPPPEAQAGGSP*GRSLRPTW PAWSNPSFLKKPTPLFLKFS*GRRIALT PKAKVSVNWDSPPALQPGGPSKTFFPKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKLRIIGPGVVAHACNPNTLGD
1319	15220	A	1327	295	3	VCHFGIYFCVCSLYFTCLYFPFLIFL*V TLTFLVIFYDFTVLFIISL*YFNDCSRD CNIHM*LLSLPVLIFHCCC\FVFRDRVS LCHPGWSALASSLL
1320	15221	A	1328	2	392	RQASRPP*SAPPAPAGKEGSGE*PPSPK /PPPPPPKVVPPRGFPFPPAGPPPPPP KKSPPPKTNPPPPPP/IKPPPPPPPPPP PPFFSPPPF
1321	15222	A	1329	378	7	TDDLILKFI*ERYKPNQF*KRTKLKDSL PDFENYKAKVVKTRW**YKE\KHIDQW NRIESR*QIFNIASII/HIEKEYLCNKW CYRTTKMEENMNLKPLP*TIKFNSK*I TDLNIKTITIWKL
1322	15223	A	1330	403	2	VETGFRHVQAGLELLTSGDLPTLASQC WDYKHEPLRLGELRSLTAAWAQDPVS PNK*IKIK*I/P*SEQFSGI*SIHNVVQ NRHFYPDPTHFHHSKVKPLTHYVVSPTS FLSPTPGNHQCLLSVSMDFSIL
1323	15224	A	1331	1	389	KMKSAIDLEKIFTKHISDKGLGYGLYK ELL*FN/R/RCQTTQLKMGER*TNSTMT GMSFEWVSKHMKRCSAFPSLVTREMQ VH/TTSFLVERYHYTPTRVAVIKQSDQV \W*ECGIRTLIHC*WECKMIAT
1324	15225	A	1332	392	3	NNFMPSA/PPPPPPFFFGGPRVFSPPP FFKPPPPPPFFGPGQKKIFSPPPPLKFF FFLRPPPPPPPPPPPPPPQKNLKGFF F*PRPEKKKKPPPGGVFFSLFFLRCSV ALSPRLCSGAISAHCNLCI
1325	15226	A	1333	394	1	SQVVGPTAIHYCAWLVFKEFLGHFSKTTI SAPLLK*TSRAETSKSFS\CPRMERA EGRMFLGKSLKQIVLLF/LISGSCVT AS*FL/CFQTESHSVAQARVQ*HDLGS LQPLSSRLKRFSCFSLPSRTRG
1326	15227	A	1334	416	1	LTLLPKPTPYNTRKENYRPIISLINIDAK IL/NILAGKIPQYIKVHN\NMGLTPEMQ GLFNI*K/RKSVNVI CHINRKEEKKILL INA*IVFDKNPTMI*KNSWQ\GEYKEIY SNILLNGKMLKACHL\KTRIN*GCQLSP DAW
1327	15228	A	1335	391	57	WQVVCNWDKNLYQKEKQDNVREK/WAT DLIINFHEEMQSVNNLQKDTHPHSLVI REMQIKTTSY/HLLAKILNSDNSSYW*G CGGMGTL*CCWVVSKEIHALWEIVWFIY SK
1328	15229	A	1336	285	2	IFFFPWRGEII*HLSLINKSRQNERAH \KDNDFSQIISKLKLMYKILNQTTI KYMFPKKHRTSIKIEHILGSKGSLNNC QRISVLQTRV
1329	15230	A	1337	34	391	AKIASLYSSLGNRANSVSKQNKTKNQ LKN/IKTAGGLGVVAHSCSPSTLGGH\ DPGV*GCREL*WCRCTPAWASG\ETLSQ K*INKGKERKKMKNCWWMNSLIQLTS FSFTKTDWSS
1330	15231	A	1338	292	1	GGGISKTPGGEGAINPKKPPALPPGGKK EAFSPQKKKGERA*RDISSEDI*MAN KHKSCPPLLMIREMQIKSTMRYRFIPI RME\ILKKQKNS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1331	15232	A	1339	369	16	DPWQNEQLSRVTCGPERRASMFRT*YK VIIAALMAYSVGPRAVSCIRALWTTYG\ IMDNYKRHERRFLKPL*WPGMVAHACNP STLGGHGRHERVGRVRSIPDCVVRVAAG VKASI
1332	15233	A	1340	394	1	TQSGVQRHDAGSLQPQPPRLKQSPHPSL PSQDHRRVPPCPARPCSSHDSYVLREG PCGRW/HESRGRVFLVLFPS***LSLMRS GGFKKGFFCTSSL/SCLPST*DVTC SLPSAMNVGFLQPHIFMHGF
1333	15234	A	1341	400	161	KIGENLPCESTKRPWKIDKIQFWPPGKV F*/SPPPPKKILFFPPPPSGPFF/PPLP PLPKSFFPPKPNPNLPPSGFDIPPP
1334	15235	A	1342	377	3	NRHFFKAETLKASKHLKRHLPLLVIREV QIKTNTNICHNIATRLAKM*KADNTKCWE SCEPVLTFY\C*WEYKLVQPL*KMVWQK PKVCVPYYLAILLQHIPEGTCAS/CY* DIHKRLLTAMLFAM
1335	15236	A	1343	170	369	RCNENKITKEVYFGEIFVRLDNKEKNTS FFYFYFLFY/CWR*GLALLPRLVLNS*A QVVLLPWPPKML
1336	15237	A	1344	385	2	SDLRRSTHGLPKCWDYRC/RATVPGR LFIPLMVSLKHKSF*RPYILFLLSSL MLLVSYLRNH*LIQGHKDLLPMFSSKSF MILVLTSSILSLFLCFVFFVLRQGL/N SVTQAGVQRHNGSLQPQP
1337	15238	A	1345	1	281	HMATKHKMRC*/SEMCTLKPQLNTTTPD HQNG*N*K*LVNFKGWQ*FGAVWNLIHC W*CKLAQPFWKIDLSIKAKISMSYSHV VRKIFKLKNK
1338	15239	A	1346	176	1	SVIWNKEP*IAKILKKKTIVGGLTVP DFKTYKAMVI/KTV*SWLKDRQRNQWY RED
1339	15240	A	1347	398	2	PRPPGPVRRRCPS/LTATSGSSSPSSP FYLGYPQGFPLPAVLNRGPGILFWGPHK KNITLPARGR*IGSS*TAPPPFF/SLFS FLLFSFLLFDTGSYSVPQAQVWFNHS LKPQPPGLKLSSQLLRLGW
1340	15241	A	1348	9	395	GLQNECVGFLVSGFFFFFPKGLGV PPKKK/RGPNPNPGVGEFLATGPFWWTG PLKKNPAPPRALFWGPPPPPPWGG*NPP PFLARGSPFFKKFFGGPDFFFYRTNPRG PNKRGPPWFLKWGNPPPK
1341	15242	A	1349	119	1	ENVERNM/WPGMMAHTCNTSTLGGQGEW ITRSGV*DQPGQ
1342	15243	A	1350	58	396	GIRVGKVCFTIFFFGFFFFFGKGVSLPP GRETGGPPL\LIKEPPFGVKGIFLPPPP GGG\CGPPPPPRVIFVF*GKGFP*GP GGF*PPAPKGSAPPPPLWKWGNRIFG GR
1343	15244	A	1351	396	1	GPTKGPGPFLDGQGFPPPTLKQNFPPFA LFFPPLGKRLILGGF\PKPGGLQPPT* KPLRFKPGGESDCFPKFF*GRIVCFQQS LCFFPPPKKKTAFGKRFKKTLFFFF SDGVSLCHPGWSTVAQCRL
1344	15245	A	1352	1	250	RRL*SQLGRLRRQNGVNLGSGACSE RS\CSERRSRHCTPAWATKRDSVSKTKCR RHQVGS�TVRLRPGYWIRHCGCHWWP

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1345	15246	A	1353	249	3	CGATLCPPKYMKITPSFFVEIDN/AILKFIWKFPGPRIAKTTLK*KQG*RTHTFHFHNILQKAIIVKTMWY*YKHROSPPGRVAH
1346	15247	A	1354	15	416	LLTSSSLKITIHTNKGRT*SFIRENIIIFIATNLLGLLPH*FTPTTQLFINLMAIPL*AGAVIIGFRSKIKNALAHSLPQGTPPTPLIPILVIIETISLLIQPIALA\ARLTANITAGHLLMPLIGSATLTI
1347	15248	A	1355	2	416	IKYLNVRPETLKL*/ENIE*NPHNIGLGSDFFNLTSNSQGIKEKIDESDYFKLKSCTESDITTNRIRQLKNERKCLQITCDKGLIF*KKLK*LY/KQKTNH*K/WSKRLKYFSRKDIHMAKRY/MKKCSSTSIIRENKPK
1348	15249	A	1356	426	85	HARLVLFVF/LFETAYLSVAQA/GGAMAQSAHFSLELPGSSDSTATSTSQVCYHRNT/RLLF*IFCGYG/RLLCGLWSRTPRLKQSSHLSPKCDYRWEPLYARPYLSCFPENARLG
1349	15250	A	1357	2	301	GGLLEVKVQDQLGQHNTPSL/IKIYILPIYTQKN*KNLTRHGMCL*SOLLARLR*ED*SSPGI*GCREP*WRHWPVWTIQQDSKSRGEKKQVIFTHYT
1350	15251	A	1358	2	389	FLHVQSGGCELPSTVDLPASASQNAGITGVSHRSWLKFSLLDVPSP/LTP/VSSAVPLISYLATGWRQAAIAASPIFLHQLARPAQPAREAAADS*LPADSAFFPKQWTC**MFTGALPKKKKKPCFVAKK
1351	15252	A	1359	309	3	KWDHILKLNFTAK*TINKVQRQPMEW*K/IFVNYPVDKGLITRIYKELQLYRKKKSNLIFKMSKS\SLAIREMQIKITMR YHLTPVRILVYVLPKRARS
1352	15253	A	1360	300	2	KRAFH*KKMPSRFTTAREGKSMPCFK/ASGWATPVIPAL*EAKVGESLEPRSSRPAWATRRDSCLF*K**INK*KLTLGLGANAAGNLTLKMLICHKS
1353	15254	A	1361	396	60	HKVTRKSDGMLCHSGFCSTINQLAFCCLFQPGGPRGTPLP/PYKPPQKTPKKTGPGGGGLYSPPFGGGGRGNPPFGAQGF*PPSPPPPPPPGGRKKIFLPKKKKKSLFF
1354	15255	A	1362	37	385	ALFSFSFFFFGFWGKKIFFFGQGGGRAGGHSNLPEPPPPGGGAPRPNLSSGGGE*RGPPIS\GEIFGLKKTGVPPGGRGWFKPPAPKEPPPPAPPRGGISGQDPLPPPVLPWGKKN
1355	15256	A	1363	12	421	EPWEPQTLGICTHLQTLFHDYQVLMKMLVTVRYHLTPVKMPFIRKTFDTAGM*KKKGCYQGSKKGGMLI/HPWGL*MSIVKKKTWGTFFKKIQKELPWPDAIPWLGMPKEGNSVFQRMGLPSVIGTLFPPIAG
1356	15257	A	1364	278	3	CCTGEKLETFLLR*ATRCQCFHLFDNVM EVLANAVRYEKEIKGIQNGKKVKT\SLFPGDEIV/YAENPHKS*PKNSL/KLKSDCSKVNIQKPIAF
1357	15258	A	1365	265	330	WPGAXAHACNPSTLGGRGERTIT
1358	15259	A	1366	379	1	KRKLMYCWWECK*IQPGWKTVWHFLKKLKLELPYDSVILLLYTFLKES/PVYARDI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CTPKFIATLFI A\RCSLTHD*TKRMWY LSIMEYYSAIKNE/YLPFATTQMNLEDN IFSEESQA*KHGVFIIP
1359	15260	A	1367	1	376	HLPGAESQPPPV/DNSWDRPAGRTQLLW TPA/DPHSYG*GGAGPHPCPSQPGCCAP VQSCS*APSEAQSLGAADS\GPAATLPA RQLITKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKDDSGKG
1360	15261	A	1368	2	409	EEAMPKAKMG*RFPAPNSQILNAKIKLL KEIKSVTPVNI*MIRK*NSLIADMKEV* VIWIEDQTSNIPLSQSQIQSKVRMLFS SMKAERREEASEEKLVS/RGWKSAGFM RFKERSNLHNIKVGGEATSTDGEGA
1361	15262	A	1369	220	416	POPLFDWQMYTTYLHNDILVNDGRLSPG GQCSELSLCHCTPI*MT\SETLSQKKK KKMQQARGLS
1362	15263	A	1370	310	289	AFR*AFHSGSK**H*EKKVN/WNFTKT *NFTAKDIIKRMKRQPTKWEVIFANHI YLTGILIS\KIYKELRTTQ*PETQSLK
1363	15264	A	1371	3	322	HASERTHRRGKSTETTTPAWATERGSVS KQRTNKKTNK/RNTGSSIHNMVSDFEKQ VTQTF*SSMQMSNKPLKRYLTSVIIEMN IKPEYHFTPIRMAI IKKTDNTKC
1364	15265	A	1372	3	332	GKEVS*EDIMMLHVYAPNNRASKHMKQN LIEMQGEI/DE/HPVIGDFS/TPLSII DRSGQKI IKDIV/ELE/STVKQLDLI/D IYRTLILKRVYVF\FTSLSKTFATINC ILGHKV
1365	15266	A	1373	381	2	CSVAQAGVKWCNHSLSQP*TPGVK*SSC FSLPSHSDYRHE\PALFFKPFVQMGST ML*FS*ESCIKGRQPCSYTYLHSPPIF SSLFPSLAPESIKRQEPSFFPEMESCSV TQAGVQWRHLSSLQA
1366	15267	A	1374	1	385	YKKGINAKIFNKI**V\ESAISHDQVGI VLVLQGFLSI/RNKSISVTHVNRKLN/ HMLI*IDAFAFDKIQSSHGKIGIKGN FFDLLKSIYRKPMANVILNSEKMKCLPC KC\KTSQGCQLSPLFFLFFF
1367	15268	A	1375	1	357	CSGVISPHCGLKFGLGSNDLPALASRVAG IIGMTP\HAQLIKNFCCCWWR*CLAFGG *RFKTMCRPIVK*NKSINK*NRTVCMG CGDS/RQLGLRLWSPGLRNQGCSEP* WHHCTSACL
1368	15269	A	1376	1	375	HRPKFKSISLLEENMGESFHDGL/GSD LLDMAPIVQSIRDKTSDFLEIKKSCSSK GTV*IMKKQATDWE/RTFVKHTSNKGS MYEEL*NL*KL*NNPI*KWAREFSRHL/ EDTQMATKHM/KCSTAL
1369	15270	A	1377	260	400	KRGLGKTVPWPVKKNKGFFFPKTTSK GRKTLMVNPE*PKYYSVKKKKKKGGGL PFCKIFFPNLTIQTTFFWPKTNPLTK KRKKPPKKTPTFWGHFFFERGTKKTQGG KKNPFKKGGWEKLFLLGQKKKMAFFFF QKPPQR/WRKTLMVNPEP*NLLKKNM
1370	15271	A	1378	403	1	TGVSQALSLFFFKYFKPRMVEFLVEPSR *KGPSVYGLQIFFSIPKVPFPFPPFWAF/ SLV*SSPPCLSLHLPAFGVLPKRSRPR PMLQSFSPMFFARIG*FQILLNFQSL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion S*FFFFFGDRVSLCRPGWSAVAP
1371	15272	A	1379	195	381	AERYQTSRSTADRISCLPT*SAET/VFP DSGKKTGGNNNNNNNNNTNNKNNNNK ISLSLKP
1372	15273	A	1380	361	39	PPVKETAKDVNRFPKQPMNST*SDA* VDEVVCL*FQLIGRLK*SRRIA*AQBPK AS/HGQHSETLSLKNYLKKRFTLLFL REMQIKTTTRYHFTPIRMAK/SHHTKC *QGLAMLPRALNSWAQAILLHFSLP SWNYRHTTSSTQASLHVLVFIGCLGNRL LTSFAVSFTGG
1373	15274	A	1381	400	90	LPSSWDYRCAPPLLANFCVF/M*SQGFT RLVNS*PQDPPTSASQSAGITGVSHA WPAFFIMWFSSSYR/TMH**QHPV*K LHICPN**KS\LSCPQVPTIIV
1374	15275	A	1382	1	431	DNIPKKSAYYYWITLFKKG*DNVEDRAY SGTLAISIC/BEINHLVCSLSDEEQST AQTANTIDITVGLAYTILAKSKLNKL CT**MPKLSYPLF*KIL*KNKTKNIV\P NQLQIKAEPLPVEILHNCDDPETWLG V AHTYN
1375	15276	A	1383	2	432	ELSDVSEFFFITTPLSGVL*QNWGIAAF IPIELRSPTEVTFSDVGNPFEISLQS PTHFSDHQWHVVRERNMKEAL/QVDQ LTPNTQPAPADGHVLLQLNSHLFVG GTA TTQRGFLGCTRAL/RMNGMTLDLE RAQ VTPEVQ
1376	15277	A	1384	1	421	NPEALASQRAGIADICHCAWPLRLSKP QFSNL*SKKPALGDV*SSNIL*YIYIFF EMESRSVTQAGVQRHDLGSLQP\LPPKL SLLPPKLSLLPPK\SASCLRLAGSWNYM HVPFRPANFCIFSGDGVSPCWPGRT TP G
1377	15278	A	1385	2	416	IFSVDETALYWKMPSPRTWYL/RKEKSM SGFRDSEERLTLFL\GLNAPGELELEIL LI*HPEILGPLNYVKFTLSVY*WINEA LITAHMFTAWLTECFKPSVETCYLGEEM PFNILLIGNAPGYPRAPMEIQEINIIV
1378	15279	A	1386	170	1	DGVFLIFGGQNEKLNKNKDG/DLTKLPR LA*NSWARQSSCLAFSKCDYQREPPCL A
1379	15280	A	1387	47	418	FWGFFFFFLKKKKAALGPWTPPPPGQGG PPPPPPRPGKGGPNPPRQTIYGFWGQR GPPPGGGGEPGPPPPGEP\PAGPPQTGG PQNWPPAPGP*KGF*GASKGAP*KGVDP GGERSQVENRGA
1380	15281	A	1388	58	503	RPTRPGNYIMIKEFIFQKDRTI*NVYAP KNIALKYIKQLINLKGKRDRLTLTVAN ISTCP*VTDITSR*KICKGTEELF*QPA \DLIDIYRTLYPTAA*YTFSSAYNYSK IGNSIGHKTFSN/CKRNDNIQWLFSDHN GIK*BINIII
1381	15282	A	1389	2	401	LVSQVVNSKNRILKKIKNSTPVHT/RQM IRKQNNLIADMETVLVWVIEDQTSINI\ SQSMTQSKALTFLNSVKAERGEEAA\EA GRGWFTFRFKERRQL*NLQVSEPPS\AD VEAVASYPEDVAKIIDKGYTKQR
1382	15283	A	1390	294	3	KIVIFDFDNDVKNCSS*KIVIFDFDNDVKN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CSSKTVIEGKVS DCKKIFSKHISDKYLI SIIYKELSNLNNNQPN*KWAKDL/NNM SSKHKIKCSISFGKMQIKTQIRNHYIPT DAW
1383	15284	A	1391	3	422	PLFKKEEGTNFPFPFPGWRFFPGGKSFS PFFPPPPPIKGGPKVSQKGRPFFFFF F*DGVS LCRPGWILFPQVTEALLRGFL ALSSLCFR LDKFFFFF*R*GHLLSRWDY RHEPPLRLIS*RTKE\KGLIMLTRVL
1384	15285	A	1392	3	400	FLYIKDIYR*YKTFQINNKLKIYFK* EKDLSKLF TKDVQMTNMHI*MGSTSLII KQM QIKTTMKHSSSLPECLHFNANITC WKRLGPAGTLILRW*ECKSVKPL/WETP *QCLIQLSMQENYH/DPATPLIG
1385	15286	A	1393	409	2	IVRHFSKEDIHSTNEHMKKGFLSLVKEV QIETTMGHHHTVRRVVIKTDIFASA\N TKC*GYGKTRTLINS/YWECKIVQPL/ WKNILAVAYKIKHTFFPPRIHLSGSQKS HFSIYSKEMKTLRQHKDIFMATLSON
1386	15287	A	1394	409	24	KSPFFFFEKGFPSPPPGGAQWGGFPPPE PPFPVVK*FSPPTFPNKWGNRPSPSW/P G*LFFPCSPGGFPLPNWFLTPPLR*SY PPGLPKRWGFKQKPMGRG*RAFFCPPKI SKKLWSGKKKKGRPLAI
1387	15288	A	1395	83	411	QRDSVSKTKQKKINNKSRDLDNRHFTKE DRWM/ANKHLKRYST*LVIREVQIKTTM RYYYISIKKSKINKPDHTNCWQCGRPG TLIYC*WE/CKMVPSLK*TFW*FLKRLN
1388	15289	A	1396	308	14	NFFFFYSWSNIIYCQKGTAFTPISDKID FN*KIISRQK*QYMLIKSINK/DITII NTYTSNNSSPKIKQTLTGLKGEIAPST IVVGVFNTLSIIK
1389	15290	A	1397	321	1	KQ*CSIEYS/FKYTR***SKL/WPGAVA HAYSPSTLGGRGGRIT*QGEFKTSLA
1390	15291	A	1398	183	48	KWPGAVNHACNPSTLGQGGRIT/TLRSG V*DQHGQHGESPSLVGRVR
1391	15292	A	1399	18	422	KAGMAILDKVDERTKNITE*/EKHFI ITKGSVREENISVLNV/WPHYRASKHMK Q/ILIELHVELGEHTIIVG/DFNISFSV LNRIDKESARRR*NI*NNINHQLNLVDI Y*KTNTTNGRTTFFPSAHKLFTIIHI
1392	15293	A	1400	28	339	YSCDHNSVQPQTPLKQSLCQPPPE*TAG ITDARHHIWPFF/LKRSFVFIAQAGTQ WRGLL*KKKKVGGFKKGSCLTLPGRGDY RRFREKILIPGRGFCNELI
1393	15294	A	1401	390	1	FGLGKHLHMTSKAQSIKEKTD*LDFLK IKNFNFSKDTIKGMKROARNGEKIFPRH QS/DDFF*WAILDTFPKEDKVMANKHIK RCLRLLL\SMRYHYH*NKKT DHTKC*R ERG\BLELLCCW*EYKMQ
1394	15295	A	1402	149	402	RFWIHLRYKRVPPLLPVITWKEKRGF VFVFVF*DRVLLCHPGWSAVPWS*LTAA STSWA\K*SSHLSPSY*DHQHASPCLC N
1395	15296	A	1403	1	403	KRKSVPELIC/APRC*APCSYRPNLPSS PGPHLDVPGPTPTSPPRPGPARGPPAA RPKEPAEPGKEERRGL\PAFPG
1396	15297	A	1404	342	3	KEDNLIDKGGSPKQIFKVN*TALY/YT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ALYSKKIPERTLIAGKEKIMPGFKASKN R/TLLLGANAAG\DFKLRPMLIDHSEL*/RPKSTLPVL*KKA*LRAHLFIALFTKH FKPTVE
1397	15298	A	1405	498	66	KNYAKSTLEPML*KWNSKALMTAHLFTAW FTK\FPMPTVETYCSEKKRP/SFKMLLL IDNAHSHPRALMEIYKEINIAFMSAKTA STLKPMQ\KVILAYKSSYLRLNI\FHKT TAALSSDSSDASGQSKFK*IWKGFTTR GRTRGSAR
1398	15299	A	1406	3	411	VSPCLGRSQTPEIK*SSPLGLPKCVDY RHEPLYLASMGLNCPISNLGQCIPP*A AWWSLLLGC\PILMLNLVQTPDLPSVLQ PRAPGPR\HPPVSAS*VAGTLGTHHYAW LSMLLGSTL*DVFPFLSPSLIPSEE
1399	15300	A	1407	361	2	IRVPQKKKIKSPGRGHKIFSF*RGPPF FFSFFFLRQKESHSVTQAREQWHDHGS LQSRLPQPK*FSH\PPPPHPPVTGTTPLF IYYYYYFLRQSL/DSVALAGVQWHDLGS LHPRVRPRV
1400	15301	A	1408	393	2	PGFNISVLKKASGGLFFSPLGKKGFFS QPFFFGSPRVFPFPFPFPFPFPFPFP L*KIFFSPPPGLKFFFKRAPFPFPFP FFFPDRVSL/CCPGWSAMVQSRFSATST LRAQAIL
1401	15302	A	1409	393	60	LNVPNPNL*SYLDKHRGMLYHILQSKF LSKTSKAQAEVTLCKWDYNKLMFCTAK KTL/IKVKR*STE*KKIFVKY/STTK/G *TYRIFNKLNNKNNTQFQNRATSRSKM AE
1402	15303	A	1410	422	2	VNDRKMDGWMNGWKEGR*TQKKKGRRK REKERSMFLGRKEGREKEREEREKESQ KERQKRGKARKEQRQEARQGG/EREK EREERERGERGERGRKSSS*TGSKVVK IILLAVKMLVHLKSLHLQKVCVFSFSS
1403	15304	A	1411	398	64	PGFFFKKIFVENFFGPHQFFFPFPKGN PL*PPQRPQ*\RPGVFPPLKKGSK KKFPPPRGTQPRWGKPLLPKRPGFF GPRVSFFCLIEIGWFFWAQVPKKKKK
1404	15305	A	1412	391	125	EPAPFFFPFPFGKRGFFP\PP*FGYPPG FSPPPFLKTPPGNFFLGPKKKKFFFPF GEKICFL*RAPPFFFPFPFPFPFPQA ICFFIE
1405	15306	A	1413	3	387	TPDLK*LTRLSPK*WDYRRATTPG\LF PFKCFASLGSISM*YHSPVCLASKLRIL FDSFSPSATAKHPLTSFAAAWLSPFA LIQPHSSSLYSSYCPVPILF/ILYF IFLRQSL/DSVAQAEVQWRD
1406	15307	A	1414	409	1	KRSGFFFF/SFPFKGGSFAKFFFLGSP VFPFPSSPP\GFFFPSPPKRGFPNP FFWGAPGFFPPLF*NPFPDFFWGPKK KKNFPFRGKFFFKGPPPLFFFPFF FFFFPFFFYKIISIKGEIGRSSVR
1407	15308	A	1415	3	385	HRPFPVVGSLSPRAAAEGVPGPPAVLAH QHHAQFLARP*LPHGAGLRTCSPCL LPPPPWAPVWPEPP*ALPPAP/AVPG PIN
1408	15309	A	1416	2	238	PGGRGCELLPRHCTPAWVT\SKTPSQK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						RKKREKPGSL*EKTLLFFCQTLVFGPKKK NGPPLLGRVWAKRKGFFHPLKN
1409	15310	A	1417	3	394	NKHLKRCSTSSVIREMQIKTTNRCHFSE *KHW/IINMCW*ECGQTELSALLIRC*\
1410	15311	A	1418	307	357	WDSEMVQPLWERKEYLKEITAESSWDPA IPLLDI\YPKRNEASC
1411	15312	A	1419	341	3	LETRKTAETIKRRAGFEK*NLETNKNGN TISQNLRDVAKEVRREKFIAMNA*\SKK KEKP*INNLMLSLKELEKDEQTKPKVRR KKKILNIRAEIIRD*KNSGKD*KKSWF
1412	15313	A	1420	405	1	IFVFLVGRGFPPLTRMVLIFWPHDFPPL PP*VIEGLFH/LPAFRPGAFLRKMVPPY *KNKIPPRKNTFFFLKPPPPFF*DR VLLCHPGWRAVQSWLATASTSQAPAIL PPR
1413	15314	A	1421	1	399	WGELVPSSGRVHELFSALRSERDTSV CSCGGQCHCPGAIPGAALKAACRGDPAS RVGVBTGSTMGNNGFFSFFIFKPYFFRD RVLPCHA\AMAQS*LTAASTS*\VKSSF CLSLRSSWDYRCVSPHLANFKTF
1414	15315	A	1422	168	414	QPTLLTELGLRPVPPHPTMNLILY**IN TILHYSYKNYFLFLRLRQGLQLQAGVQ WQNHGSLQL*TPGVSLSSWDHPNPNANF FIIFFLERQGLTLLPRQVLNS*AQ/CNT PASAFQSAGIIGMSHCSEWPKN
1415	15316	A	1423	369	1	EWREKAGESLEPG\GGGCSLRLCHCTP AWVTEQDSSYKKKKKTPGGGKGVF/C*K LGGGINF*KRVFCFGKGPTKKKTGGRA
1416	15317	A	1424	403	1	EHFCKSQDRDSVPKKKYIYIYPMVSFMP INLTNWKFLERQKLS*QIEEAIENLNS IY*/PNESEFII*SLPITKAPGPYGFTE FYYSFKGEAMQILHKLQKRG*RHSFSN VIKTLKSKPEK
1417	15318	A	1425	401	3	KNTEHSKRYSIQORYCGFSSREFFHFLV HMKVMFPLFKCAIALCLKQVYTVFFETE SCSVTR*/EVQQQDHGSGQPQPPRFQ\H PPTSASQIAETTAILENFRKICIFLRLQ SL/HSATQA*VQWRNHGSPQAPPPG
1418	15319	A	1426	386	27	FFFFFKNFPFFQVEGKGRKL*QFPF PG\LKNFSAPPLPGGN*R\RPPFARLF FFFL*KRGFSPLNQGGLGSPFFSPP\R APKNVGFQGITPPPGNFFFFFFFSEAES RSVTOAGVQWREPGS\QPLPPGF
1419	15320	A	1427	398	2	CRINGVLILC*CECKMAQTL*I*FGNPL QKLDLTCDSTIPLLGIYPRDMKTYVH\ KKTCT*MFTAALLIITKSWEKLLRPSEG EWINSRHPYDRIVLSNYETHNVNKIORH YAEAKTV
1420	15321	A	1428	401	70	GLQVHATTKFFKFFVETGSCYIAQAGLE LLVSSNPPG/SSPPKCWDYRCETRRWPF LFKFSLPFVF*LNHLFCLHLLPLFILK LNLPCFMYLFIIPALYSLSLALFRND CDLSPHLEVKKYFSKKDRL
1421	15322	A	1429	388	131	HHAQLRCFFNSFVEVGVSLLCCPGWSQTP GLKRSSHNLNFSKCWDYKR/AAITLPSFF *IALF*ENPPNCHSLPTPLSPPKLAALG NSCLHPWLPQPPVKGLSDSFVCMHPGS
						RGGGCLQRH\RGFKQENWFNPGGRGSS*

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PRSMYCPPAWGAQGGSLSQKKKKKKKKS KNYQKILSTQKTQKSRVFIWVKHCTRH CBK
1422	15323	A	1430	184	413	VSFLFDYFLFF*RW/RSHSVTQAAVQ* CDCGSLQPPILFYFLRQSL/NSVAQAG/ VGSQPLPPGFKQFSCLSLLSIWD
1423	15324	A	1431	76	533	SCKRTTGRQFPDLPTRPPTRPQGFALVA HAGG*WRDLRSLQPPPGFKRFSCLSSV LWCTKAFNDFQEIYSFSS*I*GFDSFE VNFFLEMGVSL\FARAGLKLGSGLP ASASE/SGGIIGVCHWAQLL
1424	15325	A	1432	373	29	RQGFPPMGRVVLDSLKKKKFQIPNSKIF PGGGAPLVIPPSREGEAGKFF*P\GGKG AIKQNYC/HCPPTWGKEGNFVSKKKKKK EKKMHQK*RCVKDQQT*MLLFFSLKSI YYFK
1425	15326	A	1433	389	73	TDCPAIGRNHRDPVRPLLSPPHRKI/YA NLYYYIIVRIITLTIQSTDL*ISPVLV LTRVCVCVCVCVCVCIILPS/CYPVCRF MYPTTVKQVQNISIGQEKQKTKT
1426	15327	A	1434	402	39	QAGLQLLASSDLPALASQAGITGVSHC ASPSISL*APLGLDTFSDPFCFNDLDSF EEHWSGML/SECP*GTI*DLSEFS*VYW GYGFLEDHRGKVPFFITSYQSYTPPTQL IIADVKFEQLV
1427	15328	A	1435	105	387	EFKSVAGYKINTYKSIVILYNSNE*PEN \KKIIPFIIASKRIKYLKI/QFAKAVQD FYAENYKTW*RIIKEDLNK*KNVLC*WI GRL/NI/LKMLLP
1428	15329	A	1436	242	2	FGGGFFWVGT*PNKMGPPQIKNLF/TR PPENF*KPF/LPFIAPFSLGFLGVPPFF *DIVSLCCPGWSA*AQSLAAALTSPG
1429	15330	A	1437	411	0	LLFVAQECCLKWFSALGGPGVPCS\LPAN QQPSVWVP*QS\EHVTVLQRFLWFLG PAYGQIWEVPVSTLK/PPPGFK*FS*V SLLSAWDCRCTP/PTDPAFNCIFSRDAV
1430	15331	A	1438	41	412	FFCTD*GSLCCSSWTQTSGLKRSEHLSF PNCWNYGH/RASVLGLIFFFFLRKKT/C P*KKFL*NEDLLCCQLGLELLAPRDS LGPQSVGTANVT*PRPW/LLFL*TONYLN SSRVRFSPAPLKYEK
1431	15332	A	1439	1	406	HAYNIV\NPSFVSLTGALSSLLMTYGLT MGCHFLSITLLILGLLTNTLT*YH*WRD VTRESTYQGHHTPPGQ*GPRYGILFIT SQVIFFTTRFF*AFYHSSLSPTPQLRRHW PPTGITPLNPLEVPLLNTCVLLR
1432	15333	A	1440	3	422	MEKVSVVWIDQTSNIPLSQSLIONSAL SLFSSMKTE*GEEAAEKFASRAWLMR /FEERCHHNKVGQ\EAASGDREATGSY PDDLAKIIDDGYPKLHIFNIC*KPTDT DIVDETALC*KKPSTYFLFFLKQSLAL PP
1433	15334	A	1441	375	2	KVSSPRAENVILYNCPPLFFFLCQD/CH SVTQAARQWRHSSSLQP*TGL\ASQVAG TAGAHLPSQNLIGRGIRSLA/SVAQTG VQWRNIGSWQPLPVRIKGFSSLSLKSSW EYRCPPPCPD\LFIFL
1434	15335	A	1442	397	122	GQASLELPTSGDPPASASQSVRITGMSH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CARPILGSCISLFAYPFCFLKCF/CC REVILL*CSGWS*TPGLQSSGLSLPKC WDYRCEPP
1435	15336	A	1443	3	299	WEKMFAMYLSD*ATVSRPYR*LLQLNKT KYKLKLSQS/MNRHFTRGDVAMANKHTK RKSTSLVIREIKTMRYHYLLKRMAEVQK /SVKWCQECG*GGGKCG
1436	15337	A	1444	10	410	CTLFLSISPDAGGICTMLLFQNTLNF ISLALGVSDKCFNSFLIMTIVRVFYIH GKKCILYCSFGCAHTMHTLMHTIHLK QFPLRRGLTLLPRLECSGAITAHCSLDL LGSDSPP**EMFYIMV\EMFYILPPRV CTHTYAHTDAHTHTPETIFFETGSHSVA QAGVQWRNYCSLQPRPPGLRFSSYLSLP GS*NHRHVPP
1437	15338	A	1445	431	9	GPAQSLDSSVSPLGTISSTVKWRHNAYL AGLSGGI/PCDCFLGPRVWPWGSGICQWH WAVSPTLS\PTVRPPLFRETLYFT*V*V PPLETCPO*HISHCRCVINWCEDTHTPK KHLVCVHACVCVCVCVCVCVCLGRSRQS EH
1438	15339	A	1446	85	416	PGCLSLPKIWDYRCEPPRPFFHFISS QGPLTDFFLTPLEQVQISPTAKGFLKKI PFFFF**RRGVPILARVVFKS*PHDLAA SASQKFGITGVSPHVHPIFLY/CSSIQG PLTDFFLTPLEQVQISPTAKGFLKKIPP FFFLRQGLT\QWSTHLGLPKCWD*GCE P/PMPGLHCEFFKG
1439	15340	A	1447	376	3	IKSEIITETSRKPIEKIS/RAQSCFCGM VYEIDKLLARLDRKKMKTQLNNIRN*RD EINTDFTDIKRIIRENYQDYGTGFNNL DETDIFLERHQLPKLTQBEKDNLNSPIT IKDIBIIV*NLSTG
1440	15341	A	1448	2	192	SKWIKNLNKLKP*DS*KKPEGNLHDIR FGNDFLDVTPKN/MATKGKIDN*TLPKF KMLMRIWRN
1441	15342	A	1449	411	3	VFLPPLPPFCFLNFF*GKGGFFFKIFF* KKKGVEGPQLGPPPPGPFKKFFFF*IF LKAPLFVPPTLKPLF/CPEKKKNWENN PPFFFCFFVKKTFYFFFFFLRNRVLL CHPRWSVMV*SCLAVASTSWAQAICP
1442	15343	A	1450	413	1	EA*TGWCNPGGGACHEPR*PPCPPPWA TERGFVSKKKRQEK/SRIMECFQDNLP GFFQIFSVMKNKQEGR*FWTK/VKMTKY NA*NVNGS*YWKRENEECYDVVKLF QSILS*YVKAR*KPGCWLMAIPALW
1443	15344	A	1451	4	384	DPATPLLGTYPREMKTYVHIKTCTOMFA AVLFTVAETSKRPKCPTDE/VNKI*CTY I/MTYYSAMKRDE
1444	15345	A	1452	3	390	LPDHPGSSVSTPRGVITGRGFWLLFPW VSFFFFFLLKRISLLPNWRGGGQNL NKSPPPRGF*NFLA*PPQGRKKGPPHP PGAPGDKNP/QPFFFFGKKKIFNPPTG GEKKKPPSPFKWGGGGPN
1445	15346	A	1453	37	381	LILYINVVCVCVYIYTHOMGSHIVAE AGVQWCNLMGW*p*TPGLK*/FLLSSGD YRLTLPHLANLYIFFFFEQRG\FFFLL KLV*NSGPKATLPRVGITGLTHTPRPYR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GDLFF
1446	15347	A	1454	3	400	TEMVLHTEMVLHISVWDPDLLDRPGRGVT WLMLTAELFLYGGTEAFSSSFQV*GPCS ETVECFSD/L*A*GPP*NT*SPIYRFAS FLLAFCIYLLERSP\SVTQSGGK/WQD LTSLOPLPRLK*SSCLSLPSSWE
1447	15348	A	1455	77	398	RAEIVPLYSGLGNRVRPPSQKMYIYYEQ LHAHTFGNLAEMDKLVERYKVLXKFT*E EI\LNSPVSIIKREF\AVISLPQKETLG PDSFTGGFYIFKEELMPILQRLFW
1448	15349	A	1456	397	69	CPPGLSGLPWVA*AVPP/RRPAPPPPP AGIDAGLGDDPLQQTTHA/PPAAAGSAP AGCAAGPARGAPRGRSPRRGSGAGAAPP PWPPAAAAASSAGGSSAPCASSPAAPPT
1449	15350	A	1457	400	2	ALFFWAPKKKKNFSPPPGKKFFFKGPP PLFFFFFFFFFFFFFFFFFFFFFFFFFFFF FF*RRPIFILFYFLNQKNIPRDFFFFFF FLRDRVSFCQPGWTAMV*SQLTAA*TP GLKQSSHLSPSS*DYRWVPPC
1450	15351	A	1458	343	11	QGVHSRKYKEISKLS*KKNPTRKWAKD TNRHFTKDNIOEMKNMKDVOARCSGS* F*KN*NFKSYAL*PKCSEI/KKSVTGTN WRNSQIYDKLSTLQNN*WIFSRSLYNFE
1451	15352	A	1459	109	401	QNYRQLGQWDRIESTVIDPKYGLIFD QSAKATEWRKDS*NHQT/WWKESFTRV KALEEITKRKVNLSASISVKTDVHVIVK *LKKKKKKRGGRFKE
1452	15353	A	1460	42	424	CPAN*NSFSRDR/SLPMLPRLILNSWPQ VLL/PWPPKVMGLQ
1453	15354	A	1461	419	69	IFPLKKKKRGGVGPPLYPPLGAKRGG SP*KQNLKPPRPHKENSPPFYKKKKKG RGGAPFFPPPLGGTKKKFLPPK/IKVS FNPNLFPFPFPFGGKKKFFFKKKKKK SRNTVWF
1454	15355	A	1462	1	277	CHTNFLCMSFPPAISHHPLMPHPVSRS VAQAGV*WCDLGRG/CSELRSCHCTPAW MTERDSISQLIRKKKKLIKIKKKKNKNK SVIFLGGGS
1455	15356	A	1463	382	3	KAGGSINQNSPPPPPPGEGKKKPPPKK KKKNPFWGGPRILPHNPPPFER*R*KI FLGPKFLTPLGPKIKPLFFFFLKKKKKK RMTY/HSVAQGPLLNDTLQAG\LSKA* RSPPKSKSMGQSFHRN
1456	15357	A	1464	561	86	NDPILSLKAEKTFGKIQDSFLIVSSSL NKPGEIENLLS**KASTRONPIMNLRV\ LNVFPLRS*TRQVCLLSPLLFNIVLEIL AHIISQEKIKKI*YKEEKLPLFTSS SLFI*VKNLMEFAKKLLELINEYNKVER YKINIKNILLAKNTWTLKF
1457	15358	A	1465	3	221	RFHRVSQDGLDLTS*STRGLPKC/WD YRLEPPCPAKTCLILNGSC*VFLCYLSC FKAQERPSQNSWGAFTL
1458	15359	A	1466	2	396	WWPAWHTPGLKQTSRFLSPECDYRRE PP\PGLVKFLL/IQYRVVTHVGLGDWV QDHHPIEICLHKS*NGIVFAYNLRT SSLTLFYLRRLG/SAPQAGVQRHKL LEPLPFSFRSS\CSSLSSWDYR
1459	15360	A	1467	349	413	RLGL*PRKDITD/HVSLRKDTG/WPGAV

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						AHACNHESTMAGHRRQIPRSGV*GQPGQ
1460	15361	A	1468	403	2	LPVEWKGIGFSGFHPPLRLKKFFSPTP PKS*D/YRGGPPPPGYFFFFFLKRGFGP FGRVIFKFFPPPGVPPPPPPQNGFKGRS /HPSRALFFFFKRVFF*YPPFFFFEME PRSVPOAGVQWHDLGSLQALPPRFM
1461	15362	A	1469	423	3	IEFSFFAPSKDKGAILGPSTLPLPRFNN FFCPPPPINKDIRRGPFRPNFFFFRKR GGFPHWAGMFLSNLQEGPPPSPPQ/SV GF*GRN/HPPRAQFFFFKKFFF*CYPPF FFFEMEPRSVPOAGVQWHDLGSLQALPP RFM
1462	15363	A	1470	13	427	RTRGLVFDKTEFKPKPKIKKKKA\GPFL RGNRSILKKKATFPKNLFAPNPGPPKI KKVLSDLQKNLNPFRMGNGFTPSLLK* NKSSKQKITRDRDLTSPLDQGD*KIY KTFYPKTTETTFSSAPHGFI/S*FDHKI
1463	15364	A	1471	378	1	FVRPPFFFFSSSRPFFKVGGPLPPAPQ FFFKTPRGNPDLRG*KPPPTPVGGAGK SPPW/VPPGFPPKGGGVFFFOQGL*KIS PPGEAPP*LVWGGESPFFKKKSRPGVV AHACNLALWEAKAG
1464	15365	A	1472	412	53	SRLSFFLSSEPHGPPSLGPFATNKVAF C*/PPPPF*PSPPPKFFFF*GPKSVIYF YQR*PPTSRIFFPKGGAGPP/PPFWGFV NPKKK\LKPFSPKSPPAKPKNPEGTKL GFFKKKKKKL
1465	15366	A	1473	116	34	DWNIKPVLSNVMTGLMSMIITLLQLF LL*LFFFF/WELTFFGKGFHORVDPSPQ GSLGRGRQFFLLTKTEYHIFFLIKVENS KTEGAGLAT*IK
1466	15367	A	1474	42	428	EIIMESINRFDVITF*NFCL*CYLMSKI NRQASSW/ENV*QYVGEKILIFLIYKE CIQINKK\KLRPKIDTQVKDKQISEBGM QMANQHMIQC\QPSVLNKMQIEIAEGH HLPYQINKDSKMMVEERQ
1467	15368	A	1475	87	433	PQSSPFSDHCSVQRLFLHLVKVSTYRLQ KIRKIHKSPGNNEYFGGFFLFFSFLFFF ETGFNFVPOAGVQGD*LQPLPLGFK GFS/CPQPPRTFFFFFLRVWGGFIQKK KFLFV
1468	15369	A	1476	212	430	SLILMTSNGIHFIYFLFLLLFFFF*DR VSACHPGWRAMS*SYFT*ALTSQVK\QS YLSLSSS*NRYHTAIMP
1469	15370	A	1477	493	2	PGAAAHACNPSTLGSGGWITRSKIPEH PG\TLWNPRSY*TKMCGLEAP
1470	15371	A	1478	454	492	HRVGEBRF/CLFETESHSLTQDRVQWHD LGSLQPPPPRFKQFSWYHI*PHAW
1471	15372	A	1479	2	213	IDQERERLMEGRERDRTETDAEKDMGRE /RNRERERERLRG\RRERRRRDRMT*M PRERERENLSLYRETYRDFTEWVMDR ERQRLKRRL*AVIVPSHSSLSGSRKTP FQKK*REGERKSEFLIORDI
1472	15373	A	1480	77	453	SFGDSLTLSPRLAVQWVYLGSL*PPPE LK\YSPTSASQVIHYLLFFFFFGKKVS FCPQGGGEGPPGLEIFAPGLMPFFCL NPPKGWVWR/RPPTMPKLFVFFIKRGF SPGEPRGVSFPEPGT

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1473	15374	A	1481	398	96	KRPVVCFFSPPPKKGFPPPLIFVGPFRFF SPPPVFK/SPPPFLEFFPP*KKLFSPP PRKIIFF*KPPPPFFFFFFFFFFFFFFFFF FFFFFFFFFFFFVIFLLLS
1474	15375	A	1482	484	64	QKQOMANKYMKICSPLFVIREMQTNTTI RYDDIPTRVAKNKTNK*RSNSTKYQEC ESARP*ICYWWKYMVQPLWK/S/VWQY LLKLNI*LPYDPVILLSMYPSQIKTCI PTKTCAQMYLVTLFIITKNQKLAHSARV G
1475	15376	A	1483	2	400	YNKKGQGVAPRYDUDTAANFPKELAKII DEGGYTKQQSFNIDYALYWKKTCKSY SWR*IH/SLASKDRLT/LLVGNVVGDFK LKPVLHCSKNPRVFENYTKSTLFLVCK WNSKAWITAHFLTANVAEYFEPT
1476	15377	A	1484	459	65	GGPPPHKTIIDFFFFFFFFRGESPPPPKK KKKKKKG*DNAEDEAQS*RPPPSI*BKI MHLICALTEY**LTAEIIASNIHISTG SAYIILTEMLELSKLST*WVPKLFYPNQ LRT/RAEL*MVILNK*DQQF
1477	15378	A	1485	2	518	PPPPPPQFGLRGGAAPPPKKKG*DNAED EAQS*RPHPSI*EKIMHLICALTEY** LTAEIIANNIHISTGSAYIILTEMLELS KLST*WVPKLFYPNQLRT/RAELSMVIL NK*TSDP
1478	15379	A	1486	122	501	PRDPPALALQAGITGLKQSYFLSLLSS WDYKHKPPCAPGYLK/VFFLEN*YLALY VF**SYQGSTVLTPPSLIPRHSSPGVS VQLFQKK/DLQHGCLLTPSISGYSVTWD GVQWRDHGSL*P*PPRF
1479	15380	A	1487	491	425	IPKNDI*AEPRINKR/CAKRMVRKGF EAESTICKALRYEEIVCSNTEFVHGWL *ENRGQIMKGFGNSVEKLBHN*KFYEG* LLYRFE*LAGFIVFQQ*VSKEIVKAWP GTVAHACNPSTLGGRGWITRSGDRDHP G*HA
1480	15381	A	1488	441	17	KKTNIYDQLIFNKGAKSTKLKNSLFNK WCQDKIS/IQKMKVDPYLISNI/NLKW LKDLNVTAKTIKLLKENTGAILHDLGPC NAFLDGKPKAQTTKKQVK*TSSKFKSR CQWLIPITLWETEAGGSPELRSSKPA WPT
1481	15382	A	1489	413	1	LFWKEMVFLFWPGRVGNPGFK/GWLRLR PPPF*FSFQPFWGPVGLFPKNFY*P PGGAHGNPPPPGGKG*GPRVGGGKFN *PKFGPCPPGWATKQKPVFQKKKPKNI KNRTVKVPKVTKFIIYVPYLVGVS
1482	15383	A	1490	359	407	RHRMITFFT*IVTQNFY*KKMDIQIQ ED*RTPN/RDQHKHTPRHIIKLSNSQ/ NSKRILKTRKK*LVVY*GTHIRLSTYFW PKS
1483	15384	A	1491	397	39	RKFRGRSFAKTLFSGPGQG/PKGNPLI PEGPPPPFFWPAEDGGFFFPQGPPQG PIRGPPFLGFPVPPPEGEGPPPTGP*K PGQKRPKKRGWSPQKKGPKKTLFFFFF CQMESRSVT
1484	15385	A	1492	378	1	FGVFWFLAPRRKGGFFPSHLIWPVPGPS PPPGV/SNPGPGIKFGGPIKKIFPCPPR

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						GGKFGPFGKAPPFFFFFPDQGVCSVAQ AGVLQ*AEIVP\FPPT*ATEQDPVSKKK PTRPPTRPPTRPPTRP
1485	15386	A	1493	3	428	IKSP*PDRFIAEFYQTFKELVPILLKRF HKI/EEGTLPs*FYB/ACVTLIPKPGKD TTK
1486	15387	A	1494	3	417	ILNNARLKPFLLR*TTROGILLLSLLEN KI*VLEFLAGAISQEKEIKVIQVRNEEM SKTLFSQTT*S*GRNPFIKIPKMSVV N/NFIKVTEYKVSIIH
1487	15388	A	1495	429	4	PFCLGSKRFPFFFPNPPRGKKF*KKKKIF GPPRGGPPPLFPPLWAPKGGGPPRAGGSG PPPPKGGNPLFINPKKN/PPPPGGAIFQ SRFLGGVNPKIFLPPGGKFLTDPGFPPS LPPGGKKKKPRFQKKKKRKRKVKKKY FL
1488	15389	A	1496	3	433	FSKEDTPMVNKHMKD/CCTSLVIREVQI KTTTRYHLMPTRMAMCIYIFNYILFLK/ SKNNKC**RYREIGTLIH/AQWKYKMLQ LLW/KTIWQLRLMLNTKLSKDQE\IPLL GI*KKKKKKKKRGRFGINFTDPGVE RINFYNSAPK
1489	15390	A	1497	3	326	WPACL*AVAAVALLVPEATRLTMGNLT VCTPHSIAELLSSKG/DLWLTDNRLK YQALLLE\DLQLRTFTCLNPATF/VPBE TGEPEHDCWVWVQTKRNNKDHCLYSL
1490	15391	A	1498	345	22	KSKWLDLHGKCKTLKR*YRKPTK*\LG HGNDFLDTSNAWFI/RKIDKLDIFIINK NVCSGKVTVKRMKR*TTDRDKISSKGIS DKRLLCIKIYIKILTQQ
1491	15392	A	1499	194	432	PVVVCVCVCVYVCMCVFETQS/HVARAGM Q*HNHSSLQL*TPGLKQVSCNLSSSWD YRHTPN*FFFF/CNFYLERGGVS
1492	15393	A	1500	2	417	RD*FMRFK\EKSYSCNIKIQREASANV ETMASY*EDLAKINEGSYTK/SQIFNV DEVAL\KKMPTRTFIVRERKSIPGFKAS KDRILFLG/ANAPGNKWKPVLIYHST NPRAFKNDAKSILLVLYKLNSKAWRIAH LF
1493	15394	A	1501	414	0	SSSSSSSSSSPKWTTGALQP/LLSRTP LKDSSEESSQ*AEL*AVHLVVHFAWKE KWPDMLYTDSLAVASGLAGWSGT\WKK HDWKICDK/DWGRGMWNNLS
1494	15395	A	1502	3	125	RLGLPKC*DYR/RAATTPGLH*F*SWKE QRQ*IALGRKPVNRNNTQKYIHIYTY TH/PIPTNVYICITYTHIHTPV*YTHIY IIYLFKVLVFGFLRRSLT/SVAQAGVPW RDHSSMQPRPPYKQLTCH*LASQSARI TGGSHHTWPALILKLERTEAPVISFRTE TSK
1495	15396	A	1503	406	172	DIILDR*RQKQRLRLRQKQRETETE/RR DRGRERQYRQQRQVQRGRQRQLRHR Q*QRQIDRLRQQR/RAERDRGRGRDR GRDRGRDRERQRLRQQR*RRQRHRQR /REDRQRQRQRDRGRDRRETRDGLDR G*DRGIDRGRCSDRGGRDRDGLDIGSDR DR
1496	15397	A	1504	3	420	ITGVSHRAWLPS*FLKFFVVVEMESHVS

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						AQAGLK/PSGLKRSSHLDLPKCWDYRHEP\PHLAFFQFF
1497	15398	A	1505	407	1	PTSIYHSKDPGSLKSYTKSTLPVF*RCN NKTWLTAYLFTAWFPKFFKPTVETYC/S RKKSPPFKMLLLIANAPSHPRALMEMHKE IPVVFMSAVTSILQPMQGVVLTFSYY LRNTFCKAIAAIDNDSSGGSGQIQ
1498	15399	A	1506	1	408	PPGFKPFCLSLPSSWNYRHPPF/RPG*F FVFLGGTRFHHVGYTASQHLTSRETHAY ALQ
1499	15400	A	1507	2	416	EPRSHHCTPAWQLSKTSLQKKKKKKRKR MVFTGRKKGLFFGN/LKNLGTLSREYPL GPGIKNRLAQKRKPLFYKKRF*NINPGG GAHPGGPKSWERGGGRKI*TPVGKYASN PEYHICIPPGKRNONPFLQKKKKRRAD
1500	15401	A	1508	276	14	SPPPYFLLIR*GRKGRGQF**LRLFFIY NLRQCL/DSVSQAGFQWHNHSSLPQRT GPK*PSFLSLPSSWDYSHAPQLLAFYGA NCFN
1501	15402	A	1509	1	391	NIFKEIMSENFPSLMSENFPSLGKEIES QIQEAQRTPNKMPKRSTPKQVLIK*V RE/MLKTAREK*IVICKGTTLRPAVDFT AETLQIRRE*DDTFKTLKGKKKKKTL AKLTFFPSILVFKKTRGGS
1502	15403	A	1510	2	419	PRVRSRATNVIKSKYKQHKKKNTSK*IKD LNVKPEPIKLL\BKTTGEKLLDIELGND FLDS/TPKTRAPKANLTP*NYFKLKSFL TAKETFN\KTPTKRGANHISDRGLISKI YKELTIQ*QKNLISK*AKDLKRHFSK DV
1503	15404	A	1511	392	122	SVSLCVSLQSSGMFRC/LPTMPLRR*RQ ENPLTSAGGGCSEMRSHPCPAWVTQD SVSKK*INK*IK*/Q*LRQNVKIKPSPI FCEQGKRRK
1504	15405	A	1512	2	281	GGCSELRSCHTPAWTT\SETLSQKKK RKKICIECNTLKSH/ILSFVCGGKYHSP VSTCL*WSLGRSLKRSLEHQNLDNP YPIFQNETNIH
1505	15406	A	1513	242	382	QGPNLG*LHPPPGGLKGFSPLTLRLSWK NRLPPQHPFYFCFRKNKV
1506	15407	A	1514	1	388	RTRGTERDT/RFRERRERDRGREGYRW RYRERERHRERES*V*RDRVRDGRVID RERERQSERERLR/RERDWERDTYIVRE TETERETEGERDIERERDVRDRYM/RD RDRDILRE*ERDRETALDSEK
1507	15408	A	1515	4	285	TRXQICNGDKTALY*KEMPSRMFPAVE LMPGFKASKDTLTLLLRPNAVGDNLKP MMIYYSENPRALKNYDKTQLCLYSTNGN KAWMTDYRFT
1508	15409	A	1516	415	2	MGDRESLPSPRVFLFFLAPCPKGILFHP V*FGSVRSFSIERCYR*QORNEFWGPI RVKASSRAG*VVFSSTAPPLFF/CFFE TESCSVAQAGGQ*CDFSSLRPLPPKPKG FLCPSLPDAW
1509	15410	A	1517	1	324	PTREPMPFRHAAPAGLELLSSSDLPTSA SQSGGITGVSHRTWPILASNNY/SMDKL CAI/CERFILPFLKNILLWILILFIFIY FCLIK*CITINFQNSILPHSHILYI

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1510	15411	A	1518	2	163	ACRYPWLNFLVLLVEMGL\TMLASDLERS G*PQ/CDLPASASQSAGITAESHGWP
1511	15412	A	1519	425	52	VLRGAQFLFQEARLKWDFGPGGMAPP PPPLGV*KGPLPKG\GGPNPPGPPRGNP VFSKKPKITPPGGGAPEVPPPWGGGAEK FFYPGGPRVQGT/RKTPPPPPGRQKGT PLPQKQKKKKPWSL
1512	15413	A	1520	3	404	THASGKSNIRGLTLPVFKTYKAAVIR/ TVWP/WLRANTNRQNL/DGPEVDPYKC SQMIFDKGAKAIQ*RTDNNLLNKW*/ES *TSTCQKKKKKNQFR/DPAFLIYTKFNS NGRKNLRVIGKT*KVLKKNIKQNWGDLG
1513	15414	A	1521	332	39	TSRETNFQDLDTAFLNEVGVLPLWRKG KGKIDIGIGTKEMP*FPI*LLMFSYIVI ERERKPE/LSLSPSLECSGMILAHKKN LPGSSDSHDPASRVAG
1514	15415	A	1522	482	0	RARTSGVLLCSPGWS*TPDLR*SLCLSF PKRWYRT*ATVPGLLYSLYSRFP/DE LKGCEKSRTPA
1515	15416	A	1523	1	417	NKC**RCEKGMPPVYVWYCK*GQPFWK TKERFFKKNL/NIELPYNTAIALNMRP Q*I*SQ*RKVCSCMLCAT/PTPNK*IKT MW*VCLVEYSSPLKKN\LLFSTWINLE DISSNK/LRHRKSSISRHHLL
1516	15417	A	1524	1	397	RDSTVQGHFTPPVQ*GLRYGVILFITSE VFFFAGFL/WSAFTRSSLAPTPQLGGHW PRTGITRLNRLEVPLLNTFVLLASGVSI T*AHHS�IESNNRIIQALLITILGLY FTLLQASEYFESPCTISDGIY
1517	15418	A	1525	2	376	LKAKTGQKGLLHQTVSKFVNAKEKFWK ELL\KSATPVDI*MIRKRTSLITDMETV *VV*KEDQTSHPILS*SLTQSKALNLF KAMKTDGRKGAVE*KSEANRGWFMQFKE RSC/RFCNIKVQG
1518	15419	A	1526	3	386	ESMLKAKTGQKGLLHQTVSKFVNAKEK FWKELL\KSATPVDI*MIRKRTSLITDM ETV*VV*KEDQTSHPILS*SLTQSKAL NLFKAMKTDGRKGAVE*KSEANRGWFMQ FKERSC/RFCNIKVQG
1519	15420	A	1527	127	388	KRKSQINNLLQFKELEK/QEETKPKAS RRNKKKIRVDLLKIKKGKPLEGVKKKG GFF*RTNKRDKPLLKLPKKKGGGRIKTF HKTS
1520	15421	A	1528	3	402	HENHMKICSTSYVIRELQIKTTMK*YYT PVRTTAIONTDHTKCWQG*REQ/GSLIY CW*QCKMVQ/PLWKRVMQFPPTKLKHS LN I*SAVVLLGIYP\KSGKFNVTCTCT*M FLAK*PQCSSVDEERKKM/WYMYGFE
1521	15422	A	1529	2	365	IEKLYRSGAKFFCRDRVSLCCPGWSRTI GLKQSSCFGFPKCWDYR/R*AALSGRL LLTISSH/REQIEQETHYPEKSAKL FMQ DGPPRRK/HPPTRPQASNIQNK FSFFLR QSL/NSLAQAG
1522	15423	A	1530	1	418	GTDTE*ACDKIQKPPDKRLNLG/IRK KHLQDKYL/WKNPIASIIKSRRLKSV RLRPGDGRQCSPPAWLFNIILEGLARA IR*EKQKQKQGG\QIGKKEVNLSLFIED IMLYIENLKESTKPIIIINBFSRKEDF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RP
1523	15424	A	1531	381	3	ILQGFVIRKKSIFQKACHTSDLWTLTN LSCLHMKGLPPLRLYSSCTVLLFLRKPV MRKTTLSCCFLT*DFFLPLPPCFR*F ILLIF*LYFCKDKVSLCCPSWSKLLP/Q QSSCLSLPKYQDYKA
1524	15425	A	1532	38	479	DEACGFQDPYLTTPYVKTQWIKD*TRNKG IQFLEENGKN\FDIGFSSDLLDMTPKTR ATKVKL\NDIRLRNFCASKDTINLSLLC R\KR*PVEWEKISANHISDKGLISGIYR QPPLNSKTSHLI*K*ARDFNRHFSERDI QSALYRWVL
1525	15426	A	1533	105	447	LIFCRVFEVLHSLHLPQEICLSLALFSR FTFCVLIICEVDVWSVIFKVPFCSKRNV AVHTMLYIYIFVSLFI*PQNWQPKCPA TVERINKMWYIHIV/EYYSANKR
1526	15427	A	1534	76	471	VWVCLLSLEGSQSKFGNSIEFGVLLSSG GFSAWRLFFVYFLRQSL/NSVAQAGVQ QWRDLSSLQPLPPGFK*VLKQRGVCLFV CFETESHSAQAGTQWCDLGSLOPLSPE FKRFSCL\SLSPWPSG
1527	15428	A	1535	45	338	SNNEPFLDWIVM*RKVDFIROPAMTSSV VGPRRRSKALPKAKLAPKVMVTIWWSS ARLIHCSFLNASETIASECTQIQIDDMH *KLQRLQAALINRK
1528	15429	A	1536	425	1	FFNITFHSVSFSPLSQKCIITL*ILLKS IVKNMNRNFQSLVRK*AKDMNRHFTDD HVQMAS/KHMKRCSLVIGEMQIKN\TVS YHYPPIRMIVRNSSNTKCW*GCGQTGS LMRCWW/NK*NQLLWKTGIPPHGLVSTR SRVF
1529	15430	A	1537	4	443	ETFVDHYQCGGIRPFSDLQLHAGRTTAL FKAVRQGHLSLQRLLSF/VCLCPAPRG GAYRGRQVSLSCGGLHPVRASWLLCLPK *AWTMEGTSTPASLPCLISDCCASNQ RDSVGIGPSEPGAENLLVPRFLSPSEK RSIWVG
1530	15431	A	1538	487	3	TQNGGVLLSAPRSVFSPTTLR/CTLQAQ C*AFWGGTQQAASSTAAMAAMKPLGIW AGGAAGILPKLGFQD/LPLSAEADPAGK ELSIGRQRAWREQPDQSAEPFSSQAPRP GYPPSPQPLSMRRGPGANFRLARPLRGP VRVRLRRASSERQKRSRGSGPLG
1531	15432	A	1539	394	489	IYLFIFETESRSVAHAGMQWRDLDSLQ SPTG
1532	15433	A	1540	475	202	PGGGWFSPDPNFSKENSQGGPPVSHPP PPPGNGEGGKTPGAGHSGI*NPPPLKI N/LEKGGRGPPGPNPFPKPRGG KKKKKKR
1533	15434	A	1541	14	468	LSMWNSRLKARRLVLSQVVNA\KERF LKEIKSVIPMNTLMVRERNSLI VAVEKV LVA*VKEQTSNIPLCQSLVQSKALTL HSVKAKRG*EAABEKLEAGKHWFRLF KSRHLNLIKVOGEATSTDGELQQVTYPL VKIVGEGDYPKQ
1534	15435	A	1542	479	141	RKTDSDWLIK\SFSTAK*AIINEADGQTT EWEKTFANYASDKGLISRKELQINKKK ANSPIKK*AKDTKKQPTNMKKCRTSLII

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						REMQIKTTMRYHLTTESE*LLIKSQGRA L
1535	15436	A	1543	17	474	NPKKKKKKKIDLLDTYYTLYPK/AEYTF SSEIHKNWLYIN*LRANLNKFIN*KIKT ILSDHNRQQPEINKCNKTKR/RVT/TQK FKNLILSNYVWKGELQTQIAEFLKRNVN KNTIYLNT*NTIKVLNCGGST/ALNTYI DKNFKKRVP
1536	15437	A	1544	89	481	ICLVISLRQENATSVACIVSCLSEGS ASENLVLHNASPNSCGLGIAFTCLCNV SSGNKITDCYD*LSSS/WLGFFFFFLK KSFLFVAQAGGQGGNLG*PKPLPPGLKQ FLPPPRANFCFLEKTGFLE
1537	15438	A	1545	1	300	PPPPAPXXCRPY*XPWXXPVYHSSWRHG SGAAQGAVALAGFGVGROGPGAASVSIP LCPENQGCREPGPSHAVPAPSALPSLRS LTGGQIGGTAAQAVG
1538	15439	A	1546	2	436	GAPKIKSIKGYND/RLCTTKFYNLDEM DKFLVRHKLKFLI*E*IDNLNRWITSQE TDW*I*QSSSSSSSSSSS/PSSSSSRPN GFTTESYQSFEDKLPIICKLLKKIDKE \GHFPLQL*GITQIPKPDYH/IENYRP ISLM
1539	15440	A	1547	54	419	PATWEDHLSQGGRCDCSEPRLHCTPAWV RE*DPTSKKKKK/NDQ*LLIP*S*RR *RSSHQTSHLMDWNSEAGR*EATFLRSY SKL\KEELELLLLDNDHNSD*YLL SIYSIPGTVLS
1540	15441	A	1548	37	339	KRWKCLRA*LLMRPRHAD*LNPDGVGYS EL*SRHCTPAWVTEQDLVSISTRKNER HTLEYSHQHYSG*P*TG/EESEYPSAL* QREIIDYSFIQGMTDQL
1541	15442	A	1549	477	1	PGSHDLGSYT*PQ/VVSSPVBVTSRDAPS HPSAPKFCSNPCRGWLTSSKQPKRLRT SAVGPAGARGTFHALGAGAAEAGGHS SRPEAALCRPLPLPMTLTSHPLLSGPG RLAWGCNGRR*IKGGG
1542	15443	A	1550	430	8	CWFGSSGTPDLK*STRPGLPTCWDYRHE PLCPASKTFLSPQIETPYPLNNAHSR RPALVNYSLSVSMDLPIL\AFHTNGIT GYVASPAPFVRWGSHSVAGVWPVNLG SL*PPPRLK*SSRLSLSSWDYSHMTP LN
1543	15444	A	1551	2	419	ETSPSLQGWLGVLFPKRGAKTSRFLIIR PQGSFKDGDFFNPGEIKTPPAKKKK KDSARSPPARLQA*GAGLWDARASFRP FQAPVPLSAQFRAQPLAVGTSRDGSSG PTPGQESAV\PWREKHPQPPQPG
1544	15445	A	1552	2	387	FRHVAQAGLELLG\SSDPSVSAQSTGI RGMTYRAQPG*LFNSKNSILSGPKV/L QDYM
1545	15446	A	1553	393	2	KNPIFFFLKQGFPPFP*LEGRGKFLGPC HLCFPGSKKG\LPHPQLIGAPGPPSP GFFFLKRGFS/LFCPGGSFSLRRKGPPP PALPKF\GFLRVTPLAGPGNPSFFFFF RDGVSLCHPGWSAVAASRLTA
1546	15447	A	1554	1	427	LLLLILYAIVEAVT*TEGAGYPLPGSY SHRGASGHRAIFALHLTGCCCI*GAMHC

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						ITTMIDIEPPAITQYHTPLLA*SGLIT* GL\LVLSLPVLDAGITILLTDRNLITTL FNPDDGGDPILYQHLL*VFGHPEVIYIRI LPR
1547	15448	A	1555	3	382	TLYLLFAA*AGGL/GSALSLLIQAELEGQ PGNLLGNDHIYNVIGTAHALVIIIFIVT PIIIGGPGN*LDTLIAAPADMALSRNN ISL*LLTSTVLLLLASAIVEAVA*TG*T GYLCLAGNYSHF*ASV
1548	15449	A	1556	380	3	EVSFCCPGWS*TPGFKQFACLGFLPRCWS YSREPAPPAAKACFLDI*VK*WFCK*GSP EVNSRPGLYLYLIYLIKQKKGVK**PARY LVLFFFCFVFVFVFVFVF*HRIS\SVAQG GVQWCDLGSQQPPP
1549	15450	A	1557	100	254	IPTVPTY*TPIKSFPHARIESSGPGYSW PVDSAK*VPLAVVSLDSR\RDSGNLVHP LMRVTN*MKRHVLVTLTQS\CYS
1550	15451	A	1558	2	289	APGVSTMEDEMGGGLEBPQRRCSCQRS HHCI PAWATE*DCLKFNKNKKNYLLLS LRTQSYLYF/C*VNYS*KLSIKLAGGT GEKEH*SQKRKSK
1551	15452	A	1559	24	354	PLPSASPGEATPVPTS/ACPKNKIKLY HLKKKKKKKKKKKKKKKKKKKKKKKK TKKKKKKKRKQQLNE*ETG
1552	15453	A	1560	376	2	AARGSGVRDPLEBAVCLFSDLQLRAGR TALLKALKF\RQGHLSLQRLLLSF/VCL CPAPRGAYRRRQASLSOGLHPVRASR LLCLPKQANAMAGAPPASLPPCSWSID CCASNQ*DSVGVG
1553	15454	A	1561	3	408	AASTVFLPFLEKRGIDFGFLFFFFGEKK FPFLAPGAGGLFSFPEASSPGLNPPF WPNPPEK*KKGPPPPPPGFFFFFF*KKRG FPGG\PGGAPFPDPKIGPPGPPKGGEFR GGPPPPGPNNFFFFLKGGKGGGGPP
1554	15455	A	1562	355	161	FKPGDGGCSEPRWCHCTPIWIMRDSVS KPKQSKTKKRNVFT/C*D*VF*NNNINY INCFS*RALYLILEKQFM
1555	15456	A	1563	410	1	TPPPPPNFLGTPLFPKKNAGKGLFPPPP LGFPPKGQWPIPPQRFPLFPSPKRAD* KPKPPPALKIRGPNPGVFPKFPGFCSFF PPPPPPRGGGLIFFLPP/TK*SGG*KKP KKKKKECPKKQKRGIDQLTSNLGV
1556	15457	A	1564	2	374	ADRNLTNTFFPDAG/GVGDPILYQHLF* PFGHPEGYILILPGFGIIISHIVTYYSK KEPFGYIGMV*AMISIGFLGFIV*AHHI FTVGIDVDTRAYFTSATIIIAIPTGVKV FS*LATLHGSMNK
1557	15458	A	1565	396	0	TI FLI FL RHGFAVVAQAGMOWCGLGSLQ PLFP GFRLFS/CLLSSWDYR*ROGFTML ARLVLSN*PQAI\SASPSQSPGITDVSH CA
1558	15459	A	1566	186	452	KQKCNFKTLNTKYQLPFFFFLERNF CFC PPGGEGADFTFLEPLPSGAKGFF\CLT LQRM/WE*RVSPPTPLNFGFLVKGFSL CGSTGF
1559	15460	A	1567	453	37	KTALYWKTKPSSTS IAREEKSVPFGKQG AHFLFRGKHKFKLVSKLIHYFENP/R/A LKNYAKSIL/PYKWNKAWMTAHLFSP/W

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						FIKYFRPTVEM*CSYNKILVLIDTGLDH PRPLIETK\FINLHVCVLFNTTPIVQP LPR
1560	15461	A	1568	453	39	TALYWKKTPTSRTSIAREEKSVPFGKQQA HFLFRGKHFKLVSKLIDHFENP/R/AL KNYAKS/TLAYKWNKAWMTAHLFSP\WF IKYFRPTVEM*CSYNKILVLIDTGLDHP RTLIETK\FINLHVGVLFNTTPILQPM PRAQ
1561	15462	A	1569	1	352	FGTRRRERERERERERERERERGRGGA GHQIPSI EGQHKIVGAIY\CRBC\GEK ISGSTSYIKVWDIRDSAKCIRTLTSSGQ GISGDACAATFTRAITSAGGEH*INQIA LRPSGT
1562	15463	A	1570	394	3	TLDWPSRGGSTGKPVYPSVCCCCCCCC CFNFCQAEAKNNAEGLLNQAGRTKDGS FAPSHDH*A/PRGTEV/DLLESTLQTSI KQVESKPR\EQARTGAGGQKEKATQNP KSVLTSMYTKSQSGEGRLEPNR
1563	15464	A	1571	399	2	KHQLPVFWQYNKKAWTTRTLFLDLHCC FVFEVRKYLASKGLPFKVVLIIDNAPGH PPRTP*VQY\KGIEVIYLPNTMSLI*F LDQGVIRTYR/SHYTOYSMORTISAMQE NSNKENI IKVWKDSTDDAIVA
1564	15465	A	1572	37	400	RGITTGEAASADQETADKLSDAINKIME EKG\Y*LPEQVFNLDSTLFWG\KKKPQ RTLLSKEKKRAPGFKTGKDRLLTLLFC/A NAVKLIIRTALTYKAENPOALKENVKHQ LPVFCLTTRGL
1565	15466	A	1573	84	485	AGHKDSRPHQTQEPSSLHLWDPAAGLQ VELPASP\GRALALLSPWVVDGTGRPGA GGGTRRGSGSPTGAHGAGGRMLMHGGLQV PSPAPREGS*GPARYQAQRMWARTAGGP STPSAGASRVSPHCPGP
1566	15467	A	1574	3	463	TPAQGLRDPNSMRKHAYCGCCV/CITLC VGAQKNRAVCGLYSTCPRLCVYEHEHI CVNE*VCEHVCERESVRVCESTH/LPLC A*TCGPIFGCMSEKHVFSYTPCVHRVCV CVCVHLGCCVC/VCVVCVCVCVCVCV
1567	15468	A	1575	1	383	FLSFGFAPQAGGQGHNHG*GPP*P/PKA KGIFPPHPPEKREQRVHATPPGKFLDFF FFWKKGGLNLGPKKNLPGGKKNLLVSP PKGGGKKKETPGPGGVFFWGGIFFFFPP PCSPG*PLSLLKKPKGG
1568	15469	A	1576	35	469	RIPRCHQPVGPLGCREGAKPQGPDPAA DSHPPASPAH*/P*SLHRDPIPGFRGP CRRNAGAGPRAHTAGICAPQPN*SRHH PWAAAPAGDSDPTTSLGSHVPVGRKSSD GCRQRALCTPGSPAPSEAEVGGSPELRS LRPAWA
1569	15470	A	1577	473	62	SLEINPYISGQLIFNQHAKTNH*SMRKE \SFFNKWCLDN*ISTGRMKLDPYLKP IKLNSK/LKDLNIRDTTMINLHDLGFGN GF*TMTTK*AIKEKIN/WDFIKI*NFCA SNDIIKKVKRPNTAYTCNPSTLEGPR
1570	15471	A	1578	59	426	LERRSFGAPLSPFFAPQFEMKGFSGP* KFFSPKALNFGGGVVPFFPPPKRFFS KNPQEGFI PPPLKKKKKTSQPP/YKFGP

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						PKESFKRAPFFFFFKGGPFFPLVSNQWT GKPRLP PPPPKETQNPSSFOIGGQKKGK GGPQSFSFPIKKKKKKGGHSRSTSPRV
1571	15472	A	1579	2	419	KANKTKNAYFEGINKMDKPOVILKKKY/ REKT*IPSGEEKGIMSP/NSEDTKR.II KECFKQTYAHRFYSLKE/MDILLESKHL PKLTQ/EETDSLNSPV
1572	15473	A	1580	129	403	YMFFIPINCQDHPK*KKKKKKKKKKRGG /RPFKKTLRGPKLNRAEKNKFF*KGSI KKKCLEILKKLFFGGEKNCKNPKKKK PSREKKKF
1573	15474	A	1581	317	76	PRFFFFPPPKKGFSPFFFPSPRFFP PPFLKPPPRFFFFFGPKKNFF\PPRP LIFFFF*APPPFFFPFFFPFFV
1574	15475	A	1582	259	377	PREMKTLYPTKKGLEYISHYH*WVGCKM VQPVWKTWQFLKGLNIKLP*DSAVPLV GM*PREMKTLYPTKKGLEY/MFTLSLLI IANK*KQPKCPRMNKW
1575	15476	A	1583	1	415	PTRPITSSICLRQSVLKALIAYSISHI ALGV\TAILNPTP*SFTGAGILIIA\HG LTCSLLFCLANSNYERTRRRIIILSQGH QTLLPLIAF**LLARLANLALPTINLL GELSELRTPFS*SNITLLLTGLNLIGT
1576	15477	A	1584	216	406	LNLLPLVLGGSSCLPPPCGCGN*KPPPPP G/LFLEKKGFSPCGPAGF*PPALRGPPP PPLRGLI
1577	15478	A	1585	383	3	KKFGYFFYWIG*KILK*FPG*K*SLPHR KSPFFFF*GRVLLCPPGWRGTTKGHS QVT\LPAAAMTFQV/K*SSPLRLPSR*G YRQASPWGNGFFF/CLVESLSMLPGLIL NYWATAIKPSGPPKVLG
1578	15479	A	1586	126	413	NPTLKK*KMKENRMKKNEQSLRDL*DTI KLINRCILGIPKEERKKGABGIFGEIMV GNSSNLIR\ENINLNIEVAQ*TLSRIN* KRATLRHVIMKM
1579	15480	A	1587	242	409	GWMIERFNFFFLRGSTLVTQAGG*GG DFG/SLRPPPPGLKRFSLTLPRSDYR H
1580	15481	A	1588	2	338	EIEKKGKGGKRRG*RSNKKRGGRLGQ KY*SPPCPRLSFFLVDEKGEVLQDSL GWWKTP/SGCPBMTDSSQPY/YRAFYVL KN/ORVGFSVDVGEIEKDQDVEKNQDPS CPRL
1581	15482	A	1589	360	0	NNFLEQLKFPKPKKITTD SYKAPRPPFF FPPSQKGVFPPTLFGFPFGFPFPPLN PPPGFF/CFWAPLKKFFFPYGG*TWVS LKGPP/L/REFFFFF*DGVS LCHPGWSS SAQS
1582	15483	A	1590	75	412	VEGQHCNFCAAQETINRVKQHTLELET FANWSPDKGLIPRTYKELKHLNRKHSY *KWADDLDRHFSKETYPPTKTSCTQYC *P/SITIEN*KLKTSNIKTRLQGGHKRL ER
1583	15484	A	1591	309	1	FSTQGAHMQVCYMDTFHDAEIWTSIEPV TQIVNMLPNR*FFNDCPHFPFPFCSP/ LVSFLLLLLRDRVSLCCPGQSRVSGFK*S TCLGLPKRWYKCEPPHVA
1584	15485	A	1592	2	415	LSISLSIFSFLP\FSFLLPSLSLSLFLS

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						FFLFLSFFPPSFFFFHFRASLCHLGWSA MA*SWLTAVSTSQ\VKQSSHL
1585	15486	A	1593	3	396	HSAFLFFL*DRVSLCHLSWKAVAQSQLT ATSTLL/VLKQSSHLNLP
1586	15487	A	1594	300	62	KMTGVLKSSCGKSPKQVGVLCVCVCF/ SEKROGLAS/VAQTGMQWGDHSSLP PGLR*SSCISLSSWDYRRVPRRAPG
1587	15488	A	1595	1	412	FDRPAADQKAASALKASGVQQAQMAKQTY HDWSLQDWKVLWMTH*VS\QEQDPTNL YISNPLCMDELQLENMLKPPGQVISTR ILRDYSGTFRGDGFARMESTDCKDAVIE HYNVLLIMTPPGVSAPTEPLLCKFAB
1588	15489	A	1596	428	2	QSESREPENFLPTSTSSLLLVHCLSR CVVNSTLSCVPHFFHLTFNSHLLTSQP RRVHFC*LSLSSIIISWKLNLTPGVPIR \ASEIFGLRTIRNFPFLSHSVLPFPLS ESHVTOQGVQWHELGSLLQPLPHGCQWL SCL
1589	15490	A	1597	2	442	QGSLS*PHPPMLK*SLTSAF\NYRHVSPH LANYFLFFF*KQLAVLLGLALN*AQ/C HLPALASQSAGITGVSHGAWLFFFLNQ CYLI*FLILIF\ERRNSPVAHVLVNGGD LGLLKPPPPGLMGFSCNLRLRSKYP ATSPGYIFC
1590	15491	A	1598	419	121	NLGYPRVSPPPFLNPPPEFYFGPPKK FY/PPPPPAQKIDPP*TPPPFFFGTDG SHYVAQAGLELLASSDLPASALQSTGIT KHEPPHLAETIFLVFL
1591	15492	A	1599	45	397	DRVSLCYPGWSAVV*S*LTAAASNW/V K*SACFSLLSRGDYMCMTHIANIKKNF LGRVRGSHL*SYHLKLCCLK*RTKEGFL SFFWKGRHFLGQKNILNPRLKVPFLPG PPKGLGY
1592	15493	A	1600	3	397	SRRPGRFSLMLTSLWSH*VCRAALAARE EQWSGCFKSHF*LEVNFWSGIDREV/C GY/LKTVLGEDLNDYVSTQI*D*LMKPR CPEKQDESLLKBFGGGA*RLNVVHRPGA VAHACNPALGAKGRRIPRSG
1593	15494	A	1601	244	2	KTKTSFHSLLIDSCGYLLSYSNFI*KKM IFK/YLHLRAVPRHVIVRFTNLERQEKV LRAAREKG*VMHKGKPIRLTADLSA
1594	15495	A	1602	435	2	PQEAIYTPHQPTYGAICRIARIHGSRD Q/SVEMKWHPQLTITPSGP/LGKSLLP PVALCFADLEVFIPKGGMLSPGVTTISL NWKRLRPWVILQ*RTPLARVIPPDIOR EIRLLNNERKKSYVWNTRDPLGLHLVVL PCPMVIK
1595	15496	A	1603	288	8	EFPLIREMQIKPTMRYRLTPV*MD\R*W *GCGKRGTLVHCW*CKLVQSVCSRSSK NITIELPCDPAVLILGMHTKERKLRCG WTRGVGPGYC
1596	15497	A	1604	411	236	LIPSEHFFFSG*F*AFDRSSLAPTPQLR RHRPPTGLLPLSLQGP\LLTPSVLLS* GGRFKGNFTPPGGQKIFPMGPPKSNP GPGV
1597	15498	A	1605	2	437	KCLRISPCAGFRRPWCPSFEPVRCVWPL GVPOVG/PEGP*GEG\GFEGGDVRLWQ GKKKKKNTLKGKRGWFPKGRGFSLT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WFGPQGLWEPCLNPGGPLFLIGGQKGP KVLIGKGTGPKKKNNRPRKRGSLGPP GKDDFPL
1598	15499	A	1606	31	467	EFFGRRFRGGGCSELRLRVCTPAWTEG DSISNNI*LVNEN/HTVNSWKCSDS
1599	15500	A	1607	418	32	VGQVGLELLTSSDPPASAYPK*WDYKR\ DPRAQPNPNILKAQSNRSPRQR*PASS FSNQNSCMHRCISLP*VLFLIFFKNRP* NNSFGYNSSGWWSGLNILNSC*FWFLPG NSDTEIRICRSFHRGREV
1600	15501	A	1608	379	3	FPILSPSYNPSSTELP***SLQSPLEFP YDFFSVNMFSFLFFNLKSHITVAQAGVQW RNHGSQPRSFQK\HPPASASAGTTGM CHHAW/LIYLCVYLFLEMRSHCVSQD*V QWHNHSSLOPETPTK
1601	15502	A	1609	456	99	PFPTFPFPPHSNWGLGLGCGL/EPITMP SGLGLKGSPS*SPPAHRLSGAQLCPVLR APVLGPSQMPGPKKKPTARGSPWRKGV FVMSGQSDPLGPSSCQELGPRQSTQGT PGA
1602	15503	A	1610	1	420	FRFSDGAAGQKCSSPPRPGRGRAEVLIT SQTGRQGRGAPHISDNGQPRDAP\PS* M*WRPGRGAP\PS*VGWRPGGDAPHF\Q TGQPRGAPHIPDDGRPRGDAPHFPGDV GAGQRLQTRHFGRPATAAANKVKVVTSLR
1603	15504	A	1611	426	3	KNPFLLEAKVSFNPKWPPALPPGEQRDS VSQKKKKNLLIHKKAHSH*FFICRE\C ESALLLHQNIHAGGKSYVCNK*GRGFRN KSHFTYQORTHSGKKAFL*KECG*DFL*K AILTAYQKTHSGKKSFCVCKEGR*DFTQK TK
1604	15505	A	1612	428	273	HHA*LIFKIF/CVETRVSLCPGWS*TP ELK*SSLLGCPKCWDYRREPPIRPTT
1605	15506	A	1613	311	4	ANKFKNLNEIKFPEAHNLKFTQEGGLN NPVSLY*KN*TYSLRLFP/KKKSGPDD FTGEFN*TSKEEVP SLHKLLQKI*ERN LPNLFHKARVTQVSKSEM
1606	15507	A	1614	338	88	PNPPPPSKGK\GFPPTPGRKKKTRPPP PPGKFLGF*KKRGFPFPPFGRGP\NPAG GPPPPNPPKGGGTGKEPPSPGEGVFFFF
1607	15508	A	1615	2	162	KHGGTCLYSLLLGLRLRHESCLNLGGGCG RE/PE/SHCIPAWATE*DSVSEKKKYL
1608	15509	A	1616	3	399	PEVREYLTSGRLPPKVLLTLDNAHGHSE PQRENTGINVFYLLPNPRSLIQLDQG VTRTFKSHYTWYSTERIANAMEENPDRT S*KSRIMTPL/IDAIVMTEKAMEAIMP TKIISCWRLCPDVVHDFTRFT
1609	15510	A	1617	390	1	KRNCFGPFLTTPPPGQRLGGFKFLK\HFF YYRGERGGFFSPFNKGFPFPPFPGWGF LGALKF*RGVPPSKPPPGPGKFKLKP FPPRKS YGGCFKFLGGFPFEGPPPQK KKKKNTAARDLEPNAN
1610	15511	A	1618	468	0	MKLVNIWLLLLVALL*GKKHLGDRLEKK SFEKAPCGCSHLTLKVEFSSTVAEY IVAFNGYFTAKARNSFISRALKSSEVHN WRIIPRSNPSSDYPT*WP/VALKKKKK AGV/LPLENYSIITRV
1611	15512	A	1619	421	2	SSRLSLPKCWDYRREPPRPAQPRILKKI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						S**EPFFLILKCI*LRTOGLGRGHKGKL NSTYVLHKFMD**LGQLMNGLNMLDESS FCNVLKHTKQ\WRDYYFVCLFVCFVRQS L/NPVSQAGVQRRDHGSLRAPPPGFAPF S
1612	15513	A	1620	406	2	GTKKASSNGFINGPGAARKKSQTFAFLA KPGAFPSILLDEKNRPQIKPPACFP/SI RESQTSYPVFFFWSPSCGFFFFWGKPEP LLLKEAGKVPLFLFLFGFL*DGVSLLCQP GWNVLRSQLTAESNPHASAHAS
1613	15514	A	1621	411	0	PPPPKKKPSGPPPP/SSSSSSPSPPRKF LGGPRVFFPPPPFKPPPPKNFWGPPKKK KPPPPPGGKKFFF*RAPPP
1614	15515	A	1622	2	403	TARCGLNFPCCSSSLPFILAS*VAGTTGTH HHAQLILLIFCGDELSLM\CPGWS/PNS SHLGLPKCWDYR
1615	15516	A	1623	298	411	LIINVCWPGVLVAHACNPSTLGG*GGRI/ TMRSGVRDQP
1616	15517	A	1624	263	2	DSVSKKKKNFKE*LIPVLLKLFQNIIEE GILPNSLYKAGV\LIPKPKDKT*RKEIY RPISLINIDAKIVSKILANKIQ*FIKKI TDAW
1617	15518	A	1625	3	281	PFSCSLSPSCWDYRRPPRPANFF/VYF YKKNTRTQCFTVKHGFTVLTRLVLIS*P CDPPSLASQSAGITGVSHRTQPHTVFFL NNPALPKLQT
1618	15519	A	1626	300	20	NEGPRGFPPPGPPKRLDFRGGAPRPGF* YFLKNFLGFFWFQKNFLVFFLGKNTPPP PQFFFFF/RDRMSLCHPGWSEVAQAWLK AALTSQTPAI
1619	15520	A	1627	394	40	PQPAASLFSFGLFFFFFPVFSPPPPFK TPPRIFFFFWPP*KNFFF\PPPAFFFFFF LGAPPPPPPPPPPPPPPP*DRVSLCRP GWSAVAQS*LTAALNSQT
1620	15521	A	1628	386	3	IFPTRCTHLHGLTNKLPSCFFDQAKKN PFCS\HHSRGVGLRARLFCERLTIEGAG TPACPAP*FGEPTRP/EGRVRLTPAI PALWEAETGS*YVARTGLELLVSSNPPL SASQSARITGVSHRTWP
1621	15522	A	1629	401	93	ARGVLPLNPPFWGGGGGSP*GKNSKPP RPRGENPPFLKPKQLPPPGGGPPPLF LGG*SKTTPPPKGGAPINQKPPPGPLP PGKKGAPFPKKKKKDKNIRTKKKARRS GSLLSQSHPRPR/RGGPPLTKNPPLAS PPQEKRGPPFQKKKKKTKI
1622	15523	A	1630	417	47	PPPGTISSPNF/QKNLKRGGPGGNPRN PPPLGGQRG/RGLWAKKSRPPGPPRGNP PLFKKKKINGGGGPPPVPPPRGARAGK SLYPGGGPPQ*PQMGPPPPPGAKKGF PKKKKKKPKKPKRT
1623	15524	A	1631	416	54	EYWKGR*IDQWNRM*FKMDOHLHSQFI FN*ATKAIQWGKESLFRNLCLKNWLTIR DK\IYLDACLTTY*KINSSWHSAGFL* SQILRLRQEASLSPGI*VQPRQHSKTP SLKKFFFKFFS
1624	15525	A	1632	2	373	LVFLDNMLKLLRHSALASACFPEDLAKI MDEGGYTKGQIFKVHGTAFCWKMPST FVVRQSVPGFK/ATD*LLLGANAAGN\

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KLKPMPIYHSENPRVFKNYVKPILPALY TWNSKA/QMAAPLF
1625	15526	A	1633	3	383	NIWN*KAWMTVHL/FIT*PTEYFKSTVE NC*EKKKILFKI/LLIDNTFGHPKALM EIIYKEINVIFMPANTISIL*PMDQGVIA TLNSYYLRNTFHKTIAFINYDSSDRCGQ SQLKNFWKGFSLDAIR
1626	15527	A	1634	2	182	GACTQLIGRLRQENRLN/SGDRGCSEPT LHLCTPPWATE*DPVSKKKKKNPCPKLK KGPPP
1627	15528	A	1635	331	1	LFPFPPVVLKSGPGPN*N*PPLKGKSGFP LKKKFFFFF\FRDWVLLYCLGWSQTSG LKRSSCWDYRCEPHLTPNF/SYF/CRD SVSL*PRLEGSGSIIALCSLKLDSSTP H
1628	15529	A	1636	80	381	KLKCHAHHSRGFYKYSFLQLGASQFPQ VLRITHPHKGSWAAPRS*G*SQC/SHFF SFFPETKSHFVVQAGGYGRNFT*LQPPP PGLKRFSHLSLPSSWDYS
1629	15530	A	1637	381	38	SKRQGFHHVGOAGLELLSSDDLPTMALH PTCPLQKCWDYRC/DATAPNLSSFTFMQ EKCLAF\PLFSSAPHS*PKAVIEKD CPGL*IW**VARSQRMNVFNFIK
1630	15531	A	1638	3	295	PGPDGFTAEFNQTFKE*LIPIVLKLF*K IQEV\FPKFSITLTPKSNKD
1631	15532	A	1639	48	380	ILGKAISFTIE*KGLKYLGIIYLTKEAG LHTENYKMLLKKELKKDTNIWKILCQ/W TRRLNMVKISV
1632	15533	A	1640	343	23	SWLTAT/FCPLGSSDSPASAGVELLTSG DLPALAS*TAGITGVSHRTRPALSINTS TLLCSSPYCPPHLQSLQGTTPQVFFLKA QRTGCLLQGVILTSAENPCNKH
1633	15534	A	1641	3	397	LELFSSAHCCPSLTVMQYYP\RTSHD CQREKSPHRTKKKKPLEGVFLG*KIKTN LENPPPLPFFGGGPPPKGGGPFKIV*GG WFWPWGLKIPTLPKGPTPRPPWGLGTF GGEKPLRAFPLOFRFGPE
1634	15535	A	1642	2	308	NKWR*GNWISVKIDNFNFLMPYTNLS* IRDDLNAKATTIKLVGENIGENLGIGKN F*ERTLKA\LRGKKMDKLDFTIGNFCF SKDRIKNKNKARRGGSRL
1635	15536	A	1643	16	386	EKKKLSLFTENGIPYL*NPKESAKRLLS LINDFSKV*GYKN\DEKSVAFNLTK
1636	15537	A	1644	533	3	PLSLSLSSLSLFFL*DRACFVAQAGVQ WLDLGLSLQPPPGIK*FS/CGGNVAVTP RLSPILTLPAMTEVRLPSSKIQTNKEKNT VMSEIYQSLM*MGWG/M*VRMCVKFKKP WVDN**VSMGCLLPSFLPSFLSFLS PSPLSFFPYFFETESCFVAEAGQWLDL G*LQPPPPAVP
1637	15538	A	1645	341	19	GIGGRPP*FOLLGRLKQEK/HLERGKGF NEPKSRPCISAWATKGDGCFQKKKIHMT LQQIQPKQSWKTDISQFRIDYKTTIIKT VGHGIWIDIFINGIELSENINQCS
1638	15539	A	1646	279	3	TFYHNEKDNNKCWLT\GKI*MLTGCIW ECKMVQLPWKTAWQFL/R/DVNI*LPYD LAITLLSIYTRKRTYVYTKTCIQMFLA VLFTTAKRWKQP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1639	15540	A	1647	392	1	QKLEIMLREEGMLKAKTGQKLGLLCQAV THLVNAKEKFLKLVLLQGTHKW*ESET AKSLILFNSMKAKEGE*AABEKFAASRG WFM/RFKERNCLHHLKVQGEAASAVVBA VANYIEDLVKKIDKGGCIN
1640	15541	A	1648	425	148	SQSLI*SKALTLCNSMKT/ERAEEVAGK KLEASNF\LKFKKRSVCV\RNVMQGVKVA SLDGEAAASSPEDLVNFIDEGGYTKQOI FN*DKTSFFF
1641	15542	A	1649	271	462	RRQKKRHKRCILSPLLFDIVLEVPARTI *QEKIKIGIQIGKEV/KIISLFADDVV LYL
1642	15543	A	1650	70	398	RPEASLRHMCNLNAGQLLSKRARLGALSL SFFFWKKSIAFAPQPGGGGNLG**KPP LPGLRGFSGLTLRN/WE*RWVPVPPPT\ NFGPLIKTGFPLVGOAGFDLRLTIGALR
1643	15544	A	1651	425	3	FEGEFPKVGFPPLGPRFPSPRVPPFGTLPPF PKRGPRCFPPQPGAPPPKIWTTPGALPQG GVGPALPG/ALQKFGPKNPGGFFSGPPQ MAP\GGFPGGP*RPFRGGAPFFFFLRRQG FPVAQARVHLPGSSDPPISAPQVAGTTD VC
1644	15545	A	1652	385	2	KGNNPSPPEIKFFFFF*KGLLEPLPQGG GQWGYFRSLQPPPSRLKLFSCPNLPSNW EYRGP*\RL*LTGRGTSGSKTKVPTP CGPFNLNLGLGTQARNFS/RLVFFFFE TESFPVAQAGIQLRDLHS
1645	15546	A	1653	242	3	KNKNFGINRGFFFTFKVPGFFFFLGRVK LFFFFRNLKFFLKAAPP*\VFFPIGPSF FFFFFLLDRVLLCCPGWNVVQSL
1646	15547	A	1654	3	285	HFIIYTKDLNRRFSKEDI*IIIKHV/KK CSPSLAVREMQIKTTVRPGTVAGTCNPN TLGGQGRRIVQDQLKQSKTSSLQKKIL FRLARHGGTCP
1647	15548	A	1655	1	373	KVSLFFFEQGLLCCPGWSAVVSSLPQ CPRVKQFSHVS/LPSN*EYSCTPNTFSL QVCVSIHKYI*YIYIYIFKFF/CR/DRT LARLHRLVSNANSQAILPPWPPKVLGLQ
1648	15549	A	1656	189	2	VQPGQQRNSISKTKNKTQKLPTRKSP GPD*FKEELIPILHKL/F/HKIEDKGTL HNSFYVVTI
1649	15550	A	1657	385	13	GGPPFWGARSPPKL*NPPPPRKKPPGPP PPPGGAPPLGGFFLFFPPPGGPPPGGK /SFSRPPFFFFFLGGGGQIFLSPGGG PRGVFSPAPPLVPKPAFFSKKKRGS GGEKPBADGYFIK
1650	15551	A	1658	352	2	HLSSLNWDISIRAPP/RPCVIFKNVPLN IFFL*RGVTMLPRLVLNDPPISASQVAR IIDVSHWAKLRVS/CYVFETGSGSLSQ AGVQRYNHGSVQFQPSRVS*SSHESLWK YRYPPRR
1651	15552	A	1659	265	3	HSGQRDEGRMRCGEWLESHGVVRARSCM TLKTSFLTMAKI*NQKCLFMDIEWIK MWHIHTMEYSAIKR/DEIPSFVATWME LEVIM
1652	15553	A	1660	1	163	NQQNENRKTIEKIIGTKT*LPKIKIKFD KPLARWT/RGKKNIQITNIRN*RRDVI
1653	15554	A	1661	56	320	KFFMYSAGESTKIRCLF/SCLEFLRLR/Q

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ESRSVSQDGG*SEPRSCVCTPAWATE*D SVSKKQNKPKKLNKCPASSLLITLP PARHKA
1654	15555	A	1662	3	421	GIITDTFPNLEKGINIQVKKV/RRPPSR FNPKKTTSRDLLIKLPKIDKGS*KQKE KTSKSARLPQPHGLLGLGLKSASSPIK KERKQ\QITYSGAPIFLVTDVSVETLQV RREWHDFVKVLKEK/DFYPRIVYLVKIS F
1655	15556	A	1663	362	2	VIFADEAQILKKEDKLDKFKMKTSVHOK TLSTEYKDNHREKIFVSQISDKELISRV YKGLLKLNNLTKNLLIFYF*RLGHSVTQ GRVQWCNHSLSLHPQTPGLK\NPPTSAS* AAGNTGVHL
1656	15557	A	1664	79	355	IHLPSLIGDFNLFTGISLLICLVLFVFI FETGSCSVAQ/S/GVQWHNGLLQPRPS GLRQSSHLSPSSWNHRHGP*FIYF/C VEIRAHYHP
1657	15558	A	1665	47	384	KEKASGPLINFFFFPKLCKLAPFFFLPF FLWGGGGGKFSRNPQKHFFR*KRVFVNF FFFFFLRHCLTVSLSHCHPGWSAVA*S QLTAGSNFW\VKQSSHL/LPSSWDHRH APP
1658	15559	A	1666	163	601	IFCKGGVLPCCPGLADLHFSTNSISFY YSSGLLRMTNKTETPMSTIPKGVGVAWR FGNSECIFQELPLTLHLLSTMLASFH SHEASANALVGRSLTVGWGCRGVGVSD PAAWLWRDLKGC*DKSHSVTQSGGQWC NLSSLQP*APRLKRSCLSLPRSDWHW VPPFLANF*IFCKGGVLP\FAQGW
1659	15560	A	1667	418	3	SVCLGLPKCWDTRKPLCPAPFFFY/BG SITLIPKSEMHLPRNENYRSGFLN/M/ DAKILNRILANCISN*I*NH**KVFT PGKDWFNRRKPTDIIYPH*QNREESL VSTDMAKVFNKIQPVLRRELTIBKGNF LNL
1660	15561	A	1668	411	1	LRLHVGRITT\LFKAVSQGHLSLQRFLL PSVEICPAPRGVYRGRQASLSCGGLHR VRASQLLWFLTQASAMAGPPPVLLPPC SLI*DCCANNKGGFIGVGFEPFVGVNLY LVSHLLRPSEKPSIRVGVT*FSRC
1661	15562	A	1669	151	1	PLEKEABITGP*PHAWLIF/CFF*TESR YIAQARMKWHNLGSLQPTPPGFK
1662	15563	A	1670	1	389	TFF*KLKMINLSEEGMLKAKISQKGLGLC \TVSQVNSKEKFLKEIKSATPEST*MI RK*NSSVANTENV*ERSRTSHNIFLS*S SIQNKDLTFNLSLKAWRGQEVABEKSEA SSGWFMRFKERSHLHTIK
1663	15564	A	1671	1	363	ECTGPKIAKIILEKKNVGGGLPI/PNFK I*YKAPVI*FWLKVPVIPSASSAILMKT *Y\YFKDRNQDEWYRLRVWKINSHIYQ LI\FSKGTQTIQW*KSLENK*CWNWLF TKRMRKLD
1664	15565	A	1672	203	2	ALNKRDMPS**IRRCNII/KCLFSPKM N*VFNVIT/IQCPSGHFFFTETDKSILKF IWKSK*PRLAKRTL
1665	15566	A	1673	15	378	NYHHNQNEHMYHSLPNFFFFFFFGKGA PG\PKGGGRG*REP*IPGGKGNPPL*PP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KEGGPPGGTTPPGKPGKIWDFWEKGGFP LSPGGAGTTPGPKGDGPPWPPKGGGKPGG TKQPGPKKFF
1666	15567	A	1674	2	349	LFLTVLARLVNS*PQ/CDPPALASQSA EITGMSHRAQPRGIR*I*CGSYTTCPL LLLT\YLFYFSTESHVVIQAGVQWHD GSLQSLRRLT/CILTLPSSWD*PHVTL PG*FCLF
1667	15568	A	1675	348	78	LGPWVPPVIPAPLGG*GGRSPRGFLT NPGPKGKPRVFLKIQNLPGV/RGRPPLFP /GSPGSGGPKSP*PLGPSFPLT*NFSPP FWGPPGGPK
1668	15569	A	1676	2	385	TSRRDYRP/GHHNQLIF*/SFCRDGASL CCPCWSQTGPIKSSCLVPRCWDYRCE PGL*I*MGKNPT/LFSNGL*CDCIPLIH SIADIRKKPHS*LQGL*LCHQONSQTES CSVTQAGVQ*CDLGSLOP
1669	15570	A	1677	386	1	KSTRPVLYKWNKA*MTEHLFTA*FTEY FKATITETFCSEK*IPKILLICNVPSH PRALMGMYKEINVSMPTDITCILQPM DQGVISTFKSYLRLNTFDKAIAT/DS DSSDGSGKLLKTFWKGTI
1670	15571	A	1678	2	193	EGGRIFNNSFFEVILTLI/PKPKKVER K*SYHPISIMNGDVKILAQTLLNQIQY LKRIIHYDS
1671	15572	A	1679	561	830	TLLLGT\NAVVDFKLKPMLTY\HS\ENS RGL*KSWINLGLTVFYKWTNNAGDDR HHLVYRHGFTGIF*GSQKTYCSENIPF KILLFIDN
1672	15573	A	1680	415	2	TSCAWLSLYPVLYRSSSLPRFIFCHFK HLWYKNITKAAEINTNFCCYINRVLLC HLGWS/ATVSS*LTVTSKLLGSRDPHT LSLPSS*EGRCITPRGLDNLNLSRDGG GIRGTSTLPRQVLNAWPAILLVRIT
1673	15574	A	1681	1	78	RPRIRHEVGOAGLKLLTSGQTPASVP*C WDYRPEPPCPALHISYK*NHAMCGLKCL AVSA*RHVLGFIRG\WHVECCFPFCS*A GLKLLTSGQTPASVP
1674	15575	A	1682	414	162	GGPGGPIPGA/AGLRPPPPPLGNPPPP* KAKICPGGAPPVFPFS*KGGGESP*PP RGRGFFIGVQPLPFLGHKRGFLPKKKK KI
1675	15576	A	1683	378	129	QPFGRNFYQIFNFPF/PPV*HSPFLGP KFPPFSPGGGQWGPLGNPRPPGAKGGST LRGPRTGGSRGGPPGPGKFFFLKQSLA L
1676	15577	A	1684	3	374	GISVLPGIGAPGNKPELFEEVKLYNNAR EREKYNMAELF/AVVKTMQALEKAYIK DCVSPSEYTAACSRLLVQYKAVFRVQ SEISSIDEFCRKFRLCDPLAMERIKEDR PITIKDD*GNSLS
1677	15578	A	1685	2	373	PFIRPETIKLEEIPGGKLLDLGLGNDL LARTPNKINTWDHIKLSFCTIKETIN TMKKQPTDCEKIFSRLLSDKGLM/SQMC KELVQLN*KK/TDDSVKGWAEDLDRHFS KKDIKMANRPGKVL
1678	15579	A	1686	378	201	HATCLANF\CSYG*DRVSFFCPGWS*TP ELKRSTRGLPKCWDYRCLGRSLLFPGA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PPDH
1679	15580	A	1687	1	404	MCVNPGGGACSEPRSCHCTPAWVTERDS V*KTNKKVKRRKKIFHANS/KLKRVM AVLISDKIYYKLKKVRDKEYI IKGSTY QEDISITNTYTLNT*APKYMKDTLTBLK EEIDIYAIIVGDFNTLLLIICRG
1680	15581	A	1688	307	33	DEGSCDAHAGLKLDDSSGLPASASQSA GILGVSHGARPLISSYNGTSHGGLGPAL VTSFNLSHLFKDLLSLQI/HVTF*GMGL GFAGAKLSL
1681	15582	A	1689	11	394	IFILEARTRISSRTFFKS*INIHAPVNS AI*LIGIFFREKK/STCPYIYTQMFAS LFVTAQTRKQPKCPSTGE\WSKNLWN
1682	15583	A	1690	20	391	SEKGWYSCTKWQSMKLGITFFFFPP PKNPPPKSGP/QKGPFF*GKGPWP KRGHKN\RGFPKQARPPKPVFFLIPGK RGFLGPKGG*NPGEKRNPPWP*KGK NPGNPKGGPHLTL
1683	15584	A	1691	72	392	IKMIGSLFFGFAFFFFGKKTFFFPQPK R\GGKP*IT*TPPPGN*RNSGSPPPQKV GIKAPPPLPK\NF*EFGKNGVTFPPGG FEPPTPKESPSPVSPKGGKTNAP
1684	15585	A	1692	389	161	HGGACLRSQLGLRRLREDCINQGG*GCS EPCTPAWVTE*D/SSQKNQSKIKKSGL DNSFSIG*GILGLSTCDRYS
1685	15586	A	1693	286	363	DGISL*PRPFLRQPSQPS\LLSNWGC STPLCLAGFFVVFETGFLHVAQCLRQG FTMVAQS/ASQKIHT*GAFETIQVLFY WGGVGFQWRFFFFFETESHSVTQAGVR GCSLSSLQVPPPG
1686	15587	A	1694	1	356	ELLEPRGRGCSERRPCHCPPVRAEQDS VSKKKRERKYLFLRFNWSRLRIFTYFC */HPLQHNQNIISFTLQNSFGFSSRQYC PSPLEIIFLTPLTENLLGLFMKGIIQNW FFGVGLF
1687	15588	A	1695	3	298	KYFETNENKNIQYNL\AVKLVFRENLT VVNACVKKKEERFQVNNLALYPKN*EKSM LNPKGKIIKVRSEKNDIE*KNDENQ*N *SWYFEKITWQTLTD
1688	15589	A	1696	3	405	RLWCGWRNRHLGS*NRVENPETGLHRYA QLIFLTQVQKQVGEQPFNK*CGGTWAP TGKT/MEQPPKASSSSSSSSSSSSSSC KM*NIVFFKMGENLWDH*AKSYEVRTKA *TIKGVKDLDFIKIKHFCYGN
1689	15590	A	1697	6	392	LQRTLLVGLFNAAGNLKPKMLICHSEN PRALKNYAKSTLPVFFYKWKIAMTV*T VAAWLTEYFKPIFENYCS/BKIPFKLF LLTNAPGHPTGLMEMYKTTNVGSLPAN TTSVLQPMQORVISTPKS
1690	15591	A	1698	390	3	AIIESDFLTTSREVAKKLRVHPFVWLWV LEPIGKVKVKNWGP*KLNK/NKKNHCI EVSSSLFLCNNEPFLDGIVTCDEKWILY HNW**SAQWLNREVPK/HFLQPNLHQK KVTIVVWSAAGLIQNEH
1691	15592	A	1699	1	245	GGGGEYSKIIAIIKALKNTTYLGIYLIK \DVPDLTYKNYGTMLREIKYLEK*RARP CS*TERFKIVKMSI/LPNLIYRNTI
1692	15593	A	1700	2	324	GTSGTSGTSGTSQTCRISRVSTSSWTS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: In USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						GRHLQCHVSKAESWFWLSASSCSTGSP ISLSGS/GSSLSNSSKNLTLPCLFSSLL S*P*ANPVDSAFKIYPGLSSVGSCL
1693	15594	A	1701	183	372	PGVLLCWPGWSAVTVHQCDHSALQPRTP RLK*SP\STWDYRYTTPCPA
1694	15595	A	1702	29	382	GKRFPSCSWEPKFPFLTQGGFPPLHPGQKK KPGSKKKKDKSKCW*G/CREA/GTLTHY RQELMVSQFWK/TVWQVLRKLNVELPY DPAFLGLHPTSTQKR\DTMFMA/ATIL /ISERWKQPRCTS
1695	15596	A	1703	1	382	KKVKIIGEAAVEFPDTIKKIIBEKEVLP L*VY\NADESGLFWKKLQRTFISKEEK \SMDRLTLIILCKCSWVEQDGP*ALKE KGEHQLPVF*L*NKKAWTVRTLFLD*FH QCFVPEVRKYVASKRL
1696	15597	A	1704	2	330	KLNNLLNNNS*VNTETKAEVSSSLLEIN EYEDTTYQNLWDAKAVLKGGHVAPRHP LQEVKK/RLKRFQINNLTLYLKEL/EKE HINLKASGRK*MTKIGDLFGLYFVLNG
1697	15598	A	1705	100	342	APKWSIVCPPELVGWSH*/PSRMKPWT TROGFTMLARLVNS*RRDLPALASQSP GITGMSHRTQPLLINLMEIFTEILS
1698	15599	A	1706	600	211	SCSVARLEFSDVIKAHCHL/RTPLGKQS SHLSHLSS\WD*GRVPHDLANF*IFCRD RVLPRLLQAGLEL/LASSDPPS*ASEKC WNYRHEPTVPRQNLGLKTTYGWVFLKK YILTIVSVFSLMCLDHCLLM
1699	15600	A	1707	409	1	RGPPFFSPGKAPLKLGSNSFFPIKKTRA PKKPIFSPVSP/LNFPKPTGFPVPFPQ MGGFFF/CFPSLFFFFLPPPPFFFSFP PPPPPPPPPPPLFFF*DRVSLCHPG WSAVALSQLTAALTSMDSSNSPTCV
1700	15601	A	1708	154	2	IGKPLAGLTK/RKRENT*INKIRNEKGD MTADNTEIQSIIRDFVS*RTAHQ
1701	15602	A	1709	263	37	SAQLHPLNIONHRQSILLHDFLKKQD/ G/WPGAGAHACNPSTLGGQGGWITRSGD QDHGP*HISV
1702	15603	A	1710	390	42	YAGGFRAIFFFPLPREGAKNPNFPVGGP PFGGPPFFFFFAPSQKKEPGFFGKGVF* GGAKGFPNARGPFFF/G*KKKKGPKNKT PGFFL/MGPPNPGGPPPRGEGGKIGAKK KKKSIRL
1703	15604	A	1711	3	167	YTCVFVCLCLCDCMC/CVCACMYICVCV CTRVC*VCVCMCVRVCVQALTVLCKSV
1704	15605	A	1712	116	391	KRNFFFGPGGGGEGPKFN*RGPPPPGVK GIFPPSPPEG/GKKKGAPPPGIIFFWF KKKGVPFCGPGGV*TPDPGGPPPPGPPK GGAPRQGPL
1705	15606	A	1713	401	47	HHYATKFTHAHTCTCIQDTCNTCMQHT QVHT/HTDTHTRKVSVCVLIMAEQE RPCPHC*GGEAGACGVCAWLGLSS*TW RNRKGPAAHTVRVVGQEQSAGCAHGLVFP RSYLWT
1706	15607	A	1714	1	400	CVESCEVDIEMVSCCV/CSG*SAVCSGT ASAHCSLPPIGSRDSPASACQVAGTTGM PH/LYPGVPLKPREGLQFTLPSGQLEI QPTCENKR*HVPCAL*VQLTDIRPN*RY QFRVAAVNVHGTTRRTAPSKHFC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1707	15608	A	1715	413	3	LNTPEPQRSFFIVNSSEMILLVECLFVT SGWIYHERFLNPGREIDWATCYSETGPC PVTQDGVQWSNHGSL*PQTPRLK\HPTT SVFPVA/RQGL/NSVAQAGVQWHDLSL *CRLPSLKGSSHPRLPSSWNRYAPPPC I
1708	15609	A	1716	421	144	RLECSGGITAYCSLNLPGPSSSPASAS* VAETGGLLHKKKIVETGSHFIVQTAFK FLDSSDLPALAC/SWDYRSELLCPACFY NFCLFINIPC
1709	15610	A	1717	3	384	YSACVCVCVWVDVSVHRCMSISGH/ARI IRVGPAHKAQSSCRPVPAGCCTSAQTPP WCSAATADEPPR*GESLPGAYPGSHSTC CPGCCLDW*HSLPSTEPACRAGAPGGG H*AWLGCGGRAGRPG
1710	15611	A	1719	3	615	PVGSWARSSGAGWPPGSPQSVSDGEAGH SIPAPRGQCSRHRAEGRTARVCLSHCSF SGPRPGLVPIR*SLGRPDVAQIVPDSQ EGRKTGIHAEAVMFPLPGKGVKGCAGG RLCPSSPPSRCLDLGRRGMPPSSGPAGP RPSGVGSDLGRPGAGAATSSSSSSSSSS SSSSSSSSSRDGEGP\TGSVEAPGSL GPWLPSQPS
1711	15612	A	1720	320	3	GLKWLNLKDNSLYLILAKVDDCLDEK* YADKMLQYTKSVWVSRSRGQGVGEKK QATEAAQEWELRK\RLYWRKECDALRAA REEQKELRDVRKAKKVVCVRV
1712	15613	A	1721	44	373	KAMGQTLWKTVMQFLTKEEIGPM*QSCP T/DLALVFLGICTIDLKAYIHTETCTQM IIITLLIIAKNRKKASCSSVGE/WNKKL YYIRTMESSSLR*NELSSYKHWGGGS
1713	15614	A	1722	135	396	AQGLFCTSVKLASEQPLRILFQDKRNK \FEIYGTSG*L*SIIIICNNLQSKFOMY HHKIMSSLGAVAHACNPSTLGGQGGQIT RSGD
1714	15615	A	1723	4	383	LNLRAXAKILLEENIGIHLPDGLDDDLF LDITPKSQATK/AKIGN*GFIKLKHFA AKNIIKKMRQYKEWKIFGNHVSDDKL VFRIYK*HLPLIIKNSSS
1715	15616	A	1724	2	405	NSRTSLILNQNL/IKLSEKGTWKAKTG *KLGLLQK\ISKIANAKEKLLKEVSA TSMNM*MMRK*NNFIPEMQKVLVW/I* NI/PLCQSLIQNKALTLFNSIKAERGE A\KLEATKRWFMRFKESCLHNKVKQDEG
1716	15617	A	1725	90	400	SQLLRLKQNSLNPRESSKTTTRTKVS HWHKNRHVNQ/YNKIENSGINLHIYG*L TLNKGDEASQYSS/DILFNKWCQKQK \YLDPYLTPCTKISSTWTISGFL
1717	15618	A	1726	390	1	TFFFKI\KKIL*FIWGPFRPKIANVFP *QNKPKIEGIPLPFGFKIYYRALVTKTAW F*HKNPPIGQRNKVENSETNFHPPELN FFFP/YRGAKNHGWGDSLFNKWCWENW ISI*RRMKLGPNLTPYTK
1718	15619	A	1727	3	365	HASAKSNLRWIKLNLRAKTIKLEENM GENLWDELSSRGFLDRT/PKLYSILKL RK/WNFIKIKNFCFSRDT*KS*MAGKNI LSGKDLYSEYLLK*CNLIIRQSKTST*M FIAALFI IAKH

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1719	15620	A	1728	368	2	RNCLNSEGGGCSSEPRSRHCTPAWATEPD SVSKMK*NKKINK*IMFLY\EQQSETEY FKLPLTLA/SRNMKFLGINLSKGVQDLE TENYKILLQEIEEDLNK*RNKTY*WIKL NTVKMKSILSKR
1720	15621	A	1729	326	30	NPFGGPKKGGSGREIKPPLPPMGKPLF F*KTNNKWWGGAPPVPPS/SGVLSQKK TFTLEGGGPNKLNPPALP/ARGPKKNF FQKKKKKTQNPQSOREE
1721	15622	A	1730	1	374	IFNADKIA\FWKKF*KPQGTSVGREEKQ APGFKAGRNLTTI/L/GASAVGFMIRA ALICKAANPQVLKGRDQHLPVFRLLYN KKAWTRTFLDLCFHQCFVPEVRKYLAS KGLVFKVLLILDNGPC
1722	15623	A	1731	389	1	FPPKIFFFTSTLFFFPFFPPPPFL*P/ SPPIYFF/CAPKKKNFFPPPGKNFFFF KTPPPFFFFF*D*VCLCCPGWSAVAQ SWLTTSVFRVPVI
1723	15624	A	1732	118	422	DIITHLFKWLKPKK*EKGLNILFTKEDM QMEKNLKRCLT*FVVKELQIKMRYHYPP IQMAKI*KN/STISIAWQGYRTIGTLF/ HC**EQPFW*FLSKLNMILPYNPA\IML LSIYPNALKKHVHTKTCM*MFIAALFII TKNWKEPRCPSICEW
1724	15625	A	1733	407	1	NIRGPFGRGLIQWGLLIWPKDSFPILGY PPFPSPKISFFFLARSCGAPNHFPLPN QSPCFPPQSFLLGEEKKEFLPGYSLAPP FN/RFGGS*RVKRGNGGPIPMGESFLFF F*DRVLLCCPGWSAVA*SRLTATC
1725	15626	A	1734	322	362	TAIYIYII*LFTDNIPSHPTWIEIYKE INIFVPANTIPVQHRNQGVICTFRKTI TVTDCDPANGSGQSKLTKWKGFTILDV KN/IRDSWEKVKIG/TIN/GVRKLIPSL KNDFKRPKT
1726	15627	A	1735	49	395	RGGPGFFFFFSSKKSQILPPGWKGRG EPRVNGTPPPRGKGNPPAQPPQEGGKTG PPHKPG*FLCFLKKGVQKGG*GGPQ/A PGPKGAPRPGPPKGEGKREGPPGPTRN LYYAH
1727	15628	A	1736	417	2	FLFFFFLFFFSFASGPEILFTCL*HT HIHFLFFYSKST*PPVFAGGMFQDPQW LPETKMVPNFKKRTTLT/YIP**KLCE CDLSNFFCFF*DRLLLCRPGWSAVA*SR LTATSTFQAQANRTRG
1728	15629	A	1737	316	338	FFFLSFYFETESYLHHP*GFIVKLSKVK DIEN\LKKTARGNYQVYTKGASIRLAAD FSAEISQAWREWDNMFVKLKEKTNWQPR IYKTLFVPHF
1729	15630	A	1738	197	379	QKRAQIDKAFICRDIAL/P*PQ/MYYW ATVTKTAW*WYKNRHIEQWNRW\PPPI KSQSYSHL
1730	15631	A	1739	4	401	RGYRHAPPSLANFCIFSKD/MGFTVVLN S*PQ/CNLPASTS*SAGITGISHCTRPO MATFLIGPHKIIPWSVLWPNL
1731	15632	A	1740	94	117	KDRPMVPPVGAGEDQADEFCRGHASLWS QLVSAPTTPIPLPGRDVPSRATFFPAAL AAQQPP*ASPYPLPPGLGAGHASASPT VPFSPISSTGS*ESAL/PAPRPGGSG

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1732	15633	A	1741	3	390	VDQFLISHDLSKLTEDVHNLNSSTTIG \EVEFKVKKL*KKKSSGPDGIGKIFY TVREEVTPIL/SYLF/HBIEKETLVNS FYEARIL/IPKPDKNK*TNIDAKTTS KVLNRIWQYVKIIQHNVGVFV
1733	15634	A	1742	3	442	DLHSRVEPRVRPSVRKQ*VLLKVLICA SKDTLKRAKRQPIGWKIFVNMHPDKDL IPYKINMQKSGVFLFTNNSYSSTTDND INKWAKDLSRHFSEEDIQANKHM\KR* SVSLVIREIKIKTTGR*LFTPKCWQG*G EIIITLVH
1734	15635	A	1743	411	2	LPPFKHPPPEIILGAPKKKITLPPPRPK KCISLKGPPFFFCRYRVLCCPGWFST PGLKQSSHLGLPKWWDYRHEPYCTQSSF SLSFFLKQTGR*WFDLSNFFFY/CYCFI YFSRDRGLTLLPELVLSWPQAILL
1735	15636	A	1744	1	393	RPGGPPKGRSREQGREGRSRRRRPRAP WARSHMWGARVFSVPSFDQRQSKCVQ SSYKQQLPARARDGTGNLIRGAPLFFF* DGVLLCRPGWSAGFKQPSRLSLPSR*DY RRTPPHPANF*ML/CLRRSLT
1736	15637	A	1745	395	0	PSAPSFSTRL*LGEPPGFPPPPFLKPP PRN/SIFGAPKKKFFLPPPRGKFFVSLK GPPLFFF*DGVLLCCPGWSAGFKQFSHL SLPSS*DYRRTPPHPDNF*MF/CLRRSL T
1737	15638	A	1746	397	1	CGNFLKREKNFEARRFLQK*AARFRNIR *VTPEITAFCL*HVASFVFLTFNPT IPQLYCLEPLGEMGGSGSKLPPFPSTKT PNPLISVNLCPF\AIKWENFFF*DGVLL LHPGWSAVAQSRPTATSTS
1738	15639	A	1747	392	2	FTKKGGRGGLSP/LPPQKIF*KKKTLK KPPFWQVWFPSPLFFEQKGGPFFFKK PFF*KRPDPQPQPPPSIFFFLLFFFR /HLVAQAGMQWRHLGSPQPPPGTLTQSS QLELPHTPPHPDNFCIFGRDR
1739	15640	A	1749	33	403	IKGFKKRGGGAPQKKGGTGAKPPPPP PQGF*K*QKRKNGSPNVFFPNPGGPPP PPPFWDKRGGPPRGGGAPPPRGKREN FFPTLA/HGKKEKKK
1740	15641	A	1750	3	396	KRQTTNWEKVFA*KN\ADGLISLIRKRC LKVKK/W*R/DMNTQFTDKGILMTNKH KRSTSLIMEMQHKAGVIFHPSDWQKC* STDNTQS*QGHEMYTIKHSW*TFDYQQ PF/SESNL
1741	15642	A	1752	30	419	NEGIGAGHEVSFAANKCRSMRKNVEVLA LNRRLDGELLSGLTSTQALPGWAYLHLL SHHAVRPLFLCFKRGWVLLCHPGWSAVA QSQ\FELGQVILRPHLPSS*DYRSIPP CLANFKNFRERARYACR
1742	15643	A	1753	16	410	VGPKSLQQVWAAVQATLPESYDLAHP IILKVSADRDAI*NLWQIPIVAS*YIP LGF/YSKAMPSSVDIYSSFEKKTHFFL TGGGGPPLYSNYLGRLGANHLTPGVKN QPGQFGKPPPLQKVQTLAARG
1743	15644	A	1754	2	17	NSSLIKHRRITHTGERPYQCSECGRVFNQ NSHLIQHQVHTR*RMVI*SR/CGKDPT QKSTLI*H

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1744	15645	A	1755	138	380	XPXXXSPXPPPCPXPLSSLFLTKCSAY* TPAHRPPPPGPFVPPPKPCCPPPPPLRP WPPLPLLTNPIPPPTLSEHPGPALS
1745	15646	A	1756	194	3	WLCIPIRHTTEQQPGPF/LIWSQPYS PLFCLFVF*DTVSLCGPGWNAVQSGLT AASTSQAPSL
1746	15647	A	1757	2	403	RVLESPTLAYTYLLFYLGATILMGVNIW KQPNCPK/GQOKIKLOYIYRMEYYSAL KKK*ILLFAIR*VNLGDI MLSEVSQ\SR KKNIVLSHMW
1747	15648	A	1758	398	65	FFFFFFFFFP*TKGLGCIHRCDHGSEFP RIH\GSSNAPSLAS*VGTTGAFHHARF TLIQSSSVHVSTHTLHPYPSLP
1748	15649	A	1759	456	31	FAKRITDKLLSLIYLAT*KGEITKALI KQ*\LKAQAKNSLKRHTIVLNMKL/CL ILLIKEMQIK/STLRVHFFITLAK\I *KLGNTEFCWQGL*GTLIHCWWECK*HNS YVGGIWQ/FSNKL VQI*YNSAISNLDG RVGRPG
1749	15650	A	1760	3	378	QFQYFYNGSVIKAVWYWSKNR\IDQ* NRTESPDKNLHKHMLIFDKGINTPQWR KDDLKFKWCWNN*TSCTQKKKKKGGGP *KEQNLTPPGWEDIIIFLFGAPKNMPGAG VKTRWGGKNGPFPQ
1750	15651	A	1761	69	384	YTSASWGGARYTASAAGWKTLLLLFLFI *DRVLLCHPRWSALTQPRIIAASTFQ\V KQSFWMHIGDWDYRRCMPPCRFNF LCKKKKTLRRQEVNQTPALVRV
1751	15652	A	1762	390	1	KFSTPGNKNLFFLKAPPPFFFCRGRVLL CCPDWYSTFGLKQSP/CFSLPKCWDYRR ESPPQAFVFFGLPSLPFSPPAPSLSQ SSSFFF*MEFHSFAQAGVKWLN\LFGSL QPPPPGLK*FSCLSLPPTRP
1752	15653	A	1763	2	390	PRVRGFFMRKFVDSYLVPTYTKSNLWITI DLHVRKAINLLN*NVRHLYDRELCNG FLEMIKKT*AAATTTKLDIFIKNFCAQ QMSS/MKVKRQSTKWKKCSYHISDKGL VSRKYVKAYNSSIRTQSH
1753	15654	A	1764	334	3	WSKRSGPPLSKNQTKKNATKPQT*KNW INEIGPII/NTSPSKERTGSNGFTD*FY *TLKEELLSILLKLFQKTEKSVIFPKSF YVKDHSSCLSGIHPKDANMEQHMQINQC
1754	15655	A	1765	259	1	KSTLFLMKKYWKSFLKKHFFLETRSL D/SPG/GVQWRDHSSLPQRTPLKQSPH LSLLSSWDHR*APPCANFRFRPKTRIG RDV
1755	15656	A	1766	402	386	FKICKSRLRKI/KVQDEAASPDLAKTI/ DYEGHYTKQIFHVDERAIFYWKMP/R TFIARKKSMMPGFRASKDKLTVLSGANA AGDLKLPVLTYS/ENPRALK/HYAKS TLPELYKWNTKAWMKIQKFPS*FT*IFM
1756	15657	A	1767	2	406	PRVRPRVKLITLLNVSQRWSSEKKKKK KTKKKKKKKKRGGR*KKKKKPRRG RVNLFFWGPKKSTPPRVFKHRGGEK/PP PPPPKPRERKPSLGVGSTWHGISPIKH SKTKSTK
1757	15658	A	1768	14	409	IASGFLFFIYFGVIGRPPKRGVFFPFG GGAPHPQGGC*KKKRGGGGPPFFFP

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						SLGGLGRFRPMSKIKTPPSAGGKPP/FFLRNQNTGGGGPPQ*PPLFGGPGGKNFSPPRGGGGGGGPKTPPPPPGGGE
1758	15659	A	1769	305	1	TKTGPFPSNRRAKKKIVPQKKKKEKKYNCFVTAPFKGIKTEATD*EKIFAKHLSVKG/LVYL*YI*ISKIYKELLKLNNEKTTIPIKK*AKDLSRHFTRYTD
1759	15660	A	1770	148	402	FSPVSLG*GRGNIYAGMSNV*EVPPEIDFOHEVKRALOTSFOVKLVKIIFFKSTI*KSLAK/WLAVVAHACNPSTLGG*GGWITRSGVKSEPGQHGE
1760	15661	A	1771	250	2	KKKKEKKIICFVTDTFKGIKTEATD*EKIFAKHLSVKG/LVYL*YI*ISKIYKELLKLNNEKTTIPIKK*AKDHSRHFTRYTD
1761	15662	A	1772	407	1	KKIRRGGGQPPLFPLIGGGREKKFFFFPKRGIFY*TKAGPPSSWAKKKKFVFKKKKKEKKIICFVTATFKGIKTEASD*EKIFAKHLSVKG/LVYL*YI*ISKIYKELLKLNNEKTTIPIKK*AKDLSRHFTRYTD
1762	15663	A	1773	1	406	KKKKKKPTTFPGLPFFFFSLPSPRVGARGPSSFFPSKPGLC*IKSGVSPAPKKKKPRKTNPKNFPNPKGGGEKFFNLPTHPGGTTPPF*RRRNPFGFAPQKG/EVSPGGGRNSRGEPRGGPKKKKKKGG
1763	15664	A	1774	2	378	AAGEWLHQSLQSLPGLKQSAFLGVSKW*NPWHDPPPPAPRFVVVVVGGVVLRSWFFLGAQAGIFFFF*IEGSHYVAQAGLE/PPRLQGSS*LNLPSSWDYRVP
1764	15665	A	1775	1	431	QQMRDKRNLFRHNK*GIRGIYLNIIKARHEKPTVDTILSGESFSSKIKTMLISPFLFNTVLGVL*ARKRKDI*VGK*EVKSYMFTNDMI\LDNPKDSTPKKKKTGYFMGGPGSKPPPPQGGAFSLSTRDPLEREFPKTAFLTGLQKKIKGPKFFS
1765	15666	A	1776	334	402	KGGGGVGG*QGPWRLAHCTDK\KBERKERERKRQRKKERKKERKKEKE*MKNNKKNDK
1766	15667	A	1777	406	3	SPSSSSSSLSFPPPPFWGGPRF/SPPPPVFKPPPPFFFLGPPKKKFFPPPAV*FFFF\LGPPPPPPPPFFWEAGFPFFSPG*GP/SGPMAGFRSLPPPGNSLSKKKSEGLGEGGNSVLTRVLLISSYQIPGNPR
1767	15668	A	1778	70	409	LISFLVSSLIVRLYRPLCLFPDPKSGHCIPCLLPFLWILLHIFLFMHSFIYCLINDRVLLCLPGWCAVVRPLTAASATQ\IKRSGSHLSLPSSK*\WDHRRCPGFFFFF
1768	15669	A	1779	390	31	SHLSLPKCWDY/RL*ATTPSQKILVFTHG*VLSLLSLSFLIPPD*TF*KMSLMRPSLTQKSSIIQHDLLDKVPITIFLRQSL/D.S/VTQARMQWHDLSLQPPGLKLSQPQAL\SSWDYR
1769	15670	A	1780	357	1	LTLFWGAQYLPKKKGKGPFFLLSLSPSPSVWGPLPQKKKSPPLCFFFYFLNRVLLCHPGWIAVVQSWHSSAHFSL/VLTRFK*SSCLSLSSWNYRCTLLEPPNFLNFWYRQGNALPKLVL
1770	15671	A	1781	122	254	RKNE\WSGAVAHACNPSTLPGPGGQIMR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SGDQDEPG*HEPPRPTDSFFLYPSH
1771	15672	A	1782	45	387	TQTPKLRRFFHFSLLKSWHYRCSPL/PQ HNGYFLTNLDIATSMFFFFKORVSL/LAQ AGEQWCDPSSSLHPQTPGLRR/PPASASQ EGETTGAHHHTWRNLIYFFYYTYKF*GT YPMA
1772	15673	A	1783	1	401	FATLARLVNS*PE/CDLPASASQSAGI TVSPAHLAISPSFPAMPSSGLGLSYPAY HPGLGLRCHLPVLTSPWSDTGPSSVLP DAGALHCPPEPQHICPL/LSGWLQTP
1773	15674	A	1784	432	1	FLFLFFFIKKKTPFFGAKPKNRGF*KPP EFFQIF/S/CPVFLGRFPKPQKEFFFPPE REMGFFFLFSPQGGGPARGFPPPLNQG EAPRAGHKKKGPNLGGRTFFFFFEMES \FSVTQAGVQWHDLSLQPLPPPFRFS CLTHAS
1774	15675	A	1785	15	434	RLSLSCCGREEHSTLPGAPWRCTETAWA DSPDPAPSPPSALPSLLPFHVYRDVCPV LCLRGWP**MVERGRLGISPTWLLGWPF PGGA/PHIKPE*YFLFAYTILRSVPENKL GGVALLLSILILAIIPILHISKQSIIF
1775	15676	A	1786	1	258	CWPETPVLK*SHLDLTKRGEDRREPVAW ASTTIFFFETGL/NSGAQAGVRVWHLGS LEPLPPIPSLFMTF*GPCPGLGSSWPLR EF
1776	15677	A	1787	399	63	SLHNQVVKSTPTLTKTSKKISHI*STWPG VVAHACNSNTLGHHGGRTA*/RSGVODQ PGHSETSSQRLRNPIYIKKCIKYLAHSK CCINDSFTVSVTSRKLIGKREVSPNNIT FR
1777	15678	A	1788	3	474	MSISPVRWNSKEAGRAANRQFPSPFWK DDSRDASPPPEPASPTIG/PIRRLAESSW TWGSPCAEHPRARAGRRKAATDCPWAAG SQWRGPAGQGAPRSCLFPGSRTAARAQH PRVAPPPPPAPLNTRASALRSQLPNPL *VMTFRPPAAAPRSPVGP
1778	15679	A	1789	66	395	LVQPLDFDIWHSRLSLWGRDLLWSGKE TMNPNLHNSIGVLQEWQGSVDVKRRRLM ESLTGPAADVIRILKSNNPAITTAECLEK ALEQVFGSVDSRDAQIKFLNTYONP
1779	15680	A	1790	413	1	PSPRALITDYS*EEGPRFWQV/EKKGQP LKPHPLGLGSPHQESPRVGPCKRGYNPF *KKRAKFFAPGENKGPPFWTGRDPTF*G KTKKKTNPCKGKGKGPFPKPGQFFFFF LRRSLAWSRLECSAASAHCKLRL
1780	15681	A	1791	314	1	KTKPFLLKKTTPPKKNKKKGSC*DKARY QTRKG/IVNLGH/HPSFLFYFILFFETE SHSVGKAGVRWLRLANSQTSPSGFQQFS RHSKPSRKDYRHPPKRPQECVQ
1781	15682	A	1792	104	409	EKQSFADFWDHFDLYFDNVK*KEGEESKA GEFNASTGWFGNFRKRL/RFKNVRVTGE PASVTQEADEFPDNFKKITEKGYLHG KFLMYHEAAKYLNFWCPTK
1782	15683	A	1793	392	2	GERERDRL*REERERERERERERERAR ERERARQGTSTVESRF/HSYCRRDQDVA RPKAKGEVAAGRGSPDGLQVGRGQ*PGP SLRPGPWREWGFPATYLAGGGPIPTGEVE

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						SGEEWAQQGEWGQALGPP
1783	15684	A	1794	405	119	IIKMAIVPKAIYRINTISIKVPMFAFFTK \\LKTIIKFI*N*KRARIKAILSKKNKA GSIPLPDFKLYYKAIIVSKPTWCWYKNRP IVLVHSRTARKK
1784	15685	A	1795	455	3	CSVQAGEQWCNHSLSQBPQPPGLKWS/C PSQLPK\\WNYRHVPPRPALTAHPALTAD F*RRKEYKLMRHRGKKWHDFTLRSKKMK AMRHEYHSFLTYPNGHLYLHWQFFFFDT ESHVSQAGVQWHDLSLQPPPPGFKRF ERVPGGNSGAD
1785	15686	A	1796	2	134	PRLQHCTPAWATPQDSVSKRRDMMTDD AI*KG**ATTNIIYHKFYNLDEIDQPL KKHKLPLQWTYBI/DNLNSPITR\\IEFV ILNSKKKYPGSDGFTGEF*D*FCLETKK RYDYRPCNLKRIISDYKNHLHT
1786	15687	A	1797	1	404	PTRELTGSSASGMMVEIFPKTYLISSAC WVKISKIDLKLFSPFFFFFGLEGGFYFC PPNSRGGSPGGKEGLIEPLPPGLKGIPP PPPKRGGEFGPPPTPAYFFFFFLWGGGV /PF/AVGGGGKPI*GNPPWPQQ
1787	15688	A	1798	2	383	SGWLWACRSPDSEPLACPAGPRQ*GAYH PGQQLMMVR*VSQCCWPTPPALHSIS\\P RP*LPPRRAGLGTCSPP/VPESLLPPW APAWPKPRRALPPA/PPVPGPIDRPA EECRMVRDWAAPPAAP
1788	15689	A	1799	35	410	ATGFSLGKVC*AFSFL*PKLDFWHLYF QASGFLL/CHNSPSQNTSCSSFGKHGM VLRVNSL*PDHPWNEFYFLNFIYRDS /SLTILPRLVSNS*AQTILLPLP/PKVL GLE
1789	15690	A	1800	65	415	KKGVLKGGPPQPLGV*GPPPEKGGPGP F\\CAPKEKPLALGEPKGP*RGPKGF FFKKGLEPGAPPPKPRGEKPPVFKGPH PFCKKGGDKREKNGGL*RRKPTLGN PPPPG
1790	15691	A	1801	417	3	NLGPNIFFPRAPQNWGPAPPLFFFLKKN FTWGGGSTPLFP/LNLGGIGGFPFGLEV YAPPSPHG*PRFFFKNQKLPPVWGALY SPFFGGWEN\\RKAPPGQTLFFFFFLK* GQDLPLMLLQLVNYWAQVILPPWPPKV
1791	15692	A	1802	1	431	QPCTPGLK*SSCLSLPSIGDYRC/RTTV PS*FFFFFLEKGVGFIPRGGIKGLDNC* LGPHPELK\\NPPQNSQEVGTGPPPR PG*LFFFFETFFFF*KGFFFLAQP*MK WGALKKTPAPSKRGGRGGTPMEPTH FLKEN
1792	15693	A	1803	256	399	AIKNIHDS*EEVKISTLAGIWKKLITTL IDDFDGFKTSVEEVTVDVME
1793	15694	A	1804	407	2	FEKANLPFLFKNSGPPNVPGRGMAGVP KFCPSKRKVGPIFFLRLFLFYPCR RPPLFWPAFGP*KFFLPQVFAPAF*KPS PKKRAPVFFFFFFF/RDKVNLCHPWS AMA*SQTLVTSVSWAQAILLPQR
1794	15695	A	1805	429	116	LLTKKKKKKPLACGESGLGGP*GTVTG V*QAEDTHVI\\VLSSAPSLSEEMTDS MPGHLPSKDSRYGMEMLTDKWTWDGGA WDSSPQGANCKRGARQASGS

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1795	15696	A	1806	2	408	FVIFVFLVETGF\SILARALACAISNS* PRDLPTLASQAGITGVSHRTWPRRSCV F*EAFITMLMVLHI PPSLLWHVFTHL ALSS*CFLFRLRGFPWAVTQAEQQGHD SLQPPPLPGLKWFSCLSLPS*NYR
1796	15697	A	1807	1	196	FRLGASLDLGGCGSVSWTPAPPLPPPP PPSAASGIS/SGSTSAAGL*SCRTAFF SFLSSFFFFFLKKINPFPFLGGI*PFG GPRLV*GNI*PPPGQ\DFLGGRGGKKP WGGGKFGQGGNFPPLPKKPPGPQKNPP \PPPPPPSAASGISMAHLQLPACDRAA QLSPLSSHLFFFF
1797	15698	A	1808	395	3	LGKMMNNPKFWQCEATGTL/M/HCWV CKFVQSFWNTDSIY*G*AAATHDSAMLL LGMHSMPTCTFVHQKT*TKMFLAALFIL PLNWKQV/RCPVI\DGVIPTMDQSTAM KMNLHAKTWMNLRLMLNEKPR
1798	15699	A	1809	7	454	IPGSTISLQPPPPGFG*FFCLSLSSWD RQPAPPR/LANLRR*T*LQSA*LWR\RG PILDEMKSFMNCNSLTEGVKGRVEMMS QNGRLLTKFCHVGQACLKTPDLK*SARL GLLKCDWYSCPPCLTQMPPSFPLFF*D RVS/PLSPGWS
1799	15700	A	1810	20	355	PQCAHGCRAPVVCVCFCCVCVCSHCV SMCMGEVSAGWTLCLCLST\CSGAYA CDWGGG/CYSACVACVCAQLLTC IGMWE*GQAGQGEVLLDLPLCLCSCWAP Q
1800	15701	A	1811	3	414	SSKNDNNSLQEFMDKIAGMKKNLGNL LENNTV*EFHRAITSINNRIHAERISD LENWLSEI\NRQT*KIVTRNEQKLRE DYVKRLNL*IIG\VFEEGGKAYLQNI FEDIVHENFPRFARDANSQIQEMORT
1801	15702	A	1812	1	443	AGKSPSPKKFKKGFGGRWS*FLGGAGG GVPPRPGIQGSNYRFF/SPPPPLGEEK KPPFKKKKKTPOKLQNGNPHYPFNPRVH GCREQQPWEKAPDATROPHYADKHVEAG EPREPPKPHSEPLFSSPRKRPLFTRSS T/SGASPP
1802	15703	A	1813	411	66	WKNNVFNKECLER*IF/IIQKKLDP\F LTRYIKIKSK*IKDLNIRLEIKKTPGKE SVTLAKWLIRSPYLSFP*QIQSKQ*INS YVLIKITKEERWSTSKEYQKPWRERKAM YKIK
1803	15704	A	1814	369	20	QEVRFPSIYLSSSNRKYVKDSNARFTKEA IQIANIHMKNCPSTLIVGETHIKTSKGY HYVPIRMALIKD\CNRRCGETGTLIHF *WEWKMVQPFQKFF*WFPKKRKIH*QFD LATRS
1804	15705	A	1815	2	675	GLAILGRRLRGEACTRSPFSSILIFMVS MGEWPGVP/GIKGTRTGAEAVPTRRRKS SIWPOTGGAGESSG/PLRGLPRQGGKPGS PRGPGSGPPQNCARWWHPQAAPLGACCF GPEPSRLPPWRQGNWCLPSTPSSSA*EG WR/PVLQPGFL*SPSSSLASICPGAERGP PGSSRP/GLRGAPGG
1805	15706	A	1816	273	2	MESHIMWPFITIGFHLVQCLHGPSMLQC IAVLHSSYLFIYLFYI*DRVLLCHPGWS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						AVVQS*LTGASGSW\LRRSFHLSLP*C* DFRHEPR
1806	15707	A	1817	40	404	GLHE\PGVQGCSEL*SHDCTPAWUTSET LTLKKLKIKKSKKKKRANPRGFERPTFG EAGPGGLLKAIISKPRVIQGTQKSGALL GFNSNGGENHPPQKQPYLGGLYAKAHSP RGGGPPSPCG
1807	15708	A	1818	392	3	EKYNMSYDIKSTNHRKNCKLDFIKI/RN CCSLKDTINKMKMQASNLEKIFAIHMPD RGLIFKRKNKSNLVR*QPPFFKEAKDL NTQKSQ*TNQ/HGSKETSLIIREMQIKT T/MNYTTSIPT*MLKIKKMN
1808	15709	A	1819	311	431	EVVGRWWLTPVTPLSLWEABAGESRDQE *KLCTTVEK*KTISN/HDVPIRSSWTGM VAHACNPFTLGGRG*ITRSGVGDQPD* HGEGL
1809	15710	A	1820	68	410	AKKNQGGPMVFGFGGKIPPKQKKVRG GFFAICPKEQVFFFWRAVVQSLNHC SLQPQPPGLKQFKQSSHLSSLSS*GYKH VLPCPANFILFSLVETGS\SIYFPGWSQ TP
1810	15711	A	1821	408	1	TPFFFLRVLRLTPLLNFGPGFPWPW GFSPGPLLKGRP/CFPIPKPIFQPGKW GLVFFFPFFFPYPRGSR*NLKKIFPNF PFFFPVFF*ILNPPFFFPFFFPFL*D RVSLCRPGWSAVARYRLTASSTSQ
1811	15712	A	1822	362	76	SEIAPLHFNVGDRVSLHLETNKQSNKQT KKTILFRDRVLLCRPGKNA/VEVQ**LP AASN/FLRLKQSSCISLSSNWIYRHAPP HLATVFNFLLIFE
1812	15713	A	1823	314	2	VISKPCPRELTCTYGVSLTQCSMFGRM KGLLLIWPVCEVRASGRPPLMGSEBP LCPAATPSGRCTQ/LH*ERAMTMVAVL SNRKGNGVGR*RNQIVAVS
1813	15714	A	1824	57	389	NLHLLQLPTYTDADSTGPTLSGMNVKNL HWSYEEKYRSITGVQWLILGSLQPLPPR FKCSCLSLRRWDYRCAPPERRATF/*FL VETAFLERLTSCDLPTSASQSADITGV
1814	15715	A	1825	410	70	VPIMSATQDYRHEPFRPAGRFLKRLKME PPHNALLLVI*PKNMKSLHKDVCTPM FSGTLFALAKIQKKPNCPSMDEWINCR NY\MHIYDGICYSALKKNEILARRSGTR L
1815	15716	A	1826	2	411	FLVEMGF\SMVVIAGLKLPTSGGAPASA SESAGITDVSHRAWPVFFFLKRLVLVG RS**A\WPHTNLIPPLPSGIKGLCPNS AGGWEKGAPPPSGKF/CEF*GRTGTTN FARG/WTKTPD
1816	15717	A	1827	276	3	GRPGADFRVRPQLLQRFLLIYLFTEME SCSVTQAGVQWCNLSLQPLPPGLQ*FS CV\K*FSCLGLSSWDYRHMPPHLDNKS IFSRNGVS
1817	15718	A	1828	1	391	LEPRRRFLQCVQDCATALQFGQSKTILS QKKKKKKGGPP/S*YQKGQCPSGKKGR GVAGKGAFGPGFGGENKTPPGGGPTGEG PPQKGVVGPSQGP*TKGNLWGPGGPKL GGKGGPPGPTKGGGGPSSF
1818	15719	A	1829	2	134	DHLSPPVVNQPGQHSEAPSL/LINIWK

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						AGCGGAHLSSHL/LREDHLNLEVOGCSE P*LHACTPAWATE*DPVSQTKLN*NIWK LAGCGGAHLSSHLGRIT
1819	15720	A	1830	427	107	VQHQPQQQRESPIIIYQKLARGGARCL *SQLPGKLRLENRFN/SGSERSHQCTPA WVTRDCLKRTGITRASSQRLSVGIKQS CLNERTAQLQVSAQSPSTVSTNL
1820	15721	A	1831	3	540	VQFPNFKIYYKATAIKTVL/QHKQR*ID E/MNKI*TPEINSYVGYLNFNKAIAI QWGNDSF\FKKWC*DNWISACKYSQTSV SASSASSSSS
1821	15722	A	1832	385	2	AGRQSETPYHNSTIMKVSQVCVDSLCL LPGSLVQDSPNI PAQRKRFLRGSFWL PLSRFSRVGWPLPHWGQRSSGFSLPR/P P*SQIPAPRSPPPAGPVPARSWVCGPRP QTRPLPAERPSRPRRL
1822	15723	A	1833	7	399	RISRSYLSEYGGSGKEHPTLGASYARIM VFG/VFIIYF*RCCLA*AQWYSHSSLLP QTPGLKHFP/AQAS*GAGTIGTHHT*L TFAF/IFVLGCFFL*NKISVTQAGGGC NFGSLQPPPPGLKRVSCLTLPR
1823	15724	A	1834	2	306	LARLVSDS*PQ/CDPPASASQSAGIICV SHRAQPAEEILKVFGLCLEPQRPPTDI FIIPYLC/LFEMESCSVAQAGVQWRIL GSLQPLAPGVKRVSCLSPP
1824	15725	A	1835	12	400	KKGMVFKQLKVGKKPPFSCWGPNNKKRD SPVFHHQDPIFFIPFFFGNGFLFFPP/ LAGGQGGNLN*PNPLPWGLKEFPPTPR GRGEKGGAPPPPINFVFLKKGGFPLGGR GGLEPPPLGDPPLPPKRG
1825	15726	A	1836	220	401	KGSFVFIPQPEGEGPFLG*LKPRFPGLK QFSCLTLRSGNYGPLPPPVIF/CGFL R
1826	15727	A	1837	12	357	GLGGQMNGSLGTQTSYEDLMSSS\FKP NSPPPTPS/VRTGHLPK*PLESSNGPPP PQVSHSFQGWARGHPSPPPQWNTFPSP PQQTQCSKTD*PPPSPPYLQEGSNA PSLA
1827	15728	A	1838	8	380	LMKTHAKLLNKRVAN*IQQYKK/HH/NQ MGFILGVQIYFNF*KINLIQLINSVKKK KN/HSSSSSSSSSSSSSPVLIKSLC NLGKNKRNFCLTKGIYKNKTE\NSMKI ILNGEQLNAFPLRLGTE
1828	15729	A	1839	2	444	VPGDAKWFSVLHLKDAFFFIPLVPESQY PFAFEWENPNTREK\TAVLP*GFWDSP HFFAQPLERDLRGLQLEDGSILQYVDHL LVYSPTQEASDQNTIKTLHFPADRYSKV SKKKAQITLQQVHCLGYILTPGTCK/LS PERVQAI
1829	15730	A	1840	1	642	EIKGIQIGKEEV/SLPADDIDYLRIDS TKKLLEVICELNKVG*KINM*T*IVFLY IGNEHLELEI/R/ELMPCIKTSSTMKYL EINLKKDV*DLTYENYKVFPREIKIT*A NQ*BILCLCSRRLNTKM/STFPQVFCVY YAIPVK/IPSRLVLVLVDKLLKFI*KY RGPRTAKTTLKKKKVVRLLTLLPKSY KITVITIGWYGPQDRQVD*WNRIS
1830	15731	A	1841	3	423	HRITSE*DLHLARELIW\SMYGSLDHKN

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						YDAELDRMAMPCLCAIAGALPPGYVDAS SSSKAEKKATVDAEGNFDPRPVETLSVI IPEKLDSEINKFAEYTHEKWAFVKIQNN WSYGENIDEELKTRPMKR\PY\KTYSEK D
1831	15732	A	1842	33	179	YMLGGRGCSDLRSHCTPAWVT/TA*LS KKQYQORQQNRLQYHLQYERKK
1832	15733	A	1843	349	10	LAGGLNSMEGER\LR*ERECTQQQMVH DKYCKDLMGFGTKPRHITPFSSFOAVQP QQSNALVGLLGYSHQGLMGFGASPPA KSTLVESRCCRDLMEEKFDQRK\QWVLK CR
1833	15734	A	1844	15	856	AAEQLSFIYKLPQNPSFSTPGSSLSGTH GMQTMLGSTHLPNLTDMLGPGLGVQGI SPGCACQGRG\GGGRECCSPGVSPQG \SAVGRGAGPGGLTRSGSGAASALVRP GEKGCWCRTASGAGPQRRQRTGPGSWG LSFSQTSEEKCPSPAGSAGAPVCQRRQ SSFAGGCGTGAGAPGST\GDAHPAQGS GGPLRSLPAVGGPRPGPSFLKTSGSGSV PQGVFILWSLT*RALAAPGSQGPAGLAV SCTGGRGYRDPQAPGTGAG*HGNSTRLR GP
1834	15735	A	1845	402	2	SKARROGRPLRQG*APG/AARIPEQKRI GGP/EERRRPSARGPRATRVAGEGPKPK GQTAMAGGGHDPLPLPPARSRSQESIGA RSRSGSHSQEPAPQPSGGDPSPPPERN LPEGTERPPKLCSTLPGQGPPPNV
1835	15736	A	1846	446	32	TSRKIS*KTGNQFLMKECSNHHKAAF TKKDVLNI\LAVVKHVNTKASETFHFQ SQQAKVQQGFVKEGCELINEALNLFNNV YGAMHVKTCTCMRLDLQYIMGDYABA LSNQKAVLM\TERVMGTEHPICIRPL
1836	15737	A	1847	440	4	VDGRHVEVSKKGGQVNYQAG\KTVEIWA DKLGCNMLGTADMVECLKSTRYKELIQ AITAGGAPIAFGPVIDGNVPGDRQILM EQGEFLNYDMLGVNQGEGLKFVDGIH NEDGVTPND*KFSVSNFVDCMRPRGPN YSRFQ
1837	15738	A	1848	526	0	PRRDFPPKRQTPIPTHVSPVWEKGPWGP APLRPDHPSLSPCPAMG*K\PGLPRGCP QTQISPLFNRSPLICHHPSEP\K PGPEPPPTPSSSIPSLARFTRPGESSPL PPPQTPSGPP
1838	15739	A	1849	417	31	QATGQECGCHRGPPPGPAGETEPQAPL RLPGGTGIPWGAGILCPS*LPFGSLSP AAGRG/SGPSAGPGAANFSSP*/PACPS SSRSAPVGGAGSFRRAGPGLFYTLPAFP WCGRGASNKIIMPGPLVC
1839	15740	A	1851	3	285	YTVCEVCVCLCVCLPVSLSLCLSVSV CFFPSLGCFCVCPACVSLAECALCAT KRFV/CMAACLW*ASFVSTWVMPAVN RFRRGGSALGA
1840	15741	A	1852	128	524	KIPGLQQRSEGVGQKDDLHVTAPEVPTH GWGEAASKPTVLP PPPP/PDAPT VFFF FFFFWEKKYFFGPPPKGAGPQIYLLGN PPGFKPFFPPHPQAAGI*YIKPPPWYKC PLLKKRGVSTLAP\GFPKPPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1841	15742	A	1853	1	1648	MTVELHSGLGKGVKPERKTTVRRPFVSA GKKYACPFKKAETPQWRRLMRPKAPAA SLLATFPISORLIPLTPARKHCPSSET STWVVS KAPATPRTRGAGPTSPPRPTRR R*ACSLQKLFVVEEFEDFSLAVED AENRFTGSLPVNAGRLRPVSSRPQETVQ AQSSR/PAAVTPHC SLRGFGPARLGP/P ASLPPARPVLTA/GPSCIGAAPLRPVST SSSWIGNQRRVTVEVLREPARPQSSAL HPLLT FESQQQQVGGFEGPEQDEFDKVL ASMELEEPGMELECGVSSEAIPILPAQQ REGSVLAKKARVVDLSGSCQKGPVPAIH KAGIMSAQDES LDPVIQCRTP\DPD*DL VLWVTF LQ/PALTVP TQQLHWEVCPQR SPVQALQPLQAARGTIQSSPQNRFPQCP FQSPSSWLSGKAHLPRPTPNSSCSTPS RTSSGLFPRIPLQPOAFVSSIGSPVGT KGPGALQTPIVTNHLVLQVLTAASTRTPQ QPTHSTRAKTRRFPGPAGILPHQSSGR SLEDIMVSAPQTPTHGALAKFQTE
1842	15743	A	1854	235	223	IHKFIHQIWLAKITCQRTKV*KERSVLL PTSFSPVPSQGHYTCQQLCSLASDLSQ PDLVYKFMNLAVLHAMWNSRKVSCYPWT MIYFLHANRT
1843	15744	A	1855	373	3	IKDGIYRYFYKALDSFCLCCEFMNQFFS CMDRELSQRCFLNSAY*FPSNL*CYLCY LFFFF* LKKYFLTF FLRLDRVLLCCPE *SAMVHS*LTVP LDFW\VKSSCHSLLS SWDYRHALPHLY
1844	15745	A	1856	378	1	RQRHSPAGNTGRPOVTPCG*ISWPSITK DRTSMSSVTSGALGHTAASPHARLLPLA LPSVRTQHGSPPPGQEQTIIICPSNLPT HPSLPLGMHPSVRASPLCK/P/SPPSI PASVHASKHPSPPVY
1845	15746	A	1857	3	379	YMRKVIEVWFLLLLLFFFRGGFLGQ GWGPPAPGFSFGKKNPQGLGSSNLRGPW *TNP*PVPGGALFLVGPPTPAEFPPKNF SRGFLLV/ALADF*TRPRLVSPHGG/RG AKGTPAFLESMPPWMP
1846	15747	A	1858	452	1	GTHGLLLGSGPF\QVFKPDNPFVFGQSG AGNNWAKGHYIEGAKLVDSVVDVVQEE* ESCDCLQGLQLTHSMGSGMGTLFISKIR EECPDCIMNTLSVVPKVS DTVVEPN ITLSIHQSVENTDETYCIDNEALYDICS RTLKLTTRCI
1847	15748	A	1859	1	385	NTSSDYIFPFFFLFRNSIHSVTQAGGQW HNQGS LQWPSPRLK\CPTASASICLHMP PFLANFLIFFVEIGSPYVAQGSRDPPA LASQ/SAGITGMGHCTQP*VFLFFFFFFF SFRKKCSFPWPGGGPPIF
1848	15749	A	1860	470	17	IEMSRRVPRDKLACITKCSKHIFDAIK IT*NELASAD/DFPPTLIYIVLKG/NPP CLQYNIQYITFCNPSRLMTGEDGYFT NLRLGTHCSWLMMTMTCFRAFRIFSSQ WMSYVLRFRNGITGVSHRAHP
1849	15750	A	1861	3	790	CSRPEFPGRRFVEAVRSKPYLSLFP*SR *SFFNVPAE*TSAKDILASSEFIKQND VSS\LQKFMPEVK*LDHIHTA*ADGSW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KAELEGRGPDGSAFSPFPQKPAASRQPEL GELATFLGRVDPWYQSNVNTLCPAIHL AEMPPLDTSRTVDFFILDVITYYIRMG TQPIYFYQIYTVKIFFSDLSQDPTDIFL IELKVKIQDSKFPKDGFSPPRRRGVAEGP GAELSLCYQKALLSHRPREVTVSLRATG LILKAIPASMY
1850	15751	A	1862	192	3	SSGSHSVTQA\GVQWHEHSSLLP/LLT* PPGRK*ASHLTLASS*DYRRAPHPANF *IECREGV
1851	15752	A	1863	82	370	SLCQKRAFVGEKLVHGLLVSPSGGRVPS CPDPWGCRRPFHAIAVYSFLKLRVVIPE VSILPEDLEELYDLFKVRSRSGKMRGSRP *AGLSRG/DPACP
1852	15753	A	1864	2	325	IQVYSISHLSIYLF\IYHLSRSGSMHVSM SLSI*SIYPCMDV*MYLSNLCMHVYIYL FYGSIYRFYLSICLSVYLSIYLSIYLSI YLICHPSIFKTVIDEHAIFATWRH
1853	15754	A	1865	3	377	YSPWCKLFRELCKINVFD\LDSPLLSGK EFNDTTHNTFDHMRTEKEHNEAGWLLLS SVDKVMKENDELSDNSWLQKQV*PLK SAKTALSGSLNSCREKAIEVEKQTQSLT M*VADLQRMHVQP
1854	15755	A	1866	10	378	GWKNGEFDAL*KVYGHKAPNKS AVYKW IT/*FKKGQDDIEDHDSGRASTLRKKI HLVYALIDKD/*RLTABAIANTIDISIS LAYRILTEKLKLSKLSLQWVPKQLCPDQ LQRAELPMEILK
1855	15756	A	1867	346	1	DILVVKLQKQPNGKMLKAAKERKKFAF KGVPMRMNADFSIAAMKA/RRRWNSIFS F*KENNCHLRLLYSAKNIFP/EIKTFSD REFVTIRSAVKEILKDVLAEBERLSHVK SRNV
1856	15757	A	1868	1	377	GTFFQRTQCKGIKQ\YVVGLIKASSDP TCVEKEKVYIGKLMILAQMLKQEWTEH WPAFISDIVGASRTSKSLCONNMVILKL VSEEVDFDSSGQITQVKS KHVKDSMCNE FSQI*Q/LCQF
1857	15758	A	1869	90	384	QWLLFTEYSSLYHPVLPFFFFFFPGGRG PNPPAGGEGNETG/PNGPSTPGGGGNPP PLPPGGGLGLLSMPPPPRQILLMETKKRP PP*TNKCCSPGYSPP
1858	15759	A	1870	2	578	FVVKHALLGLDFLPGKMAPWSGGCSSL GHTGGTSWDFAVGGASWRLKVVCVKGD SHKGPATPIASCGLPLGRPCPLLAQSKA *GS*KRG/VAPGSP*LALGMGGG\DRIT LISQVHGNQVTQIIPFSTEGETKAQRSP SLPFRDLIRGRHSWNLDSTQLLGYCPLL PPPLHPAGPLPVFPFTNGEIQKENSRE
1859	15760	A	1871	1	382	SGQDAGSCLLYGAGSGAMVSGAYNPYIE IIEQPRQRGMRFYKCEGRSAGSIPWEH STDNNRTYPSIQIMNYYGKGKVRITLV TKNDPYKPYPHDLVKGDCRDGYEA*FG QERRPLFFENLIRCA
1860	15761	A	1872	490	1	ADSLSKDPGRPLHPFNWGDGRGQ*PGE TPQ*HRRSCASQDPGRSQ*PGKILPSPK PGRPPMTGEDAGPPK\HGNPSPNDQKK NPPPK*/PQGNRIHRDPGRFPQ*PRKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleo- tide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						SFPNNLGDSDNDQSRFPVA*KNLPQSSS GTRAIGRELYLPPQPGSSAFPNSTT
1861	15762	A	1873	373	1	GGGVPGALFHHKKSLFFPPPPFFFRK GL*NF\KIKGCGSPFLPLLFFLEKESCF VP\RVCEGGVILGPCKVCLPGSPFFSAS AS*VSGATGAC/RERPGRFPSPFFFFYF LVEMRFHRVSQDV
1862	15763	A	1874	3	374	YMLGKEIVSKTKIGQELGLLNQ/TSQVV NAKEKFL*ETKSATPMNT*IKRKQNSPI TETEKALLVWIEDQTSNILLTQNV* MALTLFNSIKAERGEEDTEKLEGSRYW FMRFKKKKAISIT
1863	15764	A	1875	2	364	IHSGKGESLWDLGLDTEFLDLPSKA*HY KAKNDKLDLIK*MFCSAK/ET*/IRMK TQAIHWERIFVNNI*NRKLVIYKELLKLR N\KINTIRR*AIMDRHPTK/EKPMPTN *YTKGCSISLVIL
1864	15765	A	1876	41	461	GPLYLCSSEIDPYSPSKKIKSEWIRTY WMKLLSENATIMLKSDLSQV\FCVNI FVQAAKAKIEE*DYIKLKWFCSAKAI* KAKRQTE/W/DRIFANYPCVYGLITTT CMEFTQLTSLITPTITLEPWNPRQSYHH NPT
1865	15766	A	1877	2	185	VRPTKLDPLERTQYTLPLLYKWNKAWM TAHL/PTA*FTEYFKS\SVKPD*VREI DYRMLYL
1866	15767	A	1878	1	491	IHRLWPPLSAAARPPSRESGLRCRAPRR PASAAAAATAASPS\PTAPQGPFR/RRRL LIQPPLYPRGLFTPGVPL/APGGSREP S*SLT*DARTLPLPVLGPRRALLGACP AVQAEQVDPVGHLSVLAAAPCKQP*TP PPACHCLDGEGRPSGVQAPLHKAKLYP
1867	15768	A	1879	24	449	LQPPLTWALLQPPQPKSRAAFFFFFF FGKKSQFLFGPPGGGEGEKLG*REPPPP GTGMPPPPPRERGGKRGGPTGRENIGI *RKGGVPPGGGGGQTPNPGGGGAK\PP KGGK*GGRLPPPQIKGPKRGPKKRG RP
1868	15769	A	1880	190	2	PLYCHKVGQVGLLELLTSGDPPPLSLPKC WDYRY\DHHAQPSF*LFLSVQISGIKEN HSVVQPCI
1869	15770	A	1881	1	458	FAIRAGRNLDPKEFRYLRTVIVTAAYW GLNSKLRLCLTS\LLTFQHRAGVSPYTS FGFA*TCVFAKQLLEPILC/RPCFHRAP LLPKLRGHEAE/FP*QCFFR/QALGFSP /RSTCVGLRHG
1870	15771	A	1882	3	392	YMMRYHYILIRMAKVKI\SSNDTQ*L KLIHC*QECRMVQPLWKMV*QFLIKLNI *LP*NLAILLWGIYLIEMSTYEF/RKI CIQMFMETDLIVIAKYWTQ/PQCPVAGW IKQ/IRSIHTVEYYSVAKRNQL
1871	15772	A	1883	2	473	IQGGIAAYRVDQRERSNGRQGNRRNLG TNMRNRKQKGLRRCKPRW/RSRGMWKV DKPRDAR*KSDRDQ/RGETDG*RVSGG LTA*EAYRH\HRGQ\EAASQSGRSRQAG RQTP*QEQAGNEAIEIRREBEKSRGQERE RE\KDRDADRHK
1872	15773	A	1884	138	444	CYLTLIKCRITTYINDKVIIVLTIVWY*HK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DRHID*WNRLQSP*LNPSIWQLILLNN AKNTQWVKDTLLDKWYW/ENWIYQCMRM PLGSYTI PMNQFKMNYGLS
1873	15774	A	1885	27	470	TICCYIFLFFSFFSLFFFFFGKGVSF*S PGGENTG/ANLG*WNPPPPGKGISPA*P PKEPGMEGAGHPPGPKS*PGKFGPGPGG GPSFPYRGPNTWQKPGPKWFPGGIGYP ATIPQKKQPEGKRG\PGGPMSPYNGPP KTPTHGKGG
1874	15775	A	1886	478	1	KNVQENSALQAAMCRKMLIVCQTQCVYI SGESGAGKSVAAKYIMGYISKVSGGGEK VQVRGKQKDKLGRPHLHGSAAPICTP ASV*LLPTPPASAP\HVKDILQSNPLL EAFGNAKTVRNNSRFRVSLCRPAWSSC SLRADLSTHTPTHTTRV
1875	15776	A	1887	1	402	HSLERPHYIG*LFKNIFSRD/RVFAMLA HWSRTPGLKQSTPLSLPKCWDYRCEPH PAGSFFFFFLKNGFWGCSLGGRAGGQQ *LKS*WRPNPLG*GNPPC*PSKEVGTG AHKKIANREIRTRACGGTNFSL
1876	15777	A	1888	511	124	GTRRQHFAGAHVPPPEGP*S\MLDPKLL\ DDRPARDMWIREPGLLLPRAPAQDAGKY YCHRGNTMSFHLKITARPVLWHCLLRT GGWKVS AVTLAYLIPCLCSLVGILHLQR GESCPQWVCFNPTSPSPG
1877	15778	A	1889	667	310	QLKP*ATKSV*KDTAFGIDVGNDFLAMT PKAQAMKGKIDKWGFIYR*SICTAKETI NRVKR*PRK*EKIFAKPTWQKGQIS/RI HKEFQQLN/KQKSNNLIERQTKDLNRFL SKECSKDL
1878	15779	A	1890	462	3	KWFFPLGPPFLPPP/PPPI*NPFOKNK KLTRGGCARYFPPLKSPRPRIFFPFEEK GEGSPNSKHSPAPFPWGPKEFFFRTP PPPPPPPLCSFLKNNLFSYIPKGFLLGGK GQNFHSFLPSFFFSIKKLLGLGVHVRV YCRVNSCTGFFVQMY
1879	15780	A	1891	1	455	NTCLGFGNGFLDATPKA*SMKKIINKLD FNETENFCSVKDTVKGMRQATHWEK/V RKTHILYKDLILKIYNQLLKHNNKKTST IKQ*AKDLNREDIQMTNKHMKRCSGWGR WFTPIIRALWACKVEGSLELESSLGNIV RPHRKREREIHCY
1880	15781	A	1892	1	537	RGGIQAPKEVSPEGRQEPARKSLI*TA* ETPP*SQ*/PIPEEP/TGVFMKKPVSVS LETGKHAVVPKVNKLEPDNPTIKWFK GKWLGLGSKSGARFSFKESHNSASNVYP VELHIGKVVLGDRGYRLEVKAQDTCDS CGFNIDVEAPRDAYGQSLESFQRTSKR SLYALALEDEGM
1881	15782	A	1893	2	514	VRCQRRCHE*RACGSSLVNAKKLYEDAL MARKVKQSLFSLDVETDEDKFQMSLQ\ CSLAYGTLTKILSEKRSKSYGMSSVRM RSAGQTSKAHLHQPRRVQVLPVAVNL LPFRKKGQTKDPALNTSLPQKVLGTTTE ISGKHTEDTISVASSLHYSPPASPQGS
1882	15783	A	1894	473	2	VMGESRGFSPPPTFTGCNPFVFWKQGV LFCPEGFKTLCSSSPPPPPQKAGVLGG SFHARPPPPFFFI*IPFFFGIKK\LC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SPPF*PL*KKRGIFPVPRGIFCEMESCS VAQAGVQ*YDHGSLQWPWPGF**SSYL LV*LSS*DYKCVPHPMY
1883	15784	A	1895	613	11	FRPRSPACGLHAVSSPKLPGAQALSSPG LNLVFTAGSWDAG/LLRLSPRANPRVA LPRVHTGPSST/DLSPSCPLGLACGFGT SQPACL*SPFLLLAPARPSGCAWPGLP VCSLHLRGWGADPTGCLDAWAMALAS LRPCLCPALPLSREPPSPLLNDLVLP PRRAPVPLPLGRTPHSLLLCHVQSPSEQL PSKGPERL
1884	15785	A	1896	20	449	KFGYSSAAARRQQLGWEAWL*YSFPPLQL EPSAQTWGPGLRLPNRALLVNVKFECS EVSPCVACGIQAALSMGSTSSVKLLSHP QAPLPQWHQMVFARCLCMCGAQLNVPP\ ESFTFQVSTKDVPLALMACALRK/KATV FRQPL
1885	15786	A	1897	393	3	RPTAQSKGNI*VRVAS\EALSPKLLDFL PGKVLNGEKVDVPRATRONLSQFEAQR KRECVRVPRGGIPPAHRSRSDSDSADGR ATPSENLPSSARVDKPPSVLPYFNRP SALPVMGLPPPIPPPPCI
1886	15787	A	1898	395	217	RER/CKSFR/PPA/HLQAKIKGAQ*QVN QAAAAQAAAPAAAMVSRDISLLVSSQK SKVSNYM
1887	15788	A	1899	1	375	NTVLVQ*NNKAWMTVHPF/TANPSEYFK ATVEIYCS/EKIPFKILLVFARVHSHPR TLIEI*KEIYAVFI PANTPSILQPMDHG IILSSKPYLRKASRAQRLTPVIPALWE AEAAGSPEVGSSGLA
1888	15789	A	1900	47	326	VKSI IQFN SKNEPGKHDKTFSPKQTQIV WWLGSELRSFYSYSCAAGGAEMGRSLES RSRPQRAETAPLHSSPGSGSEMLSL* HLTPTAWAGVQWRGLCSLRPRPPGFK* FCPSQHHPQPPSSWDYATRCQATKQFVF FLEMGE\VMFARLILTVELNN
1889	15790	A	1901	181	837	AGRVDREPGMGTCIKELETGSRSTRS ASRWGRGRWRLGQACRVPOGLPLSTFHL GAQAKARGGTPLACSSHLPSHVGSGLKA QRDEAMVQSGLAPAVSSTCTRTWT*GSEW **GLHIVAARRQQGREEEPRTTAAPET LCFQQTSWASSCSLEHSAQPSEVOVRAL SVPSHSPMWV\PQLSLPRDHRKFPGE
1890	15791	A	1902	1	385	YTWGFRGKKPLIHCL*EYKLVQPLWRAA WRFSK*LRVEL*FNAATSPGLVPEENK LFYQNSTCTCWFITALFITGKT/WNQP
1891	15792	A	1903	207	3	FRMEFLHLGQAGLELSTSGDPPTLASQ NVG/HYRREPLRPANTLQS*PLGLKQPS CLSLPSSWEYRHY
1892	15793	A	1904	2	391	IQPLISQRKYKTLGQNSLS/CAHP/PP HFFFLDSYFHSLLSQLKNAPPT*G*CP YWYSKSYSLIHSWSSSILPCPLTSSGF PSLPSSYQPLPCPSLFL*NSLSTLCLL FFSLLSQPSFSNRWPSQVYL
1893	15794	A	1905	3	424	YRAGCLQSLPPPLLLFLLPDVPFPPPS S\LP*VKASCGLIRSQQNVGTIPCLQNR KSNKPLHKLPSLRHSLRAMQNRILPILR IGKFF/IFFS*DGVS LCHPGWSAGVQLQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FTALHLL/VLKRFSCLSL
1894	15795	A	1906	2	389	IQRGLDKSCLITDNIPSSQSLIQKGVN PSFKSMKADRGKEAEKSEASRSWFM EKERSHLHN/IK*VQGKAACYPEDLASI IDEGGYTKQ*IFNEDY/MWKKM*FRSFL TREKLTGFGKASKDRLTPLV
1895	15796	A	1907	458	13	AKEETQSVVDFPM/VPQGVVNFVPSR NANLSTIKQLLWHRAQYEPFLHMLSGPE AYVFTCINQTAEOQELEDQRRLCDVQP FLEVVRMVDCEGARVNKLSSQISLFIG KGVRELDLSLSDPEVSDFTKMCQFCBKS AAL*DQATS
1896	15797	A	1908	409	3	EKTDGLYRASQRGKDLRRLCAQSFHASW KDGMLCALIHRRRQ\DLIGYAKLRKDD PIGNLNTAF EVAE KYLDIPKMLDAEDIV TTPKRDEKAIMTYVSWL*IVIAGAEQAE TAASRICVLAVNREKKKLMEERV
1897	15798	A	1909	116	379	HSGPRREGALLLPKCLPHAKRCLLLFKM CSDGATLCCPGWSSAAPS*LTQSP/AS TSQAK*PSHLGLPSCWDYRCIPPHPANC LDYYY
1898	15799	A	1910	418	3	QD*YATANRWFI CMLSQACFLPSL*PAH LL*L*QLMLFSFPGTPVFSYGDEIGLDA SALPGQHMEAPVMLWDESSFPDIPGAVS ALMIVKGQSEAPGSLLSLFRRLSVQRS KERSLLHGDFLAFSAGPKLFSYIRPMY
1899	15800	A	1911	394	3	ILEAYPEVKDPAVKGASSKKEMYGH*/A AEQALPVASEQEQQRHERSEKKQPVKE GNNNTNKSEKIQLSENICDSTSSAAGRL TQQRKIGKTYPQQFPKKLKEHDRCTLK QENBEKTNVNIMSKKNREDV
1900	15801	A	1912	499	141	PGLGERDWT SKYGGGAGEGSTREWASRC G/IRPGGDAGQQQPRPE*SVCPRGHSP GPGSWKASPAWHSAPGGRCSGLGVQKE GPPGHLLQPGCRTPGPGIRKERFSGYLQ
1901	15802	A	1913	127	387	ISFVFPTLPKMPQLKPETISM TGLNLF QHLNCLARLATSAYDGCNSN EV/CDL DL LY*AALFLKLDYQIRFPNYFSTKYRIYY LCLY
1902	15803	A	1914	504	0	PGPGQRKHSTAPMCLLNIAQILRFVLA NQIYKCIKRIIHHQVGFIPIMQSWFNI QNQ*\INLIHHINRLN*KNHMIISFDKT HHLFIKTFIKLGIENLNLINIKNIF/S KNPAANIILNSEKV
1903	15804	A	1915	46	415	YTSNKQLQIQILKITYNSTKKYKILINW IKDVKDQYTENQKILLREIKDLNK/YRD TSCSW/NIVQMSMFS/KLIYRFSEPPNK NLSTL*ILTTSF*FAWKYTGTYIKVMT KNRVGRSLSPNFQNY
1904	15805	A	1916	420	1	ENADCVERARKSPDSIP*\RGGQISVTM VSPNEQEKAGQLAIGVRAVRYNGV\LLA KMWRKKLHLTSLANLEKI I AIGLFFSNF ERKPPENTFLKLTAMATHSESNLSCFAQ EDIAICRPHPAIKMPEKAEQYKPLTASV
1905	15806	A	1917	384	3	TRTITSGQYSTHVIRASRVPTRS*VPVF RSCTSNRRFSQAIEPRVMH*KVHIRAST VRYDSGGHVAVYPANDSALVYQLGKILG ANLYVVM SLNNLDEESNKKHPFCHTS/

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						RRALT*YLDITNPFMY
1906	15807	A	1918	405	105	KAEAQRRREICSGPHSQADSAWHPLVTW WH*PPFVARSSQEPGVHSPVP/HVCRKI LLIRPKMALANEGNYRELRFWFTPWSRSR *VGCLTTPGMCVKHLRCV
1907	15808	A	1919	409	3	GGQEEGVFRVLNSKEFETERGKP*IPPV KDQEI IH\PTKFNHVAHMGPGDGQVLM DLPLSAVPPSQEESPGPAPTNLARQPPC RNKPYISWPSGGSEPSVTVPLRMSDP AQDFDKEPDSSTKHSTPSNSSNP
1908	15809	A	1920	9	470	APARNPLPRPCTWPTGP*CLRPAPPPVA SACLCGGTNLALWLCSPGT/PVPFLTP PCS/SCEVQQPASHSVASNQSKPAKSA AVAHECPPGGTGSADPGWPPGATCPESP GPATPHITLVVEPGKSSPTMEEEPWAP QGSPCWTVRQRTMM
1909	15810	A	1921	556	1	IQLWAALGGILRRVGRDPFSHRIGKEPS AMAGQAGNGDGEES\GGLAAPHLP *SQHAAHPLLI GPPGQNLGDSKV*GFP SPRLEENTLENGGWSKQLHGSPGSQHA GGSWKNGETSLKG/EH*ADGAGRHTMPQ SPPSPFFKPHSV*HNPPAS/PPPHGSPA ESGTSPLPMSAVSLPPGSL
1910	15811	A	1922	567	41	GGWGETFSRLGNDLQAH*SRFNAQAQE ETSR/VLAVSLINEALDKSLEKTLAL LLPAAGLDDVSLPVAPRYHLLLVAAKRQ KAQVTGDPGAVLWLEEIRQGVVRATQDA NTAORMALGVAAINQAIKEGKAAQTERV LRNAAVALRGVVPDCANGYQORDLESAMA KIQRPAV
1911	15812	A	1923	2	405	IQQCGITSSSVLHGMVFKKETEGD/VTS VKDAKIAEYSCFPDGMITETKGTVLIKT DEELMNLKSKEENLMDA*VKAIADTGAN VVVTGGKVADMALHYANKYNMMLVKLNS QWDVRLCKTVGATAPKLTTPCL
1912	15813	A	1924	510	37	LLGHAFHVQSSSGRPQLAEASGHSHLKK GECVQORTGNVGLSPNTARWGTPLGPSI SSSAPPWSFSAFPGPPGSGK*AAKDGP CSLKSGLKR/RSQGLR*TRGSGPSPMP PSPSPS/ERPPPGDEGLLPCTPRGGLPG PKINTACVCAADISPGLEPV
1913	15814	A	1925	74	429	ATIPGHELLLLFFFFFLLGKGAWPL G*GKG\GGFIRG*GNRAPRG*REFPPPT PGKRGNTGGCQPGQPIFGFLKKKGAPP GPGVPKTRGQIEPPPPWPSKRAGVTGWT LGPVKV
1914	15815	A	1926	515	304	ALAASLALALNGVFINTIK/*IVGRPRP DFFYRCFP/GMG*PHSDLMCTGDKD\VV NEGPKETSPSGHSSPV
1915	15816	A	1927	1	433	NTVGSNKKSKLYFAETEKSYLNFIVNL KGPQ*VKIILKKSSVTCTLIHSA*Y KV/LKIVVWQRDTHM/DHWNISIKQHMV KQFFDGDTKTVQWAKDCLYNNWCWEK\W ISTSNRMKENIYPTP*ANINCHQDPNSK ELYRYKN
1916	15817	A	1928	316	356	GGT*PPQAATPIS*LYLPITSSL/TLPP APSLPLQIAPISDPSPSRYS/TPTPI SLGLAPPTLLIPVPSLPVSPRLNSTA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						PP/TFLTGSGAAVTVVSLAVSLSPAPAS AMDKAQNM
1917	15818	A	1929	490	11	PTRLTCPGSHVPGPVTFFPPYETHSMF\P PCHVHPLVQPPGSSHVPGPVTSSPSPPS ATHIHPLVQPPGSSQLPNTWVHPSQMR TWLQQHPPLPAPPQP/PSFGSICSSMTH LTEYLASFPAQP/PREQAPQGGVPTSLP QW*AFOPTAPCRATQSQQLLDG
1918	15819	A	1930	1	552	RNPRKRAFPSPPIPAPPS*NQENERSRH PQSL\PFVKSRRKRAFPSP/LSPCSSFV KSRKRAFPSPFPAPPS*NQGNERSRHP QSLLLLREIKEMSVPTVSPCSCSFVKS K*AFPSPPFVLLRDHTFLPLPBPQPS TVPVGCFGFSRI PRRWHTGCAFLICH SARLLCDPRVSSCVVRHS
1919	15820	A	1931	414	3	RVPGESRK*ERVLDNRHDK*EGRRRGNI \MGKRVDTT*TVITDVTNLSIDQGVH RSIAANMTFAEIVTPFNIDRLQELVRRG NSQYPGAKYIIRDNGDRIDLRFHPKHS LHLQTGYKVKRHMCDGDIVIFNRQCI
1920	15821	A	1932	521	103	ATEPAGVRLKEGNNITESFVTGVNISA LADFSQDA/SRYS*KKKQVLVPYRDSVM TWLLKDSLGNKSKAIMMATISPADVNYG ETLSTLRYANRAKNIINKPTINEDANVK LIRELRAETARLKTLLAQCNQIALLDSP
1921	15822	A	1933	1	490	NTGWVVRKGEENGTLMVRRLLPCVPLCSS AGGLTEDEGELCAAGFPLLAEDFGQAL QQLQTAHSQAVGAP/KGGDQVLGGGTGA PPTAYPNHALSIS*IPSVSWHDEGALPA VKIRILGIIHLLPERHALLSLVQARSGL LLHGPPATGKILLNKAGTTECCLT
1922	15823	A	1934	383	151	EVAFLENLIKDDIERGRLEPLLVAAGT AAVGH\S*LGRMKELCQCVRPKMEG YMHVSQHPVPESHKMRKAIF
1923	15824	A	1935	379	1	YVPVVS KDKEYFPNSQ*GLTTHQILPYI DGFRHVQKISAEADVKNLVRITAIQILL *VGLQSYLGQGHQPGKS/CRGPGCEGWE GMVLR* AQLSLSGTTAL*HWCPSRKL IQFGIIKNLIRRLCI
1924	15825	A	1936	376	2	GCLFIYMKPTAMSSSQVARSGEVSPFTA VPA*S*K/QGHGAVLGCHITSEACFOAC FPFLRPGRSTCFA*SGC*DVERSSSHSH GTAHSP\HGTAHTPMEQHTSHSEQHTHS HEQHTSHSGTAHMY
1925	15826	A	1937	426	1	KHGETIDDLKVVYRDNASKKSAI/YSKW ITHWKKRRDDVGEEVHSSRPATSVCEET IHLVCALI*ED*LIAETIANAVGIPRC SAYTILT/E/KLKLKSLSTRWVPK/P/L LPAQLQIREKRSMAILNKWNQDHEAFLH IIAGLY
1926	15827	A	1938	2	469	KRRKLVSSIAAAIHPALSS*TRQRFLL LFLFHIVREDLVQLRIKKHTIQIGNVE VKLL*PTDNIILCGKLYRFHRSTQKVLQ LI/NFSIVAAYKINMHISLVFLYSNDE* LENKTKQTSSTIALKRIKYVGSNNKSK KFYFAEIEKSYLDFIWN
1927	15828	A	1939	468	920	IPLSTHSPGMGTSTHLSTRHLSFWTYH ERLLNPGRETDA/IMLFRWGLLMLPRL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VSNS*AQVIPPTSASQSAGITGMS\HAS GHLIFNY\CSM*WLHLRNSQ*KRCTGQE TGPCPVTQDGVQWSNYGSL*PQTPRLKQ SYHVSLSPPSSWDYS
1928	15829	A	1940	448	474	GIPGG*GSTTRNALYHVMNGEDVILTT CKHGKDWQKHKDSRCRDNTYEYK\YDF GEMLHNATFCLVHRGRRHGSPRFLEAMQ AACVPVMSLNGWELFFSEVINWSQAAVI GDERLLQLIPSTIRSIHRDKI IALRQRS QFLWESCIATAIEDPNLIGVVR
1929	15830	A	1941	1	423	NTTLIFAGGM*NVCPGPLCARLLHRS LATDPDPLLTLP*IPTPTSPSSRCAPKAP PHLICPTSCPLCSKPHWP/CSSCQ
1930	15831	A	1942	48	417	RLTMYQVLYRLHCTALQPLPRVK*FSC LSLPSTWNYMHMPQCPTNF\CIFTRDEV PPMLP\SWWRTP
1931	15832	A	1943	450	2	VHRRSNRQNMDSR*RGAMQSVESV\GV PY\EQ*TIVDGI\NSGVWEGIAYA*IBE RYPEEFALRDQEKYLYRYPGGE\AYKVE TIKLNVEAVNTRDKPTNIFAKNQAPVR MRRNSFTPLSSSNTIRRPRNYSVGSRI KPLSPLRAQECI
1932	15833	A	1944	451	3	GRITRHLPRRAEDDREREREPSPLPSRH PMFPPSVTPKASSDWP/PASSIPCQACH G/PPFVSLPRKPAHRSC\PVPPP\ASGG DTSIHSGKTYYVKRKSQPAWPVLPGGGL *APSHGAPSPSPDQHRHCPET\R*DLL PAPAPSPFSIPPLY
1933	15834	A	1945	402	3	VRLVSWKVMYP*SRSKASL/HPQITAS LTGSCVNCIVILINFFYEKISANIAM EIPRTYQYBSSSLTKMFLPQFVNLYSS WFYVAFPKGKFGYPGKYTYLFNEWRS ECDPGGCLIELTNQMTIIMAGDV
1934	15835	A	1947	1	405	NTGWRVFAILCSLKGRPRGIERV/GGKK KKKKKPGGPLGPAQGKTPKTQKGGGAQG NRGKPPLFSGGNFGNGRIFGNLPAPGP GGGGGPR*KTR\KRKNGNWDLLKGGGKL VFCEPMVGKLSGVPGV*QKNFKGGW
1935	15836	A	1948	443	1	LTPGAANASLLG\CCMEDLSVNG*RQGL WEALLTHNMVAGCRLEEVDNAYGHYEF STLAPKANLSVELAEPCEPGLPPVFA NFIQLLSA/PVVVTEGGTAWLEWVHVP MLALMEALRKSQVLNRVT*GAHYSDCI AAALRIKIT
1936	15837	A	1949	396	2	GNGRGGSVPPNSLNEDGISCAI*/RHIN WLNG*TPTIYCL*ETHLICK/DE/HRLR VKGKKKILHPNGNQKPAVALLT*GQTD IK*KAIKSNKEGHEIKGSVKQENITVG NIYAPSTRAPRYKKQLLDLKGVN
1937	15838	A	1950	419	1	RWQ/PSARPPTPSGK*GASLPARPSSGT *GALLPGCPVWVRSASSWPPSRLGSEE PLCPA\PSHLGSEER\PSRPPSHIGSKE R\PARPPIA*DVGSASAPP/LPSGM*ER PAAPPSSGR*GASLPGRPSPEMWGVPLPR RPVWDVRAPSRAPVWEVRSVSAWPPHLR REKTLRLATAPV
1938	15839	A	1951	422	3	QNHVIMSE/DAKIAFGKIQYFFKMESLN TL*MKVNFLNLIKITQKNFIANTMFTGE

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						MLE/AFLLRQGRSC/CSLSPILFIILL EVLPS*VWQEK*/IQG*EREE*NCDFVD DMIVYVEN*KKPLYNLL*IIS*VARFKV ILDTCI
1939	15840	A	1952	2	409	CAHYSKNPPQRPLRTDARLPAV/DFWSL GAILFMVCGCGPPFQANDSETLTMIMD CKYTEPSHVSKEGKDLITRQLQIDPRRR ASLQ*IENHPWLKGVDPSPATKNNIPLV *YK\NLSEEEHNSIIHRMALGDITDR
1940	15841	A	1953	2	367	IQCVRL*VHVCLCASSVCICLYVHATL CVSTCL*CVAVCM/CLLCACATVSACL /V/CGCVSTCVCVCPVCTCDCVMSAC VCT/CLCVCVTVSTCVCBRLCVPTCVCR CPICSSLNGNEWMG
1941	15842	A	1954	374	2	EAPWLLRAGRGAIPPCWSKTTPSPLLF/ PPLLPGTLVYQPVPLPPWNRLACAVTL ST*ARAGTSNPSWHLEFPVSTAPQHPSTW QSPGAGTMGDPSPSPWTSLLPGCCCHNP CHCPFPHHKPTRV
1942	15843	A	1955	1	411	NTPSPELHPC*PGL/PPLSPPPQQPPTW APPRSTQOKLPILCLLKPSAHTDAPCT QPGSTLPLHTPHTQQAQGTAYQIHTT*A APPPGAKPG*RCPPPPPSRQPQRMQTPA PGNPQPCPRLTTLTRVLPAVPPLEI
1943	15844	A	1956	33	451	RGRNTFGPLQSPPPRFK*FSCLSLRSW EE\RDYRCMPVHPANTMLASLVLS\CD LPALASQSPGITGVSHPTREPLS*FLMP LE*GHRHLLLVLLSQPPNMPP*FORFST GQLECSSFRNLIVSPSLNFHSDPPLT S
1944	15845	A	1957	3	399	YMQVRTTMSDSSHSISKINTDNTKSC G*GSTESLFHDRWEYKFVQLLWETVWHY VR*TFITLYNPEIILKR/IFRHTYKNVC
1945	15846	A	1958	47	399	AANPTLPAVFFFFFLETEPPFGPGGRA GPOSRLTEPPPSGVKPIPR/PPPPGEPE KWPD\QGGGGGGDPKPPGGGPPP*ATGQN SAGKKKKKKIPRPGAHGADPLLPGKAGG EELDPA
1946	15847	A	1959	407	238	TOAFALI/KDGGVIGGICFRMFRTOGIR EIVF*AVPSNEQVKVSGSPRRQPQCTAH S
1947	15848	A	1960	106	1854	NEAVKSKPNQTRNHKEKNYVHLPDAGP SQPASAGGSSSACRRSTKATLHKRWSS PAGPGVQPLSWQHPMPMA*GLOGNPSPQ AAAPPARPGLVSGNCLT*EMAQAGA/GT GGSLASLGRKCPHIPVPC/PVL*GLC VPGRSSLGELGGNPVTVQSFPGGAESD PW*GDAECCSLLQASFGDRAGWSIR/RG SVGRPAGVPRGKGRKPTLSGA/SGPGSV LGGFCCPEPLSREAESGMVQE**GRFWT QERTPTGR*GCKVAGYLHSSATVGHSG AGAGGSPGKTSATLDVGQGLGGT/PSGP AWDRITNGYMEKALPLCNGKVTGNTQCG AQPPASGPSFWVWQPLLLRQRLQSTGL *LLFPVGGGLQPGEG/GQFFPLSPWGS LTGRKNSNKARPGNEGTEG*GARNGAS LTWVWTVPNGGYCPQAGRDFWLVDSEFK PSLGLRAMV*NSRKAPLSFEDGRMGTV*

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PQQQEGGRASHRKGDSGLSPHSGKG*DP*G/PGGKERSISPPLPRGL*GP/VGERGRNGDWFW
1948	15849	A	1961	76	427	QRQEPPTPGHTTSGTRHPGPGGRGPIQT HSHSHLFPWLETSAAGSSPPNFLCSLPY TPLLRLLPSPFLCPSQTTRMPPIAPHP SPASPCKVP*DARGAPAGGAPSTL/RGH HPPHP
1949	15850	A	1962	375	131	FLVGRIRLLYCLRELFFVYLLREQKAKRN SQWVHTLPISRRHVDVPCSPSINNRNRM GRDKKRPFFL/CVDA* LHSPSVVIQF
1950	15851	A	1963	89	538	GLILLQKNHFGAVSSMVERG*LLHSGLF FSFPDKVSSVVQAGVQWHDLSLQAPAS GSKRFSSLDHRHAPPHLAHFCIF/M*T QDFAMLARLGTSTFIYLFCCCC\FETGSH SVAQAEVQWHNSSLQPHSPRLRRSFHL SIPGSWDHRNAP
1951	15852	A	1964	402	42	CCHYPGTPLQGRLSASHQAS/SGPQLP APLPLQVLPFLALGIGVDDVFLAHAF EALPGTPLQVGPCP\QGSSEAAQLTG*E PLGSSDLGLLMNLGASCPHL*TGEIIVL CPKGYCLDQ
1952	15853	A	1965	8	14	SSRAAACPPRPALSLPRPFVFTRRMGPO GSGLPKLPVSAPSSRMGSFPAPSPLLLA SGDRHLCPDAAALPILAIETGCDS\PPG H*PPPSPGGLHPCSPPS*PLIL
1953	15854	A	1966	521	2	YELYGIIKRHRREVSNQVRYKEHSIP PDYVSSVPTDPTWGPERREREESGHFMV DHTGTAAGGGGGNIIASPKLGATPLPPE *APA/PPPPPPPPPPPGVSGHLNIPLI LEELRLVQQRQIHQMTEQICQVLLL GSLGQTVGAPASPEIHGTGTASTKPL LPLTV
1954	15855	A	1968	111	395	YLMRGFLLHHNMVKGKEDERKTGARI LFFFFFFFKKESPPPRVEGRDP\NLGT* NPLPPKVKLSRPTPPEKWEPGAIPHCP NNLFFFRKNGGS
1955	15856	A	1969	413	101	DVNRHFSKKNKHCQ*LVIKEMQIKTKRR YHFSPTRMGKIKN\KKENKFWQGYGETG IFTHCWCEKMOVQPIKKTVMQFFLKV* LLVFGPACKELGSYYSLVTKS
1956	15857	A	1970	411	1	NLTPALCTKVHFKWVMDIKMKGTIRLL ENNTRKYLHNIKIWKGLNRTE\KP*TIK KKTDKFDYDTIKNLSSSKNKTRQIDWE NIL\YLQYITDK*IISGIHKAFLKV/YK /KKTNNPVGKWARDLNGHLIKNDIHM ACI
1957	15858	A	1971	3	828	GQACHFIFRSAQAGGSRLRIWRAKQLGL WRVCALIMPALEHSFPTRLLQNSVPGP SISLDTSL/CNRCVWEGGRG*TGPGLP SLGKVLVEGIPSESPGPTASHPCCSPRP DPDQ/LSCISAPSATPTVH*SHLTLP MGWPGPQ*GLHLSQPGPRKP*PGCSGLG GDAAPRGMEKP\PPPQLP
1958	15859	A	1972	398	3	GPFCYFSVRLQCF/RKIPAWKRAVCSAT LI\SLQGPSLSAPHVLGLAALAVHLGES RSALPEVDVGGPAPGAGLPVPALFDSLL TCRTRDSLFFCLK*ALLPQSRLSSLSK

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						SDTCSFDKIRDRHADIPPLY
1959	15860	A	1973	2	433	QDPTKMTKEELNALKSTGDTLG/RASE VEVKNEIVANVGKREILHNTEKEQHTED TVKDCVDIEVFTAGENTEDQKSSSEDTP FLGTLGATYEEQVQSQILEASLPENT AQVESNEVMGAPDDRTTRTPLEPSNCWSD LNGGS
1960	15861	A	1974	373	580	TIFSRQVLRIQNALSDKPNVSTVYSNNG SELHGTSEASV/YHWKILISTEYHKT
1961	15862	A	1975	47	413	KWKHLRGSEHWRPQENQVHQRIAEIRKA GLWSQRR/PAAAGGPRPKSHWDYLLBE MQWMATDFAQERWKVASVKMVRVARQ LQDRTREAGARREBPSRLRQTSFVLPE KSSVPGLVLR
1962	15863	A	1976	444	3	GYERSRGTTSCTHSSRDYDGFQOATVK WAMLQDFRMLSPCSKEVMHQPFYLRKVE IMAQCEEWIADIQQYSSDKRVGRIMSRH SAAIKRRTGQLREELLKPCPEGLDPDS GDAPEVCRAATGAETIMHDQV/QPSSS KVLPSDFQ
1963	15864	A	1977	281	567	PRSSLQGGELSRPWRKGNFPGPPVPPPP QRMFYDSELSFGISDPSCCF/RSAPTAD QVYGDQDMHEVVRKHCMDYLVRKWRPLG KGQGGKISSPHRP
1964	15865	A	1978	357	2	KQILGPPHPQAQPGRVVPPPHGPKDAPL WSSRAAPPGRGLGRAGPAGVEAGATLR DSSPSTWTREGLHVQAQRKPSHVHKG/ SGPGCLEDEGFPTSLRLQAQLAEIGRGN GLSVRRQ
1965	15866	A	1979	29	434	VQAEAEGLPGDTEHPQPOLMSRSLGQS DVTIKHVACGDFFTACLTDRGIIMTFGS GSNGCLGHGSLTDISQPTIVEALLGYEK AQVACGASNVLALATERELFALGRGDSG RTGARTKESH/YLPQQVMP
1966	15867	A	1980	3	2082	SSEGVLGRNMSNEEEIISQEGSGDYE VEEIPFGLPQSPGFEPQSPFEPQSPR FEPESPGFESRSPGLVPPSPFAPRSPE SDSQSPFESQSPRYEPQSPGYEPRSPG YEPRSPGYESESSEYSEONTELKTQSP FEAQSSKFQEGAEMLLNPEEKSPINISV GVHPLDSFTQGFGEQPTGDLPIGPPFEM PTGALLSTPQFEMLQNPGLTGALRGPG RRGGRARGGQGPSPNIGICGKSFGRGS TLIQHQRHTGKPYKCEVCSKAFSSQSS DLIKHQRTHTGERPYKPCRCGKAFADSS YLLRHQRTTHSGQPKPCPCGKAFGDSS YLLRHQRTTHSHERPYSCTECGKCYSONS SLRSHQRVHTGQRPFCGICGKSFSQRS ALI PHARSHAREKPFKCECGKRFQSS VLAIHARTHLPGRTYSCPDGKTFNRSS TLIQHQRSHTGERPYRCVCGKFCRSS TLLQHHRVH\SGERPDKCDDCGKAFS\R ASDLIRHQRT
1967	15868	A	1981	2	188	LPETNFAELFLPYISQHNLRKYK/WP GAVAYACNPSTLGGGGWITRSGDQDHP GLHEWP
1968	15869	A	1982	3	424	EGQAIVERMNLCLKQQLQKQGENRYR TPHKQLN\ALLTLNFLSLPKGRILSAE

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						QHLQKPAAKTEAEQLVWWRDLITESWEI GKIITWGRGYAYVSPGL/NPSRHLKPYH ERMLRKRFREDPEDPPSCSHVKTDAEED PN
1969	15870	A	1983	3	399	YSKLSFKGTLTkFRRIYSSSFYKEFGGC ISDLCHP/R/TLTNCLRGELLKENLVWG AFGCHPHFPCCYINKSQERNLLQALRHPT TVAFGETGFNYSYKCTMPVPEHHKVFKR QLELAASLEK/PLVILCQCADE
1970	15871	A	1984	1	405	RRHIGGGVRLYYIGGEVFAKLSDSATF AQTPNCNQRYGWHPGTVCKIIPGCNLKI FNNQYADLLDQSVNQGLEDY/QLTRM CTILMSLLKGWGAERYRQTATRTPCWIE LHLNGPLQRVDKVLTMGYPSILM
1971	15872	A	1985	27	452	QGRHHAQGGQSPGAGHLGPTPEPQPEPQ PRPSSQAVPAGRWEPAQE/PTRHPHRL SPASRPLGSPAPLVRSSPGRCRLHEHT IWSSTVGTSVEPAPSLGRPQAPLEPGTV TSSVRLQQPHMHTPGKIMDPKRNKGK TFT
1972	15873	A	1986	414	220	GAEQEBELLSP/GSGGCSELRSCHTPAW ATRAKLRLTKQNKTKRESYRQGNQNWGR ILGELLGRL
1973	15874	A	1987	52	412	TRERKLFFACDNVWHLKRYLRKNSFGE NLWSSRNKKKKKKKKKKKKKKTKNFST PKNFFFFKACQCMGKKNTHDFHEQNF I EHALLQQLNINFSNYIEGRVF\HPGAP IESLLLMCH
1974	15875	A	1988	2	143	EKKRGLDKRTP/AQAAFEKMQEKQMER ILKKASKIPPPFVCMWSVDS
1975	15876	A	1989	3	163	TEFQPEK/WGEDLDNTWEYIFAIDLL CCHQKWICHPLFLVGVVRAGAEVSGVF
1976	15877	A	1990	1	439	DKTAAEDAIRNLHHYKLGHNINEEAST NKSSTSTKLHVGNIPTCTNKLRAKFE EYGGP\IECDILKDYAFVHMERAEDEE AIKGLDNTFQGKRMHEQLSTSRRLTAP GMGDQNGCYTGGKDGHSKECSIDRSGR VADLTEQ
1977	15878	A	1991	1	145	VVAASKAMK/MGDWKTCHSFTINEKMNG KVWDLFPEADPVLKRLRESR
1978	15879	A	1992	2	425	NISTLKKTLESDCT\KLFSQIGGEQAO AKVDRCLSDLAETNKFRLDLEGLTEL NSTAIKPQVPWINSFVSVHNIVEEEF NDYEANDPWVQQLILNLEQMAEFKASL SPVIYDSLTLMTSLDAVELEKVVVKST FN
1979	15880	A	1993	3	449	VAGPAPGAGARPGLDLQFLQRFLLQILKV LFPSSWSSQNALMFLTLCLTL\LKSF QFTCNLLYVSWRKDLTEHLHRLYFRGRA YYTLNLVRDDIDNPQORISQDLERFCRQ LSSMASKLIISPFTLVYYTYQCFLSTGL LGPVSIFY
1980	15881	A	1995	1	410	SSRRPFTALKTKSMRDLNPEDIDQLITI SGMVIRTYQLIPEMQEAFFQCQVCAHTT RVEMDRGRIAEPRVCGRCHTTTHSMVLH NRYLFSQKMIQLPESPEDMPAQTPHT VILVAHNDLDDR/VQPVDRVNDSGFF
1981	15882	A	1996	1	154	LFFFRLLVRYTKKVAQVSTPTLGKVS RN

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1982	15883	A	1997	2	475	LGKVGKKSWKHPEAK\KRPCGKN KKLRRQTRREBAQKE\LPDKV\RWGLVTP SETPVGISNLSPLGPRL/QNPARKLP PWRFPWAQRPAH\ERANAGPKTPAQOR KVKIKKKLBEDISQGVHISVYRVRNLSN PAKKFKIEANAGQLYLTGVVVLHKDVNV VVVEGGPNAPKTI\TRIMPLRI
1983	15884	A	1998	3	431	QLRTRDRGWPSRRPEREKRTSQSARRPT CTESRWKSEEEVESDDEYLALPARLTQV SSLVSYLGSISTLVLTPTGDIKQG/SPL EVSDSDGPASFPSSSSQQLPPGAALQG SGDPEGQNPCFLRSFVRAHDSAGESSLG SSQA
1984	15885	A	1999	1	400	ALDLRGLQILVGFPPKRRVTTCSTALQ SPIEQYRKERSTAVMRTEPDSAYQASPR PYSAGPADSKKPTKGYCYNPTLP\RLIEI MTLEGTTG
1985	15886	A	2000	1	372	QNIDLVISFFSSRLQAGAELSVERVLE IIKQGVVALPKDRL/RGSCAPTLAAGR SSGGQSPCMPGLCVCSFWLTVSWLVQC KFPELKFYVBEEQPEEFFIPYVWSLVY NSAVGLYWNQDI
1986	15887	A	2001	393	1	GGTGRGGGAGGGVGAAGSASGGVGRGA GGVIADSGAPGGGVEGGVGASGGWRE/G RGTSGGVGSGGACGSV/GGSGGAGGV GACGSTSDGVRSGRTIGGLGSGSAGG GVGACGGASGYVGIRGAGGG
1987	15888	A	2002	2	362	WVTFISLLFLFSSAYSPPGVRFRDAHNSE VAHRLKDLGEBNDKALLLIAFAQYLQCC PFEDHVKLLNEVTEFAKTCVADESAEDC DK\SL\HTLFGDKLCTVATLRETYGEMA DCCAQQEPE
1988	15889	A	2003	2	358	EANRGWFIRLKEGSQLYNIKVGGEAASA DVEAAASYPEDLAKITDEGGCAKQIFN VDK\QTAFSWMKRPCRTLIAREKSVPG FKL/SKNRLALLLANAAGGFKLSVLI CHSENSRTF
1989	15890	A	2004	190	1	DQTCFLSFTVKAVTFNGVWVWLTVPVIPA LWDYRH\RPANFFVFLVETGFHHVAQAG LKLKLS
1990	15891	A	2005	1	132	GMCHHAQLIFVF/CSRDRVLHGCSQTPC LKQFSCGLPKCWDYR
1991	15892	A	2006	2	134	PMTFFTELEKTTLKFIWNQRRIQIAKAI LTNQK\NKARGITNIC
1992	15893	A	2007	315	127	SEIAFFFCFLKIILDTR/FSFFARAGL KLLASNDLPSSSSQGAGITGVSYGTQPV CFEYNVG
1993	15894	A	2008	3	325	RCSMLAVREM/QKATKRCHFLPTRIALI K/ND/GSNKCWK\HCWWECKMVQLLWKI VWQFLKKNIELPDPPEIPLRDIYPKQL KTYVHTKTCGOMFIAVLFINVPHLMNV
1994	15895	A	2009	369	3	VGQAGLEFLTSGDPPASASQSAVITGMS HHTQPIFCIFGFA/GCPDWSQTPCLKQS AHLSPSSWDYRCMPPHLANFYFCRH/R VCCPGWSQTPGLK\YPPALVSQSVATTG TSPRAWQDTILPV
1995	15896	A	2010	114	287	APLCLCLRHLRLTLKRLTVLGTAEHTL\ NPITTRGRGGQITWGREFETSLANMVKP

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						CF
1996	15897	A	2011	218	346	IMKFNLKFFFIYLFSSQSL/SSVAQAGVHWRNLGSLQPLPPKF
1997	15898	A	2012	310	1	SSSSSNTHEFGIPKYLINPDTCFLA/KVN NSSLTGLEYTETLKPQIK
1998	15899	A	2013	3	301	SDCCASNQRDSGGVGPSEPAKHTLCV/ CNSLDLIE
1999	15900	A	2014	332	3	LRDPLEEAVCPFSDQLHAGRTTALFKA VRQGHLSLQRLLSF/VCLCPAPRGAY RGRQAG/SLSCGGLHPVRASRLCLPKQ AWAMAGAPPAWPRPCSLISDCCASNQR
2000	15901	A	2015	2	325	LLLHHAPPVNLFLRDRVSLCGPLCGPGC SQTPLKQSSCLSLPKC/WDYR/RATAP GL
2001	15902	A	2016	373	3	WAHGLQPGKPKVDSLKKRKKKKKKLN TFPLRSRTQACLLSPLLSNIVLEVLN EIRQ/QKKEIKGTHGTGREELTSLFTDN MIIVDIPKQSTKKNQGSYSVARPGAVA HACNPSTLGGG
2002	15903	A	2017	343	1	EFPPVSGSRATGKSSDIRATKYIWRVLE YLRWPRGQRRLKSS/HTSLGSHYHPGA FRGDKWSCCHQKDETTGGGEDEVLLCCP GVLGCSALCRSGVRTKFGIRGRPWKERE R
2003	15904	A	2018	139	2	NSISTKNTKNWSGMVAHAFNPSTLRGRG GQI/RGQDFKTSANMVKP
2004	15905	A	2019	3	322	ARELVFFFGAYRKGFFHRDMKPKNLLCM GPKLGKIADFLARELRSHPPYTDYGST KWR/YRGNPALLRPTPMKFPYEGWLHI SGSSIWNIKTSDSNFIPFKBSKG
2005	15906	A	2020	205	377	NIVENIVFCWPGVCFLQCTVCINPETS DE/WPGAVAHACNPSTLGGQDGOITRSG DRE
2006	15907	A	2021	3	324	KKWGR/LNRPNGRRYPETRWALEEDQ CHICKELHIKTVRFHCTPIRMAKIHTTD NPQSWPRCGTGTLIHCRGCKTV/R/PL WKTVRQ/FL/RKLNIPLCDPAVLSLCI Y
2007	15908	A	2022	2	382	RVSQDGLNLLTSRSTRGLPK/CWDYRC EPPSP
2008	15909	A	2023	1	421	RWNPGGRGCSELRLLHYCTPTWVTERDSI SKIAKNK/NNKRPNNCR
2009	15910	A	2024	339	3	SWDHRRVLIFVFLVQTGFCHVGHAGLEL LTSGSQSAGIAGVSHRA/GQKHQFRPEH RFLKFGFVFRDRVSLCCPGWPQTPRLKQ SSRLSLPKSWGPAALDPDSSYLEEMVL S
2010	15911	A	2025	2	146	NTFGRSRQEDHLGPGGQACSELRSHHCT PAW/VIEQDPVSKKKPKP
2011	15912	A	2026	3	380	RLECSGGISIHCLNR/LPGFKRFSCLSL PSRWYDTRLE/PFVFLVETGFHHLGQAG LELLTSGDPKCWDYGC/DHCTWP
2012	15913	A	2027	32	296	DYMNSLMVFHSLVLASTDGFLPKTVST QSAGITGISHCARPWIPF/CFFFKNRK TRFVAQAEQGQGNFGSLNPLPPGFRGFP CLSLT
2013	15914	A	2028	2	187	FTLLPRLECSG/MILVHCSINLPGLRWS SCLSLSSWNYTCVAPFSIFYFIPLTW

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						GGTLNC
2014	15915	A	2029	197	3	AAGLSQAGMQWGDGFSREHLPSRFQFF CLKVPPNNWDYRHGPPRPVGIFFSF\LV ETGFHHPGQ
2015	15916	A	2030	88	362	KFGINLKKKKKKPQKNQFFPTFLFF FFETESHSTQAGVQWRDLSPQLPPG FKSLPSSWDYRCLPPCPANFCIF\IPDS VSLCWQGW
2016	15917	A	2031	7	131	GTIMAWAPGEGGCSEPRSCHCTPAWVT\ SETPSQKKKKGVLL
2017	15918	A	2032	1	343	LECSEPRLCHCTPAWV/TGDSVSKKKK KKKK
2018	15919	A	2033	243	14	QKLAPWPPQSAGNNRRVPPHPASMAFLT KIEKTALKFIQNHKRPQIAK\TILSKNR VGSITLFSKIHMTTVIKTI
2019	15920	A	2034	238	3	FLALPKVLGIIGCVPPHPASMAFLTITB DTALKFIQNHKRPQIA\KPILSKNRAES ITLFSKIHMTTVIKPLRVST
2020	15921	A	2035	345	2	LVKIQKEMNVFMTANPISIPQFMDQGV SSCKSYFRNKFLYV\IAAMD\TD/SSNG SQSEWKTFWKGFILDGKNTDDSWEB VKISTLTGIKKKLIPTSTDDFEKFTLV EDVT
2021	15922	A	2036	1	140	GRCC\HELRSRHCTPAWATRAKLKKKK KKREKKTQKGKGLGFNAF
2022	15923	A	2037	199	348	RSSNEGGRDCVFCFGRVSLCLPGWSAV AQLWLTATSTSQ\VKSLSHLGL
2023	15924	A	2038	3	193	NGLNAPTKRLRLANWIKSQDPSVCCIQE AHLTCRDTH/RCYLKG/WYKAF
2024	15925	A	2039	116	337	SKLLKILPRLCWGWQAPVIPATOEVEA EDHLNPG/RSRPAWATQRTPVSIKKKII LRPANGK/CHGPSW
2025	15926	A	2040	368	252	VFFFFALFYLFVFFVFFVFFVFFVFFVFF QFLGFYFRKF
2026	15927	A	2041	204	399	VSSHKINGLTVCTSPFFLSLPPSEES ACFFFAFCHDCKFPEAS/SVMLPVKPV L
2027	15928	A	2042	103	356	WHFSPQPPLPPP/PLNPPPPPTPPPP\ PPPPPPPPPPPPPPPPPPPPPPPPPL PPPPPLSPPPPPSTPP/PPPPPPPPPP PLPP
2028	15929	A	2043	3	344	LYKWNKRASLAHLFAAWFTVYFKPTVE TYC/SGKKKIPKILLIDNTPCYPRAL LEMCEEISIVFAPATTSS/LKPMQGV IVTFKSNYLRNTFQAGGEEKKEKHERKK NIIS
2029	15930	A	2044	2	349	PRVRKSPGPNCTANFYQTFKELISTLL KLFQKKKKIKKGENPPNSFYGAIPRIP NPNMDLSKK/ETYGPSVSGRNMAKIPK FLAGHFQSFGREIHHDQREFIPGIQGG FNIGN
2030	15931	A	2045	280	462	CXFFLVVVLVWCVLLFXVVVLWLCFVG FVVCVVFVFCGVVFFVFFVVCVLCVGL LGCWC
2031	15932	A	2046	3	284	PSPSFSLLLPPSFSLPPPSF/SPPPPS FSLLLPPSASLLPPCTSLLPPTSLQ LPPLPSFYLLLPISHHLPHTNLPPTS IQDPSTPCSIK

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2032	15933	A	2047	95	1	GRVDAILAHCKLR/LPGFTLFSCLSLPS TWDC
2033	15934	A	2048	211	1	EPTTMTGAKWGSSQTTTNYHMLQSLRIN VRVDFFFFTCTDR/SLSMLPRLVLNSWI PAIILPHPPQVLGLQ
2034	15935	A	2049	35	266	EVRRPSTWQPPRLRSEBPLRL/QPPRLG NIGFCHVGHAGLKLLTSSDLPTLASQSA GIT\GHSYRRASEEDKKBSMSS
2035	15936	A	2050	281	3	QSNFKRALLSILLKAIYRSNIIPIK/VP MTFTEI/EKVIKPIRNLKRLRIAKVI LSKKNKTRITLSDFKLYYY\IAVFVAA WYWKKNRLSDQWN
2036	15937	A	2051	251	12	ILRFFLPKFLGFGKPPSLEKTHFFLPF GNSLFWPPEKLGQKKVFFFFFLLRQG L/NSVSQAGVQWHNLGLLQSPPLRLR
2037	15938	A	2052	2	325	ADHLRPGVQDQPPQPGQNGKTPSPKIEK \LAGCGGGHPRLEENCLNPGGRCSEP RSRCTPAW/VNDSKTLARKKKKKKGVE KNECGRKVMRV/LQGPKAKVKPWGENTL
2038	15939	A	2053	3	166	SLLLPRVECNGAISAHCNLHL/HNLHLP GSSDSPASASQVAEVRGSLERSSSLA
2039	15940	A	2054	227	3	LNENIGRITGMSHHARLILLFCE/YRVS ITQAGV/QHDPGSLQPLPRVFKQFSHFS LQSSWDHRCAPIRLAIFWVFC
2040	15941	A	2055	301	0	QRKSHMFLTINQKLEMILKSEEGMSRVE TGOKLDLMC/QVSQAVNAKEKFLKIKG DTSVHTQMIRKQSSINVDMEKGVIVWIE DQAP/HNHIPLSHLLMRAR
2041	15942	A	2056	1	109	RPLRRLRQENRLNRSGRGYSEPKLC/HL CTPAWAT
2042	15943	A	2057	313	250	PQPPFPSPFPQSPPPSPPPSPSPSP/ PPP
2043	15944	A	2058	134	2	EKESRSVA\RLKSGSAISA\HCNL\CLP GSSNSPPSASRVAGSSGA
2044	15945	A	2059	120	326	NSLVADME/KVLVWVIEDQTSNIPLSQ S/LIQSKALTLFNSIAKAKRSEEAEEKIF EASRDWFMRFKIKQK
2045	15946	A	2060	102	413	ERTGFRHVKGKSGLEFMTSGDPPTLASQS VGIT/VHEPRTRPG
2046	15947	A	2061	311	1	FFKKQRFCKSGCKTPGKPRGPKKLGANQ FSGPTPLKNGVGFSFGPKGGFPPPPGG FPAGRPKWLTRILGKGSLLRG/RYPKK GFLKPI LGDNSPQAPKRG
2047	15948	A	2062	229	380	WYDLGSLQPMPLRFKQASRVNLPRSWDY RHPPLSRLN\IVFIVDTGILHV
2048	15949	A	2063	142	383	PQSCFSTHWQLLQKQEEETAGAVSVCVCT S\VCVCVCVCVCVCAGAMCVCAGA/CFC VCVCAGA/CLCVCVGA/CLCVC
2049	15950	A	2064	408	200	NLIQIKALTHFSSIAERGDKSTE/EKF EGSRGWVFRFKERGHLCNKKVKEAANA YAEAACSLSRRSS
2050	15951	A	2065	348	3	WVSPYSPCVVCVCVCVCVCVCRDWVSP CCPGVCVCVCVCVCRDW/CFTM/CAQVC VCVCVCRDWVSPCCPGVCVCVCRDWVSPCCTS WSILKLLSSGNPPTTVSQSAWITGRSHS AWPARA
2051	15952	A	2066	73	286	NLIRGLLESHILISMRYGYCKSYTLMSR DIPREALNKWS/IPMFCSWSRRLIVSMA

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						VLSKLIINRFNAKDVOH
2052	15953	A	2067	329	0	PSSTFLLPFRPPPPPPPPPPPPSP / PSSSSPAPSSPH
2053	15954	A	2068	221	3	ELKVLHCLDRDPSLQSSIMKVLILILI LSVCCVC/VCVCVCVCVCVC/VCSCVC /VCSCVCLCVLCVCVCVLS
2054	15955	A	2069	1	167	GTRENPLNPGGGGCSEPR\SCHCTPAWA TKSETLSQKKKKKKISNYKTPFKSYRI
2055	15956	A	2070	2	354	ARACLGLPSSWDF/SVENRPHRVGQAGL ELATSGDPPTSASPECWDCRH\DHHTW LL
2056	15957	A	2071	20	341	CIVTVNTRGENINICWSPDGQTIAGVGNK DDVVTIDAKTHRF/LKQNSSS/SEVN EISWNNDNNMLYPDTGNGCINILSYPI ESRAIYQRPFIHVHVNDLPHGDVLS
2057	15958	A	2072	353	58	LQLLTSDPPASASRGAGIADGVWFTQ/ SLNGAQAGVQWRDLGSLQPHPPSRL/LI ASQSAEIAASARPPRLGSEERLCLAAH RLGCEEPLCLAAQSGK
2058	15959	A	2073	1	338	GSRLQRVCINYLRSFPFLSQGWINFTW LFCLCVCFLDRVSLCCPGWPSTSGFKR SSCPSLLSRWDYRHPQHLASHTLTKKL /TILPR
2059	15960	A	2074	1	322	GGREAGEARGGGGGQSGRRRRRGGRG PRTGGAEGGRGAGETPGGGARPERQGR GRHSEKQGP/RTKRPKTKKQLSQNK NT
2060	15961	A	2075	450	225	TPVGRGCSELRSNCNTPAWVD\ETLSQ KEKRGVVKIGWKKRRRIISLHLPGSHE KFNNLETVKNCVNHFCRLNT
2061	15962	A	2076	2	470	TPQNKPHPTTKNTQPTQKK/PTQTOP /TTPPKTKKNTTPNPAPPNTQKNHTTK PTTQNPHTKQKNKTKPNTTQQQNKPTN QNPKTQTQQTQTQTKPPKKKKKTADT TSPNPISTKKIKKLAEP
2062	15963	A	2077	304	1	NSATPPCSPTA/KPHPTPTPPPTSFI TQHSPTKICPOAREPTPPYAHPRCP RKIIPKGRRHPLAPQAARDLNYHPI IWRGRVCVCVCVCVCARA
2063	15964	A	2078	167	1	TILQNTSTWSNVLLWQGAQAAC\NSST LGGQGRITRSGDRDHPGQGETLSRA
2064	15965	A	2079	3	364	HETRSRHSCAWCSAALWRAVASRCPS /IPVTPQCLYWP/WKVPLOCPDL
2065	15966	A	2080	303	2	SKRGRPSGHECPFLGTSSSCRHVASCTI RTPRRLCKSQLDRCSPLKERHKFGLSRS VLSAMTQSGIY/WQPPPPPFKRCFSLN LLSSWDYRHAPRRARA
2066	15967	A	2081	4	326	AGITGMSHRAWLFLYFLNKFAFT/YGLV LNFFLHKIQEPLSG\SGSGP/LSCNS
2067	15968	A	2082	1	343	PPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP PSSPSSPPPPHTPH
2068	15969	A	2083	330	88	ACDRSTIIRIKEL\BQLCKQK\SNPPI KKWPKDMIRYFSKQDVQTVTKMNCSTS LIIEMQIRSTMRYLLTTRTPHPS
2069	15970	A	2084	1	340	RVRSHGTTHLAQLIPVLLVQTGFHHDGQ DGPDLI/NLVIRPPQPPKVL

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2070	15971	A	2085	2	348	ARALSLGANAAGNFKLRFLLRVHSONPR ALKNYAKYTLPLVLRWHSESLETAFTBC FTEYFKPTVETVCSEK/I/SYKALLLI EKALGHPRALMEMYKDISIVFMPVNTTS ILQPM
2071	15972	A	2086	369	2	KGLPPSPANLFFLSVY/MGFPMFTRLIL ISCPYPPPSASPSAGIKGLNPPGWPPF SFFYQKFVRFFVLARNRTFGFVDYFSIL YLIYGCSNLYRFLLSALYFFVSFVFL TQIEAMVPERA
2072	15973	A	2087	314	3	LLSVGPTRNSRPFKGLIGRILLDPEFY PSLVSDDLFASASPNAGRILPFFFFETG SHS\TQAGVQWRHHSQ/LKRSSYLSL TSSWVYRHTPPHANCIFSR
2073	15974	A	2088	330	16	CPCFFLSALSVLVGWCFAPVVCVCV/VW CVCVFFVFCVFCFLGCVLCLCFV/VCL VGCCVFFGGGLCCVCC
2074	15975	A	2089	1	337	GTRTFLLPPSYKDPCEY/IWAHPDNPSS SNCNMLNFSTSD/PPVHSSGNWKVLSSP NRPFYYSYATPHTDPTPHLPSPNPSSP SPSYPLSDSTICOTTPPTTPTSSHTL LTS
2075	15976	A	2090	350	84	QRKENKRTRKRATERRDESRREEKAGRKE GENQEKRNKEQQGRQRRSRDRT/EEKE EAKRREHKNPKKKTKPPQKKKTEKK KTDNLSN
2076	15977	A	2091	1	355	SDPPTSASQSAGITYVSHRTWPLLEFSG TSIRLAGKPAGVLVEVTGK/SVCGGGVT KTHWNECHTGYPKCCWSSQAGESSLQPP PPGFKRFSCLSLPSSWDYRLLPP/QNFC IFSRDGL
2077	15978	A	2092	27	345	ASIPCLKKRKKKKTKTGKPPPGGPKP KRGGGGGPPPTKRTLFGPPQGNQTPGGV S/GPPKGDPPFSPIPPQQRKSPFEEKG KKGPPPPWRGVKREKGFHLKNFQK
2078	15979	A	2093	3	301	HEHVAQAGLKLGGSDLPPLASPKWDC KR/DYCANPHIFPISGPLYVFFPLPRMS PHTHTHKYTRTFHYAHKHCACLTNLLL RAQFQCHFFKGVVDP
2079	15980	A	2094	76	342	WFXXFFFLFVFFVFWFVFCVFCGFF FCFFCCVWFVFGCLFLCFLFWFCFFV FGFFGFWFFVFLVCFVFCFFGCF LFCFF
2080	15981	A	2095	115	325	MDERKKIRGGGRQGECKIHCKKKLSPG IRSYPVEN/F/VDTMYDLPAYYKLN LTNADPCAVRYLLFDQ
2081	15982	A	2096	80	227	SCLGN/CIHLYSHSPTLSFTHTHTHT HRERERERERERERICMSVYA
2082	15983	A	2097	308	1	NSTVTNENSVNIHYRTRVTEAQFTIAK SWNQPKCPSILEWIKL/WIYIYVCVYI CVCVCICVCVCVCVCVCICIYIMMEY SAIKRNELAAFAVTWTRA
2083	15984	A	2098	2	361	ARACGLPSSWDF/SVETRFHRVGOAGL ELATSRDPPTSASPECRCRH/DHHTWP LL
2084	15985	A	2099	1	221	LLWRLRHNHNLGGRCSEPRLHHTP SWMTR/GKTPSQKKTKQPMWQNLCLK KVFGNTGVREIFNGIKLS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2085	15986	A	2100	186	2	ERVYVCVCVCVCVCVCVCYQCYLPQIRSL/V ASSLKANARVCVCVCVCVCVCVCVCV SLWHPLTA
2086	15987	A	2101	305	2	HNILLSQSLIQSKALTTFNSMKA/E/RG EEAAEEKLEASRGWLMRFKE\RSHLCN\ TKVQGEVASADTBAAPSYTEDHSKITDE GGYTKQQIFNVDDKASYWNMS
2087	15988	A	2102	6	166	EQTALAILARAIQKEKEIKGIQIRKEEV KLCFFVND\MVLYLENSKDFLKVDA
2088	15989	A	2103	53	176	EIKNNRPGMVAHAY/NPSTLGGRRGRQIS WGQEFETSLVNMVK
2089	15990	A	2104	3	267	FRHVGGGLKVLTSGLDPPALVVSQAGIT GVSHCAQPIVGDFNTPLSIL/D/RSTRQ KINKDIQDLNSALDEADLLDIYRTLHEK /STEYTF
2090	15991	A	2105	268	3	PPKEHGSSPATEQSWMENDFDELREBGF RRSNYS/LREDIQTGKEVENFEKNLE ECITRITNTEKCLKELMELKIKARELRP ECRSLR
2091	15992	A	2106	3	170	GFHHVDQAGLELLTPQVIHP\LGLPKCW DYRREPPCLASPHFHQIAISQRRHREAK SARGPDGFTAIFYQTFFKEELVQILLKQF QRIKGEILL\KNHYVKPSITLIPK\PG\ RDITKLLTRSFVSLCPVLSPLQSLQS RPSLSMISLHSCFVLSASAHPHVHL CPTCPTLVLSGSHCVCCVSLFF
2093	15994	A	2108	3	370	HENWNNGWGDSTIYSKMYLYFKPMLRP Y/C/SQKKIPFKILLFDNAPGHPRVIM EIMYKDMEVF\MPVNTTF/ILQPMQORV ILTFKSYLRNTFHKTIAAINSDYSDGS GQSOLKTFWKGFIVL
2094	15995	A	2109	1	213	HFPVENESAPG/FKAAGDLLTLLGNGA AGDFKLKALLVYPSENPCFLKGSFKPNL PLVWCSSHKKAQVQLG
2095	15996	A	2110	391	3	KKKKKNPHRKKIKRWKKIFNAERNKKR AGVIIHILDRLDKQQTIRRDQR\GYT MINGTIQQEVITILNIHAANTKAVRYIK QVLLKLKTELGPNTIITGDTNTLLSL NRSSRQKNQQTLDLICNI
2096	15997	A	2111	188	365	FQNTIHCVCVCVCVCVCVCL/CVCFCV FFFLCGLGGFMCWCWDFCFLFCFYGVG FFFL
2097	15998	A	2112	3	340	RMESALDRKQFTTVVGDGTGDFHAVDEY KPHDATTNPSSLILAVQMPAYQELEEEA IAYGRKLGGSQEDQIINAIKLSVLLGA EILKMITGRVSTEVDRLSFD/SDAMVA TA
2098	15999	A	2113	11	305	FLFTDFCLFMTHILGHKINYITN/CKRN VIIT/SYFSPHNRIKLKISIRKSRKSS NTWKLNNRLLHYPQIKDEVSRIRKYLE LNINENTNF/QNLWDIHK
2099	16000	A	2114	3	387	QTNH/NIPLSONLIQSKAITA/NCMAE RSEEAAGKFEASRGWFMRFKSSY\IKV QGEAASAGVEAVAIYDPLARLIDE/GCY TT/QIFSVMQTAFFWKKPSRTFM/REE KLIPGLKASKDSSSLLRVHAAGD
2100	16001	A	2115	152	393	VYCPICWLVSFFFCFCSVLILFVMFV/CL CFSFFCFLGFVVVSSFFYLFCVFFFI

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						LGCLFLCVVFDLFLFVLFVLCFFVS
2101	16002	A	2116	2	373	ARACGLPSSWDF/SVENRFHRVQGAGG ELATSGDPPTSASPECWDCRH/DHHTW LL
2102	16003	A	2117	3	449	HEFDHAMLQAHRAHHLAIDAYHEFEETY IPKDQKYSFLHDSQTSFCFSDSIPTFPN MEETQOKSNLELLRISLLIESWLEPVR VLRSMFANNLVYDTSDDYHFLKDLBE GIOTLMGRAEKRCRTVQNLKQTYRR/F DTNS/HNHDALL
2103	16004	A	2118	146	15	FFFFYFFFLFFFFFIFLFFFLFFFLFF FFYFIFILFIYSLLVF
2104	16005	A	2119	406	3	LFSVNETGFYSKMLSRFTTATEETSIPG FKVSKDKLTL/LGANAAGDFKLKPMLIY HS/ENPRALKNYAKFTPPVLYKWKNAKAL MTTHLFTARYTEYFKPTVETY/ILLID NAPTHQRALMEMYKEINVMPANTTSI
2105	16006	A	2120	109	396	YYFYFYLVLFFYFFIFLFFYFFFIILL FYFFFSFIFFFLFVYFIFLCYFFLFF FFFFYLFYSSFFFIFFLFFFIFFFIFF SYLIFFLSYII
2106	16007	A	2121	15	413	IVLARNTNFWLSFLFPVALGILIVLKGV KYIFWPLEYQORLKMFSYSFHY/FFLG SLLFLKYGFHMYLILL/CIFIIMCFF IKYSFFFCCLYHFFFSFYLFFLYFLIF/ CYLVILFFSFLFLFLSSYCFPF
2107	16008	A	2122	1306	429	SSSSSSSSSHVLRITKDEDFKILEQRQVV LSEKBAQALCKEYENEDYFNKLIENMTS GPSLALVLLRDNGLYQWQQLGPRIVEE AIEYFPESLCAQFAMDSLFPVNQLYGSDS LETAEREIQHFFPLQSTGLIKPHATSE /HKRGPSMMVILTKWNAVAEWRLMGPT DPEAKLLSPDSIRAQFGISKLNIVHG ASNAYEAKVVNRLFEDPEEN
2108	16009	A	2123	3	206	LRRLRQENHLNWRGGGCSEPRSQHCAA W/VSNSETPQKKKKKKKKKKKNLPS ALKKTYSQRGKLF
2109	16010	A	2124	23	401	IASGRPPFFFFFFFFFFFWPPPPGGYPHFS FLKKKKKRGGGGKSLLPKGPNPPK/ WGFFLFPPLFPQKTPPPPFFYKTPPI PPQGERGGPLKFTPPGGGGNPTILLD KKRGVLGPPPPFWTN
2110	16011	A	2125	3	439	MFDVSLTFTHSLFHSFQFHRKCELST LCDGGELRDHILLPTSICPIR/DKCS PGECC
2111	16012	A	2126	1	213	HFPVENESAPG/FKAAGDLLTLGLGNA AGDFKLKALLVYPSNPCLKGSFKPNL PLVWCSSHKAWQLG
2112	16013	A	2127	104	419	NSFFFEELYNPFGGLGKKTFFGGGEFP GHTPPNEALGGKNKFTGEGGQTFPSNN GEEKSVSFWISIEKILHRALL/AHALCK NCVVELNFGQKEPPPPPEEF
2113	16014	A	2128	399	140	PPPPKNFFFPKGFPG/FG/VGPKFPP PKKRVFSQPPRGFFYPPLKKKNPPFP PGNFGPPRGFFKREPPPPPPPPPPPP FFFFF
2114	16015	A	2129	10	457	KTSWTWCPVVPVATQKAE/AGGSPEPG RSRL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valuee, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
2115	16016	A	2130	409	0	PPPPSPSPPPPPSP/PSPSPPPPPS PSSPPSPSPPSPPPF/PSPSPPPS PPSPSPSPPSSPPSPPSPPSSSS SSPPPL
2116	16017	A	2131	317	177	FFFFFFFFFFFLRLQIFFF FLPIILIFLFFLFLLFFF
2117	16018	A	2132	3	542	EPWSVAQAGVQRDL SPLQLPRFRERF SRSLSPSSWDYRRLPAHPAN/QFLVET VFRHVQGAGLELLTSGHLPALTSQSAGI TGMSRTS/RPGFLFKV
2118	16019	A	2133	146	439	LKSVSTSIATWIQPK/CPTNSEVDKCPS TVKWIKMWII/YFTMEYYAAIK
2119	16020	A	2134	95	1	GRVDAILAHCKLR/LPGFTLFSCLSLPS SWDC
2120	16021	A	2135	2	380	THTHHTH/THTHHTHTHSLS
2121	16022	A	2136	4	337	KRNKKAWMTVLHLTAWFPEYFRPTVETY CSEKKIPFKIL/LLVDNAPGQPRVLVEM HKEMNVVFRPANTASILQPMNQGGISTF NSYYLRNTFHKAIVADSNSSDGFQGNK PVSSSQVRASVYLKKKKKGPPPEGITN TAGKEKPQSFRGKG\PPFP LISPKKEPV I/SFLKNFGPCTIGKKKPHPPAKNGGP LQ/RPPTQQGGRGKKKGNNQRPLSLGLG GNRSKPPPF
2122	16023	A	2137	2	356	FLGSSDPPPASVPVG RATG /RVFFFFFFFF VEVVSHYAQNGBELLDTSNPFAVASQS VRITCVSHRTWL LSPLYKI IQVCVS/K/S PELEQSEDKS LKK
2123	16024	A	2138	2	357	LLQVRCFVSTVNRGSSCQKTIOVYYYQE AI PP SF LL SP FLM /PYTKINSRWKDSN VKPKTIK/TLEENLGMP LN IF FTYQ L LW LYLHPESQLBICSN FRALQEGNL II FF I GRVGRP GT TL
2124	16025	A	2139	379	16	NLLLLNF FFF FL ER GLTF APRA GGWG NYLTWN LG PG PN KP PPP PR P/GTPK PTLK EG LF GF KT TG FP GA Q KG PEL PG LR GP PL APP RG NG GN PPP GPL K TF N G
2125	16026	A	2140	73	411	AGVSWRDHSSLQPCLTSRARAV\SHLSF. LSSRDYGMP PPP PKKKKKKKKKKKKK KKKKKKKKKKKKKKKK
2126	16027	A	2141	46	421	LAYLLSPVMVKPNQNRWTTLQISIN KGL TCRIYKETLQLNHKKTNNPIFF KW VK KS RHFTTRGAIQANK/HIKMKLNII SVYGN AQKNTMRHYHTPIKM KM GCAL WL TP VM COEAGY ILKMYPGWTPYP GRV VR PTAP ALPPRGTFPRD
2127	16028	A	2142	26	479	QNRLLARLT KK RKGLNOAHF/IKNDKGD ITADPTEIQASI REY HKH
2128	16029	A	2143	9	166	LEKESP PPP PF PP PP PP SPF / PHGS LPKPLGLQPLRP EVSFLEYLPKLKAC EGGVIEIAASF PRIYLMGMCS RD RIQ KDIDVVIQKSAEDCL FAGVKAILKA
2129	16030	A	2144	1	328	KTFLRLSQLVLCYISSGLIDDHR RPM ALT PR HR SG IT APR RP PQ PR VG I PE PTALS PS GP PP PC ST FG RC Q VP SLER RRKEGREPPSVGRGCCGHGIS PSSDIFF HLNFLCAHPDLFVFVCS IS NLQ LI FH E
2130	16031	A	2145	1	440	

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						KKKKKGG
2131	16032	A	2146	23	422	IASGRPFFFFWGAPGGEEGKKNFFWGPR GGKKKIRGAPTPRGKGNPPPKPWGKKGG APPKNLGLFGKKGAQRGPPGWFTPGKK KSPPPGPKKGGKNGRPPGPPQIPFPK FFSTGEKNPLGKKTTPNWRLLPW
2132	16033	A	2147	3	372	KKNTFFFLTTPRGPPPPRGLSPPPKRA TPPPPPFKKKKPGFPKKKNFFPPPGGG PPPP/LPGEKKGGYF/WW
2133	16034	A	2148	363	1	FNCRWETKSHSVQAGEQWHSFGPLQ LPPGFK\BFSCLSL
2134	16035	A	2149	2	361	FFFLVETGFHQVGGGLEHLTSDDPPTF GLP\GGWDIR
2135	16036	A	2150	387	2	KKSFFLVSPARVQWDPPNPPIPGSNNF PFSTPPKTGVIRGPPARKIFVFFIKTG \FPQLGRGVLSLPQ/CDSPPAPPKGG VSGGNPPAPPPPPFFEMESHVSQVGV QWRNLGSLQPPSPGFKQF
2136	16037	A	2151	23	421	IASGRPFFFFFFFFFFFFLGGRGVFFYP PGGGGGPNFFKKTFFPPGKKKFFPPPS KGGPLTPPPPPPPFFFLKKGVIINGGG GGVKISPPGGTTPFLPQKGG/NKKGPP PPRKKKIFLFFPGAIRQRP
2137	16038	A	2152	3	366	VIWAHCIFHLGYTDRPCLKKKKGGFPG GEKMLKNFFPLGKKPPPPQIPNFWSV IEKPPRGFYLGAAPPKKFFLLKP\GPF FFKEPPPPKKKGASPLKKKFFKGKKS PPFFSDPTS
2138	16039	A	2153	423	253	FFWGGGAPIFPPPKGFFPKNPPGVFFS PPKKKKIFFFP/HPVNFPPKDFKRP P
2139	16040	A	2154	287	1	KEMNKKKNPKKKVSKKISTAFYNKTLN NINFF\FAFFFFFFFFFIFFFFFFFF FFFFFFFFFFFFFFFFRFLFLNYKQTA QLMQHSAPTRP
2140	16041	A	2155	433	2	RRVLFIFPPL/HFSPPLPFPSPPPPP PMKFFSPPTFFYFKSPHPP/HPPQV VFSEPTTPMPFITPPPPHTSPSPSFF FFFFFFFFFFFFSFFFFFFFFFFFFFFF FFFFFFFFFFFFFIISIKGBIRSSSVR VMSRTRG
2141	16042	A	2156	69	606	LWWEPLSRHAAYRQWPGTAPRGLGHKV KGPASPA\PCGAAAGSTAQG\GGGAAC LPGPAAGAVTVVPAGPGGRATGPVLQR PAGAGQPTQQGQHDHAGRVLWQHIGIRP GAHRPGPCAP/DSAPRAPGGRCG
2142	16043	A	2157	449	0	SSPGSSSSCSPPPPGGGVGFEL/YKPPQ KKPPPPPVGGPGFPQKLSFFPLPPP FFLGGGGPPPPPKIKSFYPPPKKVSF PPPEKKAFLPPPPPLPPPPSPPPQPP LF
2143	16044	A	2158	241	5	KKFSFFPPGGSQGGFFGSLQNPFGFTF FFCLNLGKKWGQRGPPRPNP/SFFFF FFFLVETGFHHISQDGLDLLTS
2144	16045	A	2159	434	2	LGSASQLGCSGVRDPLEAVCFPSDLQL CARRTTALFKAVRQGHLSLQRLLSF/V CLCFVPRSGAYRGRQASLSCGGLHPVQA SRLCLPKQAWAMAGAP/PPASLQPCSL

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						ISDCCASNQRDSVGVGPSEPRAGYNLLVRCFLSP
2145	16046	A	2160	448	84	FLGGFFFFFWFPPSPPOKEAL\QKKIFFVFFSPESNQKNFFFSFSRGGPPNPLFKGGGR\FSPWFLFFFFFWFFLVVFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFLGKCKPLKYT
2146	16047	A	2161	3	156	RGCSEPLRHCTPAWVT\KETVSQKKKKKFLTLGGKTFKNFFFNAPGTFP
2147	16048	A	2162	412	37	FFHSPPPPPPAGGAVFPPKKKKSSPPPTPLLL/RGGGGPPPPPKRGGPPQKPKRGFFSPPKKKKFFPGGPGPPGPPQKTPPPPPPPFFFFFFFFFFFSLFFFLRTLWRKGRGRI
2148	16049	A	2163	5	370	QSSCVQWLVPVPTIQEAEAGGFLEPRSERLQ/CSHCTPAWA
2149	16050	A	2164	437	36	FFFFFSEAESCSVAQAGVQWHARSLPQLPPG\SSDSCLSLSSYMCLSPRTGGS
2150	16051	A	2165	3	623	RQGFTLVAWAGVQWYDLGSLQPPPTGFKRFSCLSLPSSWNYRHAPPCPANFVFLBETGFLHVQAGLELPTSGDLPASASQSAGITGMSHCA/RPKVCSYHLFF
2151	16052	A	2166	337	0	PPPPPPPPPPPS/PSPPPPPPPPPS\PSPP
2152	16053	A	2167	350	156	AEATSKIRCQKCYIMIAGHSGTRLQFQLLQRLRQENHLNPRA/RGCNEPRSHRTWPTWYISKSLA
2153	16054	A	2168	1	337	DEKSLQSRSSSYNGYSDLSTARHSGHHKKRTK\IKKKKKKKRPFKKKGPLKTRKKPRGGLLKAHPFPGGPPPGFFLTGEGAPPVFFKKKKKPLGKGGLWG
2154	16055	A	2169	2	606	RVLRAVAHEEPDKEGKEKPHAGVSPRGVKRQRSSSGGSGEKGRPSQEPPLAPPHRRRSQPP\HGGPLPPTNAAPTVPGPVPLLLPPPPPSLAPAGPAVAPLPAPSTSALETFSPLTVAAGPKHKGHKERHKKHHH\PAFMVIPAPAEPI
2155	16056	A	2170	311	2	GLQPLGLGSVKQCMDLACVPBTVCVVCVCVCVCARAHTPVCTQGCVPSTQCVCMHVC/VCVWACTCVPVCMHTCVGVGASVCMQRNELGRWAWENDAIRQRC
2156	16057	A	2171	78	337	NTPNISYKAMSLKGPITGTFLPNYPGHKVCVCDTYLCVYQHTHTHTHTHTQAFP HI/HIYTH
2157	16058	A	2172	2	278	KNRLNPGGGGCKLRSCHCTLAAT\SETPSQKKKKRKRKRKRKRKKIVYTKIEKGNAMTGESFIHFCKKSSVPQVALSAEYRCST
2158	16059	A	2173	2	365	FYHVGQAGLKLTTSSDPPALGLPKCWDYRRE\DCAPNVKS
2159	16060	A	2174	195	389	FRVFSKLKYYDFFRGRISLSCPGWSTPGFKRLSCLSLPSSWDYRPPPCPAN\FCIFSRDGVSP
2160	16061	A	2175	23	374	IASGRPLIFFFFFFFFFFLFCRGGGPPFNPRGKERGGFLIKGPPPGGKKNFWAPPGGGEIKRTPPPGVFFFLKKKGFSGGGGKK/PPPPGEPppppPQGGKKKK

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						TRGFLF
2161	16062	A	2176	2	158	FFFLKQSLSVTQAGVQW\PVDSLQPLPP RFKRFSCLSLSPSSWDYRCVPQCPAN
2162	16063	A	2177	340	120	PRFHFLASPSEMSTMTVKAKTTVPASEC AYPKIEPFFPF\DPGRSES\FDKLGVHH HPLFPLSGEPLMILHKNT
2163	16064	A	2178	3	256	YLKKDLNVNQKTLTLL\EKQK/HLHD MRLCKEFLNKTSKAQYILKKISQY/LIK VQNFNAVKDPVKRMKROASD/WENIFT
2164	16065	A	2179	95	1	GRVDAILAHCKLR/LPGFTLFSCLSLPS SWDC
2165	16066	A	2180	1	143	ARGERERERERERERERERERERERE RERVFV/RERAALSREGRDKCERSGLF
2166	16067	A	2181	1	304	ARGQGHLSLQRLLSF/VCLCPGPTGGA YRGRQASLSCGGLHPVRASWLLCLPNQA WAIAGAPPAALLPPCSLISDCCASNQD SVGVGPSKPCVGYNLLVW
2167	16068	A	2182	3	163	FQRSTESCGWDKARSQSRSPPRQOAH GHHS/HTHTHTHAHTHTHAHTHAWTRP
2168	16069	A	2183	3	205	NFKLFCKGFFFLRQSL/DSVSQAGVQRH NLGSLQPLPAGFQLFLQPPPPGSKDTHP GVQRHDHNSLQP
2169	16070	A	2184	228	88	WFFRIYDSFFLVFLVFPFFFFFFF FFCVFTPPFVYFIQYVVYI
2170	16071	A	2185	287	3	SLFLAIPQWFFQKTIYLRKQKIVLLACQ PSKGLSIVQVVRGQLNSFVLKSDQDTP\ PRFKRFLCINFLSRWSYRHVPPRPDSFV FLVETGFLHLV
2171	16072	A	2186	252	105	VSISCHPQ\PLIYTCY/HIDGYSNIHL CTHTHTHTHTHTTRVELQGPA
2172	16073	A	2187	267	459	KHVPSSSYTWL/IFFFRGNFLKKGANFV PQGVLLKGNLSSLYPPPPRLKQYSCLTL LRIGNYRHA
2173	16074	A	2188	170	15	RSVMKDLNSHFSKENIQMANKRTKECSA LVVFREIK/TMRCHLTPIRMATIKK
2174	16075	A	2189	2	504	DVTISTCHASAKVGRVLVFDHYGKI IQK TPYPHPRGMTVSVKQLFSTLPVRHKEFQ RNKKGLG\RRSCFCDF
2175	16076	A	2190	1	565	FFETESLSPRLCSGAISAHCNLHLPGS SDSPASASRVAGTTGACHHTWV/IFFVF PVETRFHHVSQDGLDFL/NLVIRPPRPP KVLG
2176	16077	A	2191	142	382	NTPPLLFFVIRDRVSLCCPRWSGVAQF WLSATYASRV\KRFSCLSLP/SNWDYRC VP
2177	16078	A	2192	138	365	KHQYHCC/LLKKKKKKKKKKKKKKKK KKKKIKKKKHGGPFKKNFW/EGQPRNWA GGV
2178	16079	A	2193	385	21	RGEIFFFKTRKKFSPQGGRGVFPSP PKNEFFPQGGKFFGG/EGGPKVPPKKG GFPKKPQGGFKVPPKKKKKII SPGVIG GPPGNFLKGAPPPPPPPPPPPPPPP FFFLVRAVKLS
2179	16080	A	2194	415	56	PPPTTAPVFSPPPPPPPPPPPPPPVFF FRSFPAPPPPPPLFPFPPSP\PSFPP PPPTRPCPPPPPTIPPPPPPPPPPPPP FFFFFFFFFSLPPPPPPPPPPPPSFL FLFFPSRLW

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2180	16081	A	2195	35	369	MKRPSPPPTPPPPPPHLLPPFPEK KTGPP/RGFFKGGGERGPPPKKKDPPP QKQKKKKWGGGGGGGQRKKKHPQKNP PPPPGRRGGGNFLWGRPRGPPPGGGGK K
2181	16082	A	2196	2	266	SKPRSCHCTPAWATQ\ETPSYKKKKKK KGLPLGGPGGKTIFFSLKPGQKAQPKNK IPFKKKIPFFSTPKGKKKNFQGGPKKK KKKI
2182	16083	A	2197	1	277	ARGERERERERERERERERERERERE RERERRHP/RPRERE
2183	16084	A	2198	1	285	ARGERERERERERERERERERERERE RERERERERERERERERERERGAPP PRLYRERVLLKQGRFLPPVRERKK/RS PVQTLPGY
2184	16085	A	2199	346	1	VPRHGLPCFCFPHQLQPPKRRKFNRR ALTSHQTQFFVFETESCSVA/RECSGAIS AHCHL\CIMRSSNSPASGGAGSSELRR HCTPVGQQTBIWSPKNKPIKKEGCPYC QFLSC
2185	16086	A	2200	3	389	HEGMILAHCSLNLPGSGD/ASHVARTTC VHHHVQLILFIFVETK/FSHYAVQAG/L ELLSSSDP/PTSQSSRITGMSHH
2186	16087	A	2201	3	204	HECHCTPAWAT\SETLSQKKKKKKKKK IFPGKKTWGGWNKKKFLFLNRKFFLGKG LFHLKRGPLKLF
2187	16088	A	2202	69	379	KKKRVFFWGPGGSKPPT/SGNPPWPFPK GGGLRGLPPPPGPRGVIFKNFGKRGPPP PPGLKSWGPRDFFGLALQRGGISGLNNG APPPFFGVLLKLPPLFFVSKG
2188	16089	A	2203	81	379	KKKKKPPPPKKKNPGPKQEGGGLRGPP TFSGGGGKKTCPOKLKAAGG/SKKAPG PPPGAEEKKNPALGGEKKTLPNGRGPKR LRGLAKKGNPPSSFGGK
2189	16090	A	2204	1	341	GQSLFVSPRLQLSNGNRTLTLVSTRND VGPYECEIQNPASANFSDPVTNLVLCBY LLF\PVAQATSPNPRSORPGLSVPLSSK NADSPPTPRNPARHDFLPQANMRPSLD QE
2190	16091	A	2205	2	370	DAPPRPANFVFLVKTGFPFVGQAGFKLP PPGDPPLASQITGKG/HCAQPPF
2191	16092	A	2206	362	24	PRGSSSASSSSSSSSPPSSSSSSSSSS SSSPF/PPPFVLKPPPPPKKSPPKKK NPPPKKKTKTTTTTTTTLRRGLCPFGR GKRAKPPFQKKKKKKRESSFYQQVIIH M
2192	16093	A	2207	357	3	AGQALWLARVIPVLWEARSYYVRISWYR NIVAMDSDSLDSGHSKLSFRKGFPVL YAIKTHDSWEGVS\MSALIVWKSLLPS CVDAFEELTSSAEVAAQVVGIATDLEL LVGCARA
2193	16094	A	2208	280	411	GNDVYFLVFLF/CLFEKESCSVAQAGVQ WHDLSLQALPPRMA
2194	16095	A	2209	3	392	PIIYEKYTQQINEMPRKLQHQQLALVSR NGPILLHDNAQLHITQC/LQKLNELGYR VLPHLPYSLDLSPDYFFKHLDNF/LQ GKHFNQEDAENVSQKFVKSQSMDFYAT /GNKLISHWENCVCN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2195	16096	A	2210	248	417	GILANCASIKDLISRIYKKLKQIN/KQR TNDPLKKWAKDMNRYFSQBEIQGVNKH KK
2196	16097	A	2211	213	493	GKRFYFACPGKIGALQGPFKGGGPPFF FFFLTTPPNTNYLTNKLKIKSPCTFYF SNILGFYPSITHRTIPDAWTA/SQSGP VLMRSIS
2197	16098	A	2212	159	413	LAPRVIFGPPKKPPERPLFFFFETES SSVTQAGVQWHNLSS\PRFKRFY/CLS LPSNRDYKRPPPHANFCTFSRDGVS
2198	16099	A	2213	455	60	NPRREVGPICPPPKIRVPPQNPQVGFYS PPLKEKTFSTSPAPVNLGPPRDPFKRPP FFFFFLDFFFFFYTYKTSAACTRSP AQRVARRELVPSS\PLPSLCLAPAPR GPGSLCPRGSLEGDNGSSPG
2199	16100	A	2214	2	243	LTLSPRLKCNMGVSAHCFLLSSSDS/ RLR/QENCLNLGGGCSLRLRHCTPAW TTERDSVSKINKNSLKIFTCFVDAA
2200	16101	A	2215	1	286	FSQLRLRFIC/SQGGRLCCESCSPAFH PECLSIEMPEGCWNCDCKAGKILHYQ IVWVKGNYRQVFPRTKRKYSIIVQTSF ILWIQSDLEIDR
2201	16102	A	2216	173	2	ITIFFFVRQGLTQAGVQWR\DLSETLV ILPPLAPCSLSQSSWDYRRVLPPLNFC IV
2202	16103	A	2217	216	4	VYPPSFMVFSQVFLSSTHISLSFSFFWN YLFYLYLYLYLYLRWSL/DSVTQAGVK WHNLGSLQELLPGFK
2203	16104	A	2218	14	228	KRSSHLFTDDIILYMENTKHSTK/NLLE LIKEISKVTG/YQKSVAFLYVNNKQAIK KTIPLTIASKRIKNSGQA
2204	16105	A	2219	244	3	EVLNQNSGLPRWPNILRAKASLRVPRQC SRGVVFSANGAGTRYLYAKEWGGGLGG GCKLRSCHCTPVWAT\SETLSQKK
2205	16106	A	2220	162	2	INMVGNLFFFGDRVSLCHAGWSAVAPSW PTVASTSL/VKQSSFLSLPSSWNHRH
2206	16107	A	2221	146	3	GRVDGVPWRNPGSLQPPSP\GSSDPPTS ASQESGTTGAHHHTRLIFVF
2207	16108	A	2222	239	2	SYISKPKDKFPHDSSPEIKPVTVWNRNSF SFIFPPFFLFPPEKESHVTOAGVQWRNL GVSSYWP\AGLKLTSGDPPALAS
2208	16109	A	2223	2	159	LNRLDGGGCSLRSCHCTPAWAT\SES PSQKKRKKKKKKKKGGGRNSKI
2209	16110	A	2224	3	345	RFKLFSCSLPSSWDYRRVPPRPA/NFF VFLIET\GFALITSSKTERQSRLEICIFG FVGLPCREKRASERRSVEG/HERKILES FDFFFLGGTESCFVTQAGVQGCYLGSPO PPPPG
2210	16111	A	2225	103	319	FSEYRNVTNFLMLTMSCSCLTLVE/C/ WSEGYMATPCTILLLFFORHCLTLSPG GVQWCSHSSLQPTPGIK
2211	16112	A	2226	2	110	PHHVQAGLELLTQWSIHLSPKCDWF\ RHEPPHPA
2212	16113	A	2227	2	178	IFLIPTFLEMSSHYVAQAGLEFPF/KIL TSRLSLLSSWDYRRPPRLANFFAFLAK GDAA
2213	16114	A	2228	173	3	FIFIFISLFFIFFLRQSIIVLSAVQSR LQPPPPRFKQFS\CLSLSSWDYKRVP

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2214	16115	A	2229	333	1	HTPPPPPTFHSCLCTEGAPPPQNT/PNP PRNPFIIPLSRSHTRANESLSLTPRTHP HSPRPPLLTHPHNPASAPPGSRYPPR ARHRERPRERPTQREERERESVCVCV
2215	16116	A	2230	350	3	KKKDIPPVNIYAPNTGAHKYIKQILLDL NRDGF\HTITAGDFTTPLSVLNSSAESR CSRPFIIISPSLVVGLRE
2216	16117	A	2231	277	1	QMHPARGHLFQALIPVQKPAISQGMSA SGSTQVSPFLSPCFWVEVNCNTKVL\T PFCGAGTGSHSFAQAGAHWCNRGSLQPH PPGFKRL
2217	16118	A	2232	3	335	ETRFHHVGQAGLEPLTSDPPASASQSV /GITGVSLRARPGE/GSWKTVCCNMMS EPT
2218	16119	A	2233	29	448	CPSLRQAWHEAAIDEVRTGYRQLFHP QLITGKEDAANNYARGHYTIGKEIIDLV LDRIKRLADQCTGLQ\GFLVFHSFGGGT GSGFTSLLMERLSVDYGGKSKLEFSIYP APQVFTAVVEPYNFILTHTTLEHSDCA
2219	16120	A	2234	1	365	GARLILVLEETGFHYVGAGLELLTSS DPPASA/FPKCW
2220	16121	A	2235	28	460	DRLIDHISKLGTRGLQGFLVFHSCGNLG \TGFGFTSLLMERLSLDYGGKAKLEFSI YPAPQVSTAGVEPYNSILTHTTLEHSD CAFMDVNEAIYDICKKNLDIERPTYINL NRVISQIVSSITASLRFDGALNVDLTBF QTNLV
2221	16122	A	2236	614	84	LAASLAACAQLSALAASHRMWALQRLRK LLTTFBQGSININRLLGENDGSTRALS TGSALAALVKGLPEALQRQFEYEDP\IV RGGKQLLH/SPHFVKLVASRLVTLEAG HFCPCCAETHKW\AWFRYCMASRVAVA LDKRTPLPRVFLDEVAVRVCGHILQLG DTELQQHICHL
2222	16123	A	2237	1	393	GPMLAQLSVFRCGSTSAPNDLWYHFIEL PYHGESITMLIALPTESSTPLSAIIPHE STKTIDRWMSIMVPKKVQVILPKFTAVA QTDLKEPLKDLGITDIVDSSQGHFCQIT KAENLLV/SHILQKQK
2223	16124	A	2238	3	402	HVGQAGVQIGKACWELYWLEHGIQPEGQ MPSDKTIGGNDSTNTFFSETGAGKHVP RAVFVDLEPTVIDEGRTGYRQLFHP LITGKEDAANNYARGHYTIGKEIIDLV \DRIKRLA\DOCTGSQGLGFP
2224	16125	A	2239	2	478	GRGGLHRIPVVTPLTPSFARGLVPSLAR GVEARNAGAPIKSYPRPGSRLKMQNGSK GSLQNKTFHWEICDAHVNSKIQLKQ\H ISSRRHKDRVAGKPLPKYRPNYKLR PSILAALAFQKDMNPLAPLSSPLA AAEAVSSALTLPFRPFCEV
2225	16126	A	2240	255	2	FLFVKPHQISCPYTKGKISFLVLCPLNF FLFWRQDLAHPGWSAVTQSWLTAASN\Y GLKQSSYFSLSSWDYRCIPPHLGGKRP L
2226	16127	A	2241	365	11	EPFPPGGEKKRGKPPPKKTPKKDGPQK KSAFFGG\GKIKKKGAFRKKKKGGG PPPKKPPPRKKKKKNFSPPLPPKHTP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SLPQKPPTKIFLSPPLLFNLIFFFPLSPFIF
2227	16128	A	2242	3	143	PNFLSPRLDCRGITIRGHGGLYLPGSCDPS/CLSPSSWNYRSTPP
2228	16129	A	2243	132	2	MSAHCNHLPLPGSSDSPASVSQVAGIMGA CHIF\VLVQTKPHHI
2229	16130	A	2244	334	43	TSKHMKRCSSISLATREMOKNTTIGGHFV PTRLANIQKPKENAKYRQGLMC/WCWC NLASPLWKTIWHLVKCLPYSSAIFTLG \IYPEEVCLASSVPGT
2230	16131	A	2245	312	2	PFSKLPEKNFFFFFLLRQSL/SSVAHS VVQWRDLGPLKPPPPESKQFSCPTLLSI WETQTALSDQCATAHPPGGQRETLSHKI CVCVCVCVCVCVCAVCIYIN
2231	16132	A	2246	3	230	RAQAMVETSRERCLLRPPQIETR\HVAQ AGLKLASSDPPTSASQAGITGVSHHT WQPLTFCPHAKSLPFINQI
2232	16133	A	2247	2	214	GRVDLVIQAGVQWHDGLSLHPPPLP\GSS DLF/ASDSQVAGTAGRFHYAWLIFF\VF FVETGS/HTQVSNSYDVL
2233	16134	A	2248	3	139	EGVQGGCHNSLQPPTPG\SSDPPTSASI EAGTAGSHYHVWLIFLLF
2234	16135	A	2249	3	160	EGVQGGCHSSSLQPPTPG\SSDPPTSASI VAGTAGSHYHVWLIFLLFCFEGDAA
2235	16136	A	2250	319	3	GQKRYKIFLCFFFLGWLVLRLWSLTLSP RLERESVSKPKSQKPKPKFTPREF KEVLAKYGTKFFVFFGLFVWFFLRWSL /NSVAQAGVQWRDPGSLQASRP
2236	16137	A	2251	15	394	FVSFSFFPSFPHLFFSSSSFPFLPSF HFSFLPSDRPSVVP/FLPSFLP
2237	16138	A	2252	60	306	GREIRILEIMAEFLNLMKDLNISIQVA QQIPSKMNSKRPHRYQHFRSQSQRILKA TREKQLATYKGSST/VSPSPGPOTVNS
2238	16139	A	2253	3	351	GFHVDQANLKLTTSSDLPASTSQSTGI TGI\DHCTQPNFI
2239	16140	A	2254	150	2	RPRPDHSRLGAGDQPGQHSKTPS\HQK KTKTSQAWRHAPAIAGTROAEA
2240	16141	A	2255	357	1	LNLNLSLTLYAKINLKNITGTNVKHKTT KFLGGKNGANLMDTRLDNAFLDLTSKAQ LTKEKIDKLNFIKIQT/CSIKDLLGNL KRQAPEEKKILRNHISNKELVSRIHKEV PKLNNKK
2241	16142	A	2256	397	1	FSLFPVGGGQGGFFSSCKSPPPRFRAFF CPNPFRRKGGNRGPPHPGKGTLGFFFFF FRQSFALSPRVEYNLCLEGGSDPPASAS QVGGAPGLPPPAAVNFVGIFFF/CFFLRQ SRVSAQARMQWRHLGSLQAMP
2242	16143	A	2257	2	132	TLTLTPRLECSGTIS/AHCKLHLPGSR HSPASAPRVAGCGGHL
2243	16144	A	2258	214	347	KISLILGVHKICCEF/CFFEMKRSRVTO AGVQGHDLSSLQPPPPGL
2244	16145	A	2259	347	2	FFSFFFFFSEAESRSVA\RLCSDTVSA HCTLHLPGS
2245	16146	A	2260	333	1	SDQRWTENAFVELRDEGFACPSFSEL/R STPSTSGEEVENFEKLDCEITRITNTE KCLKELMELKAKAREPRECRSLRSRHN QLEERVSMEDQMNMKREGKPREKRT
2246	16147	A	2261	2	357	SPRSCSVYGIATLLFLYFLYKLAALLY

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						GLALNSFLHEIQEP/SLASGSGPLSRNS
2247	16148	A	2262	355	0	PPLPSPLSPPLSLSTFFSLPPFFPPFFPLF/CPSFSEFFFPSPFFP
2248	16149	A	2263	348	35	YFLKKGFSTFFPRGEGRGKDSRSLKQLTF GFKKP/SCPSFLRKW\ETRLCPAQKIF FFFFFLLEMGFCYIAQGD LKGSSQSSGI TGVSYHIWPTFIGHLTMCLAKC
2249	16150	A	2264	270	92	DRPARRKMFFTYSSRLFFFFFFFFFFF FFFFR\FFFFFFFCKFFFLSRWSLM IFIS
2250	16151	A	2265	1	417	FRPPAGVQWRNLISLQSLPPGFKRFLYL SLPSS/WDYRCMPPLA/NFFVVFVDV VVVVVVVLVEMRLRHVLARLDIVVLICI SLMANGMEYLFCSFAIHLPSLLKCRFT YFAHCLFLYFLETGSHSVTETGQWC I
2251	16152	A	2266	344	427	LIGLCDTNLGAIAHAKRVTLIAQDLQLA
2252	16153	A	2267	310	417	RVPGYTLGSGPLATMAGFDDKLKPHMBG AAAPILVR
2253	16154	A	2268	186	464	NSCLSHNQRLFRLEKMGPISAQEK VLHTLSGFGSLV\VGWLVFEMESCSVVQ AGVQWRVHPPPRFKQFWSLSPSSWDYG HVPPCPANF
2254	16155	A	2269	1	427	PEPPSLPPDGAKKQKTQKSKKWRICFLR KKKKKKKKKKKKKKKKKKKKGGGSKKSR GPKLTETNIILIKGGLKKMNYREIBK KLLFGGGGVIGPTPTQDIKGREINYLE AVGREKQRFISLVK/TNVA/HEATRDTI FRGYL
2255	16156	A	2270	399	44	ISFQLLLPITVLPCHVRVLMEMYKEVHV VFVP\STTFMLQSMGQVTLTFKSY\Y LRNTFNKAAALTSDSSESGSQSLKPV WAAPSSLNASKNI/RDSWEAVKIPALKG VWKKWSLKM
2256	16157	A	2271	19	420	AAGIRHEERERERERERE/ORERERERE RERERERARNIYHTYRPPRVFFFPF FFFFKKRRGFLVPTPPGGGGAQKKKTS LEGGKGVFPKGGGKKTPLKNPGGWGEPP QKKNGGGPPPRDPPPPRPLF
2257	16158	A	2272	463	20	SYNIPLSQSLIQ/SRALTLFDSTKAERN RRGK\RSGLQWEGSRGWLRFKERSHL HNIKVD EAVSYPEDLDKMDALNTKQOI FSVHKIALYSKMPSRIFIAVERESMPG FQASKDRL/LLLG/ATAAGDLKLPMLI YNSKNPRVPRAEF
2258	16159	A	2273	474	82	VGWADFLKNTSQAQATKAKMDKWDPIK LKSPTAKETISAKRQPTGEKIFANY TSDKGLI/SRIDKELQPYRKPNPNPV KWARGWAQWLTPVILALWEAKAGRTQ Q EIEATLALFSGLCQVFLC
2259	16160	A	2274	152	3	AEGRNGDGIQKSSI\RTLLSNDKNPQN IHRPRTFLTMLYQONLCHLGL
2260	16161	A	2275	32	361	LGASARYEKPVTNLILNGERLNIFFPIR/ SKTRLGYLLSLLFNIGLAILASAINQK KEIQIIQIVKKIKITQRKKKKNTKKKK ALFKFKGGPEKEKGPPKNPFKTPPVVF
2261	16162	A	2276	329	487	EFVNITIKIATSLHYKAIKAIK/AMVIW YWHKNRHIDQWNRIESLEINPHICNK

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2262	16163	A	2277	2	466	AHHSCSHLLTTAAHYSCSPQLLTTAAH TYSPPQLLTPAHHHSCSHLLTTAAHHS CSPPQVLTAHH\GAHTCSPQLLTPAHH SSPQLLTPAHHSCPHLLTTAAHHS PQLANSYRG\SPYCSSWSQTGFRKSSH VGLPEPWIFHGLQVV
2263	16164	A	2278	4	467	KNVTQGGKIHIRDKLDEMWNSTSVFCTN HMKHQTNFNAKCNVFKCGK\TACNFQ LTQYQISHANQKPYECQICGKPRKRAH LTQHNRIHTGGKPYECKCGKVFICCS LIQHKRTHTEKPYECLECRKTPRRSAH LIRHQRIHTGEKPKYK
2264	16165	A	2279	383	3	FLCVCACVCVYVCMCMCACAC\CMCMOG CVCVCVCVGLRGLGAVVCRSWGPP LCFLLGLPLKSRLLWLPRTTISICTL PSAQGGLPAPGFGKYASNTTGVKSSSV FSLSRITALSHLHW
2265	16166	A	2280	47	219	VCSELKSchCTPAWAT\SVTLSEQKQNT KQRTLGSIFFQHTFMHLKKEKSLILQK W
2266	16167	A	2281	294	160	NKTEFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFLFLF
2267	16168	A	2282	68	490	RTFAYPKPPVFGSHSGKTTIPKNARGSY PS/PPLPFPSPSPSPGSPVSLPPRLP SPSPSPSLSPISRLPSP/SRSPSPSLP
2268	16169	A	2283	3	454	CQSAPLGGASQLGYSGVVRTLEEA VCPF SDIWLCAGRITTLFKA VRQGHLSLQFR LPFVWLCPAPRGVYRGRQASLSCGGLH QVRASRPLCLPTQASAMAGAPPASLPP CSLISDCCASNERGSTGMGP/SEPGTG
2269	16170	A	2285	1	452	LKDSGRDVVSQFEGCALGKQLNLKLDN WDSETSTFSKLREQLGPVTQEFWDNLEK DTEGLRQEMSKDLEEEKAKVQPYLDDFQ KKWQEBMELYRQKEEPLRAELQEGARQK LHEL/QEELSP/LGQEMLDRAHVDAL RTHMAPYSDELQ
2270	16171	A	2286	3	266	NSSPSSGHSTPRLAPSPAREGTDKAV SALKSPQPNRGMGRGQR/PGLPS/DTAT ITPHTSGFQKQQLSLKVQTQRAKGRLS HWDLEP
2271	16172	A	2287	274	453	IYTFVKSSSKTLRPRHIDQWNRIENPEI KP/EYSQLIFDKANKNIKWEKDTLLNKW CWDN
2272	16173	A	2288	81	487	TVYFKPTVETY\CWDKKKIPFKGLLRD NTPCYPKSLLEMCEKINIVFAPATTTSS /LKPMQGVIVTFKSNYLNKTF\RLGEG RKKKKKKGRKKSFKALAAINSDDSGA GQSKQKT/FWKGFSPNAIKNIQDPWE
2273	16174	A	2289	75	469	SRGVAGAPPKSPSTSPGGLDVTGPH SSHAASPGP\PPPPEPTASSMASAP/P PAPQPTPL\PPATLGPPSAGPE/PSGS CTSTGWGYSFCCPRCRRMRWQPPQGGP AWHWWPREFP/PPRVSGS
2274	16175	A	2290	256	55	PTQPLRVELTTVTLRCDINKWDYIKLKS FCTA\KKRQPTEREKIFPNHVSNNKRLIS KIYKELIHRI
2275	16176	A	2291	497	29	SLTHRVAGGA AVTPLAHAGARQIFFLGD PHPTSSLLGWGPAWDPCAQVSDHPASS

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						RVGKTLTSCFPGGRLPWVTCFPGGQLSC LTQMHLTPAGMCSPCVCVCVCVCVCPN GMCPRCMVCVCPCRDVY/ICVCVCVCV CVMCLCPCWDVFTL
2276	16177	A	2292	141	392	SCSTEVKQPKIGVREVDVVAAPGLAPSS PQKKQTTSTSSLLSLLRLSKVRFLFNIV LDVLAREIROEKEIKGIQ/LGKEE
2277	16178	A	2293	14	291	YVGTGEGSIFSMRVINYMTRHLATLRE S\CYSR\VYPRFIEFLRFDIQSTGO/RI TSRQHPPR/DLRDALLYLNRRITLVRTR CKSVAKRPPGSP
2278	16179	A	2294	110	293	LLSNRSLATASLCGGCNELRSCWTPA\ WRQRET VKKKKKKKKKPGWGLNPPQR GKLCF
2279	16180	A	2295	96	313	WNGCYLLSNRSLATASLCGGCNELRSC WTPA\WRQRET VKKKKKKKKKPGWGLN PTPQREKLGFLKRGPGF
2280	16181	A	2296	234	2	CCLETTSLFDKGT KENTQWGKDSPSNK RCWKNIWISTCKRMKLDPLYIP/YTNINV KY/IKDLNLRPEITKLEENLREK
2281	16182	A	2297	334	6	KLFSPPGGGGGPPPPPPKGGWVPETP\ KRGGGAPNPPPPKGGGAPKPPQKKNSP PKKKKKIFCPPPKKKGPKGVFLRGPRGP YRVFLKGPPLFFFFLKKSWRPLAMYA
2282	16183	A	2298	467	8	LPGFKASTDRDN\VAGDFKLKQMLIYHS ESSSALKNDTKSTLPVLYRNKEAW/VTA HLLIPWCTEYFKLIAETCCSERKISFKI LLLI\DNAPSYPRALMKMFKINVFMSDN TTSIVYSTDQGVILTCNSYYLRNTFYKA ITAIDSDSCRMPOEGN
2283	16184	A	2299	1	449	SIYLSIP/FNLSINLSIYLSIPIYLSIY /HISVYIYL/SIYLSIIHLSAIICLSIF QSISLSLSINLSIYLSIHLSSIIYS SIIYHLSIH/LSYYLS
2284	16185	A	2300	1	445	QAGLQLLTSGDPRTSGLPQCWDYRC\DH RSWQT
2285	16186	A	2301	241	22	KWVLGTCACVHVFCVYMCYVCAWV/C VSMCLYVCACVCMNQ/VTCMCVCVCV CRFVCVGIPPHSKWISIG
2286	16187	A	2302	3	478	GGQTETLLTSQRKGGWPEALLTSQMGRP GRGAPHIPDDEQPGRDAPHLPDGAAGQ\ SAPHLPDGE\PGRGAPHIPDGAAGQRRS PLPRWGG/ELGRGAPHIPDGAAGQRRSS HPR/PGRPGRGAPHFPDGTG/Q/DGAP HFGIIPPDGT
2287	16188	A	2303	440	41	KSHHLSFLSFLFFFP/TKSHVAQ/CW SAISAHCNLCPLGSSSHSALASRVAVTT GVYRI
2288	16189	A	2304	2	395	FFLVKTRFLHVQAGLKLFTSGGPPALA SQ/SL/RITGMSHRTQPE
2289	16190	A	2305	184	2	SIKKPKPLVNLNRH/NT/WQGAVT PACN SSTLGGRGGRITRSGVQDQSGQRRESEF LRLGYGLD
2290	16191	A	2306	86	472	I IKLCKWQNK/RFEAGSLVPEMGFYVYT QAGLELLFSRDPHTSASQSAGITGAAFH QRWSVGT VLLQVDRGTPPVGDGCSRT PQ WPGQAFRLRTALKSEAHPPHSSTDVTPVL WSEGSPPCLSPPSLSFTG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
2291	16192	A	2307	133	2	RVIHVVRSHPAIP\TTREAEAGESPEP GGGCNEPRSCHCTPAW
2292	16193	A	2308	3	369	LTAFDPDFPGSTHPLTSASQVWATGAH HHSWLIFFVFVETGFHL/SELLSSSPL ASASQSAGITG/REPPCLTSPPFF
2293	16194	A	2309	253	365	TDYFYLFTYLRQSL/SSVAQAGVQWQDL GSLQPPPSGFK
2294	16195	A	2310	362	0	TKAQQCVENHFKLDANTLNKIVWRNI CHSSPNQKKYGLAILNLDKSGFRSRKDT GDDE/HFIKIKKSVIQRAIIINIYA
2295	16196	A	2311	167	2	LCYCVIFVFFIFWRQSLTSLQGGMQWCD HGSLQPLPP\GLKRSSHLSLPSNWDYRR
2296	16197	A	2312	67	482	DHLIPGGGGCSELQSHPCTPAWTA/ET LSQKKKKKREK
2297	16198	A	2313	188	437	AGFFPPENQLTNMKVRKANESDPWGVKP ESDESETHGSLSLSLSLFFLFIPLRQSL /NSVIQAGVQWRNLSSLQRISP
2298	16199	A	2314	41	325	TTTLFXRVRQGYSSLLMFLFPVCLCPA GRGGVYRGRQSSLSCSRHLHPVRASRPLC LPTQASAIAGAPPPALLPPCSLISVCCA SNEQGSVG*DP
2299	16200	A	2315	417	0	SPPRNWDYRCVPPRPFANFVFLVEMGF/Y HVARPEFGLLELPTSGEPTLA/FSKCWD YR
2300	16201	A	2316	98	288	LMAVVPATWEAEAEQESLEPGWGGEEG CSELRSCHCTPAWVT\SETLSHTHTKKK KKNGAAL
2301	16202	A	2317	1	410	LNHIPLNSLTKRKPSPHSLNLKKKKKKK KKKKKKKKKKRGGGVKKKPRGGQKKK GGEKNFPSSKGGKKKRGFEFGKNFFG GGKKREKTPQKKKSPKGGKKNLR/BERG EKNPKRGGKKRSSFRNNLRGEKK
2302	16203	A	2318	249	3	PLKASSPPKAFNFCREVGPICPPPKKKV P\PKIPKLVPISPPPIRKKLPLCPPLTL APPRVPLKRPP
2303	16204	A	2319	2	393	AHLGLPKCWDYRHEPFRPAPLFLNLSYF GLDLLT/S/GDPPALASQSAEITGVSHC AQ/PEYVY
2304	16205	A	2320	389	2	RGNSNIGGPGPLRGKKFSPPPPLKNWGT KLGPPPPPPPPPPF\GKPGFSIFFKPI LKFKGPKKPPRAPKNGGSPGPGWFFPF FLSNFTQLPGIKLSKGGKKNFASPPPPF FFFVHYKTGYPSATPDW
2305	16206	A	2321	389	206	FQWRWGF/NHVGQANLELLTSNDPPASA SRSA GTTGM SHHAQLKNYFLMVRMWRNW IAVGM
2306	16207	A	2322	371	42	SFPFQSGFFSPPPPHEFFPPPPSFFSW VGVRQIPPPKIFSSPPPPGGFFSPPPE R/VDFFSPPPPPPPPSFFLSPPPPFF FFFFFFFFFFFFFFFFSFFGVKKRK
2307	16208	A	2323	82	386	PFLTQKYFFTPPEEGFLKKPNRREGPPS PITDPTLWPNMMKGIVPKAPPIIFMGGG INMTFSGFVTTKAPFERPLRFNPLRQG FDLLTLKAS\WGSSASWY
2308	16209	A	2324	1	413	RGSGDNRHGPPCRVNFVFLVETGFLHVG RSGLELPTSPALASQSVGITGVSC/RPP PQASY
2309	16210	A	2325	58	400	SETLVSKKKKKKKKTPPPKPNPKKKKNP

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						PPPPPGAKKGPGGKF/PPPPIFQKKRGG FKK/SPPKKPPKKKTTPPLGKKGPPPP RGGPLGGPPPPPPQKKNPPPPKKKPPF FFPPK
2310	16211	A	2326	462	306	AHNLRLPGSSDSPASASGVAGTT/GMC HHARPILYLSGDASALLHCFSSAQLF
2311	16212	A	2327	1	393	SRPPSRTEKIRNFFVETGSCYVAQAAL KLLDSSDPPTSASQSAG/ITGMSHRAQP TS
2312	16213	A	2328	391	2	AWFKETKAGWIIPRSWDRGSWVSQPYSA LTSSPESGFHVSVTNGDSMTCLDGKHS L VAPHGIPQRGSSSLQDGVSPCAPMTKPY LASTKM\RLHEARELGFFSFLSLRQGLA LSPOLECSGAILAHCSLNL
2313	16214	A	2329	2	115	GCSELRSRFCTPAWAT\SKTASQKKKRG KKKKGGVIFY
2314	16215	A	2330	2	406	AAAPSALALRDGWAVRPELDLLPPCGEE VAPGAHCLGCGSPCLFLSPSHTRQSP APTSSPGLSTSPPLVPTHVSAPHSSKGP PSIPGAQALRGCGLGWDR\PSSPSLP/ PDVSPKPLNFAP
2315	16216	A	2332	226	377	KRKSXHTFLFKTLSPWPDVAHACNPST LGGQGGRI/TPRSGVRDQPDQHG
2316	16217	A	2333	3	191	CLSPGGGGCGGLRLCYCMAWVT/NETV SQBRKKERRKEREKEIKBRKKRKKERK KEKKKG
2317	16218	A	2334	295	81	FFKPPFPKKTCPEFS\FWEKRGFPPP PLRSFFQNPFPKGGPPIILKGPPPPPSL GWPPPPPLFFFFFLR
2318	16219	A	2335	375	8	TQIVPLPSNLGNKTRLRLLKKKRNEQGN IPTDTIDNRIKQIIQ/TYYBQLCANK\N LDKMDKALESHNFPKLRQRESLNI/HSA KEIHFI/ILNISTKKTDPDTGFTGKFLQ IFKEKKMAGHSGSHL
2319	16220	A	2336	399	97	FFFFFFFFKQNLA/SVTQVGVOGQYFRSL QPLPRVKPFSFPNPLSNRGYRGPPLGR VRQENCPKLKSKRFQLNKIPRLGKKKKL RFPKKKKKEKKBKIVKT
2320	16221	A	2337	411	57	KKPRSFSSCSPPPPPPPPPPPKPKKIF PPQIFWGPFPFPFPFPFPFPFPFPFP PQKKKKI\SPPPPKKFFFKTTPPPPPFF FFFFFFFFFFFFFFFFFFFFFFFF
2321	16222	A	2338	97	354	AKAPSLSLVLSFSSTFFLGIQGLALLPM LECRGAITAYCSLNLDPDSSGPPTSAPSP TPY/RIAGATGTHNALLFKFFSRDGL PL
2322	16223	A	2339	391	45	LMFPHLSHKHRSGEAPSIHWSIYLSIHP SIHPSLYHSSIHLSTIYPSTCLSIH /CISIHPSIYSPICPSVHLLAHSFIHST ICPSMHLPIHVSIOHFLSAQILPVSVFG EVSDI
2323	16224	A	2340	506	0	RDHEQLGIVRADKKKKKKKKKKKKKK KKSSSSSSSPGTFFRG/VPLKDPVG
2324	16225	A	2341	203	1	VELRVRAEPGFNFKGIYCTSMVDWIK KMWYIYMEYHAAIKG/DRIMSFVATWM ELEAIFLSKLMQ
2325	16226	A	2342	402	40	PYPKKKASPTDA\FSSSSSPPPPPFF SPPPKGFFSKPFFFSRFFSPPFFLK

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						PPPFQFFFFGELKINFFFPALKFFFPK SPPPLFFFFFFFFFFVEAGVLLCYSG
2326	16227	A	2343	181	1	QLKDOASDLLGKNGDEVKETIPSPFLPSS LPPF\LPLFLHQFLPSFLPSFFPPSLLP FLS
2327	16228	A	2344	2	407	FVASQLGCGV\RVRDPLEBAVCFPSDL QLRAGRITTAFLPKAVRQGHLSLQRLLSF \VFLCPAPRGGAIRGRQAFSLSCGGLHPV GASRLCLPKQAWAMAGAPPPASLPSCS LISDCCASNQRDSVGARPEPGAGH
2328	16229	A	2345	405	178	IIKFIYEKATA/LLNG/EKLKAPPLKLG TRQGLHSLLVNCTVLEVLTTGLRQBEKE IKGIIIEKKEVELSLFADRIL
2329	16230	A	2346	2	412	FKASKASLSPLLGANTAGDFKLKPLGIY HSLH\LKNYADSIILLVLQWNNKAWMIA HLFTAWFTEYFSPPLRPAQKISFKMLL FIDSAPSQPGVLMEMYKEINVVFMPANT TSILQPMDOGVILTLSYWLRTDFH
2330	16231	A	2347	2	397	ESLEPGRRRLQGARIMPLHSSLDNRVRL CLKKERKKEIGVLCRQWCECKIVQPLWE IVWYFLKLN\ESPYEPAVPLNINYPRE MKIHVYTNCTQIFIVALFTIAKSGKWW GTVACACKPSSE/WLRWVDYL
2331	16232	A	2348	3	423	EGCSELGSHHCTPAWAT/AESVSQKKKK PKKK
2332	16233	A	2349	49	262	QMCKGSNRRRGKRVGSRQISKKKTNAPI KKWAKDMNREF/DIQMANKHMEKCTSL IIREMQIKSTMRYHLY
2333	16234	A	2350	356	2	FVTAPLHSSLGNRARSYCKEKKKVQVAA KAVLRGKFIIAYTVFKKRKISNINLSIS LKTLEKEEHTETKADGAQYVTKI\RAKI NKIETANETKSRSLKTSKTVEGKCLRD ILLSAQI
2334	16235	A	2351	360	19	LDAQFLEVGLGELLFRSTVPTLQPPGCG ASFPVLNTLPF\SLSPSQSSSSPASLVR PWVAPPFLCPHGEPDGGPDSTSLPFP PAATGPAARLIQHPASRQPRPASHTHCG V
2335	16236	A	2352	360	0	NTFLAAFRVLVFCQMTSYSLALLSHKLAL MPLNLSDLLTRWTHCMGELFFLDILAIQ NPFHTVFFLGHPWGMESRFVQAVVQW PDLRQLQPS\PPGSMRFSCLSLPNSWNS PSYGR
2336	16237	A	2353	34	474	EGNRPCKELAARQVGCPCSCSPHWQLL QKQEKTAGAVSVCVCTSTLCVCVCVCVC VCAQAMCVCAGA/CFCVCVCAGA/CLCV CVGA/CLCVCAEAVSVCVQ/VAVSMCVC RS/VSLCVCVQGSCLVCAGA/CLCVCV CGIPPPVLCIN
2337	16238	A	2354	297	16	KFFFLKSFFFFSFFFLTTPRPPFFFPKK KKIFFFFPCKIFFFFLI PPPKFFFFFFF FFFFFFFFFFFFFFFFFFFFFXRHGG WFEEITILTV
2338	16239	A	2355	3	315	PVTPATRETEAGETL\HDLGEPGGRGCG ELRSCHCTPAWVTEQDSVSKKKKKRGA RFKESNFTTGLQRNIFPLGALKLISGA GVLKRRDGKTLGFPQFNRPWG
2339	16240	A	2356	399	154	PGQRGEIPLPKIQ/ELAGCG/GHLNPG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GRIFGEPRSRHCTPAWATBQDSICKSHS RSLGWCYKSSSVYLSTRGVWVRGLASV
2340	16241	A	2357	416	2	FFFFFSETESRSVAQAGLRT\QWRNLGS LQAPPPGFPTF
2341	16242	A	2358	209	2	KKNLVFWPRGGYFKSLQPPPPGV/SCPN PPKKLEYRVLFPQPSNPPFFFCIPSRDG VSPCCPGWSRTPD
2342	16243	A	2359	279	380	RGYNP/WPGAVAHTCNPSTLGGRGRQIT RSGDQDH
2343	16244	A	2360	415	224	FFFFFFFFFFLLITFILMLNLLPCHKFLFL QFLGLYLFLLYL\CAFFLLVALNIFITS FQQLDYTF
2344	16245	A	2361	278	2	ISDPFRFWNIYRIHTGLISLIQISENCV SCQKFOILEHFRFQIRDAQSVLRK\RKA WTGAVAHACNPSPLGGRGGWISRSGDLV HPGQHSETP
2345	16246	A	2362	139	282	KKKKGGRGGGGGGGGGXXWGGTKKKKK GGEKKNLWGGGKGGGKGGGS
2346	16247	A	2363	19	409	PKPPSVLGGGGPARYPSPPLGGPNRPVPL GPGVGAPPPGPKTPFFLKIKKIYPARG GPFVIPASPGGEGKKSPLPPRPVPLTQ IFPP/PPPPGGPNQG
2347	16248	A	2364	159	383	HSHFKNLSSIIKKLHRNNTFTEHFSLS SLNQCFNLTVFYSHLGNFKNSN/SWPG AVAHTCNPNTLGGRGGQITR
2348	16249	A	2365	400	221	GRLRQENCLNSGGRECSEPRS/HLHCAP AWAT\EQDSVSKNKKQNKQKQTHIYTVL LCARH
2349	16250	A	2366	383	14	GGRCNAPRSCHCTPAWVTERASPQKTK KQKNHTTKKRISCCYKMEDPLRQA\TF LQCPRAEGPSQKAARMELMEKQEKNOGP ARHRRQEQPLTSRPPCDHLCVVLVSQVSS TPAQGLSLLICK
2350	16251	A	2367	274	1	PRKILKARGKEHLASRGTMIRMTSDFYL QTMQARREWSKIL/NVLEEKIHQHRIL/ PVKSSFSKEEIKTFSDKQKLRGLVTSR SDLGKDVK
2351	16252	A	2368	161	2	FFFFFSETESCC\VTQARVQWRHLGSLP GSSDSPASASQVAWITGTRHYAWLIF
2352	16253	A	2369	361	198	NGRLIFVFLVEMGF\TMLARLASCDPPA SASQSTGIRGMSHNSQLKCFTEFDSFC
2353	16254	A	2370	116	300	HLNGDAVEERDFMKCTVSGITVAHCNLE FLG/SSDPSASAPRVAGITGMCHHIWLI FVILVEM
2354	16255	A	2371	2	192	MKLDPHLSPYTKVNSRWIKDLNLRPKTI KILEPNIR/ITLLIGLGKDSMTRNPKA IAIKTKLAR
2355	16256	A	2372	1	133	AGELLEPG\GRGCSKPRSCHCTTAWATE QDSSPEKKKKKKGGF
2356	16257	A	2373	43	403	LHDSPALASQGAGTTGVSHHARPAAGIN SRIGQAEDRISELEDWLSEIR\ROSGRN MDKRMKMNKQNLQEIIRDYVETKSM/NTR LIGVPERVGENGSNLENIFQDLIHENYK GKPIRLMVDL
2357	16258	A	2374	404	215	GQGRITRAQKFETSLGNVVRPGSEAQ LLE\PDRCSEPRSCHSTPAWTEQDS VSKKRRKC
2358	16259	A	2375	3	397	SKQLEFTQLYTKLNQLNKTKISDLKKEK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YPIRLFSKENTQMASRYRTKYSTWLIIR EMQIKTTFRHKLAALASSRCLLGLG\AT SAHCCTVGAPLW
2359	16260	A	2376	413	1	PKKGLFPKPIIWVTPGFFFFPFRKKPPP KKIFGAPKKKKSPPPPAKFFFFKGAP PPPPPPPPPPPPPPSGDSQERVREAM PVAGGP\PRPHSLSAFHAPGGTAWTPMH PVQTHKAQSPKLPASECPPPTTPLS
2360	16261	A	2377	398	247	RRFHHAGQAGLELLTSSDLPALASQ\SA GITGMSHHAQPSATHFQKHLVS
2361	16262	A	2378	2	143	QENRLNPGGGGCSSELRSCHCTS\AWVTT AKLCLKKKKKKKKFFGKGGG
2362	16263	A	2379	417	90	FFFFFFFPGGRLQVCPPPGILLFCFLY KGGSPPGGSTIFFPPPPGEGVPPGPPPP GGFFFFFFLE/QGGVSDGPGFFVLETPK KPPPPAPQKGGEPKFKPQVWGPPWPTF
2363	16264	A	2380	36	427	VHPLNHDQKQGASSTQKKKKKKKKKKK KKKKKKKKK/WKGGGAF
2364	16265	A	2381	402	2	NFFLKGRGWGFLPPLPRGPPPRGGPQK /RGGLGGPPPPFFGSKTPPAGGSRTPMG QKKKGPPLEPGPLFGGAGQAPFLPPVP RGGVSPSKKKKG/APPPPPPPPPPPPP PPPPPPFFFLRYNLALLPRLGCSGT
2365	16266	A	2382	166	5	THGHVIYVDQEMQMMIENM/WPGTVAHA CNRSTLGSRGGWITRSGDLMVKPRLY
2366	16267	A	2383	2	457	TSQPSLLSSWDYRSTSPRLANF\ILFFY IYFFFAFSVETGFHRVSQDGLNLTS/S /IPSIPRIPKHWDYRHDP\RTWP
2367	16268	A	2384	2	417	GRVGFSQSGNPNSSLSFTLLKVDFFVTI PGEGKDRIFKVSIKWLAIWSRMLHREAL VSGQIPVPLESV/QALDVAMRHLASMRY
2368	16269	A	2385	318	32	TMEIMLDKKQIQVIF/FBPKMGREAVET THNINYTSGETVQWVFKCKCGDESLE DEECSGRPEVGNDQLRAIIAHASADAWV DRDSGRCCACAP
2369	16270	A	2386	409	3	ISQAPSTPPRKRGRF/PPQKTSFLGPPF YAAFYQEKKFLFFSSDPPRETGDGKQK GFPPPKVAPKKKGFFKGGPPPGKKDPP SFFKHKSQPTRPPRAPALEGPRSR/SAA LQPGDRRR/PPSQKKPTRPPTRPPTRP
2370	16271	A	2387	415	10	KKGFFPFGPFIFLFPFPGFLPPPPPIF WFSGFCPPPPPLFYFFFRGGPK/HILVF PLFLLPPPPFFFPFIFAKESPPKGGGP LNFFFFGPKKN/SPPPPPFFFCMEFH SCRPGWSAKWHDLSLQPPPPVFK
2371	16272	A	2388	410	95	KATMDKSDHIKLSFYPAKETPTKVKTQ PPEWEKVFNYPSPDKGLIPPIIYKELQK YG\KKSNNISIKKWKADLNRYFSKDIQMA NRCMKRCSRPGAVAHTYNPST
2372	16273	A	2389	362	92	RFLFFFSPPPKKGFPPKPPFFFSRVPF PPFFLNPPPKLIF\GPPKKKIFFPAPGG KKIFFLKGGPPPPPPPPPPPPPPPPPP PVENTFY
2373	16274	A	2390	131	487	ATEHEKTEKSSLSFFSISKRKKMEKLH DIGFSSNPLG\RPKAQATKGKTDWTSK LKICSSRDTISRMKRPKEWAKTFANKS CNNKKPEKIDKNKKKKKKKFLGGALLKK TNLKPRG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2374	16275	A	2391	408	145	RWSLALSPRLCSGVSSAPCKVPPPGVT PFSCLSLPSNWEDRCESPPPAQ/IVFIG EGFYILHGFF/RRGPKIRCFISGCPPPV LSFPT
2375	16276	A	2392	1	203	LFFFAPSVETGFLHVQAGLEPPTSGDP PVSA/FPMCWDYRHD
2376	16277	A	2393	386	16	TPSAGGRHIELSLSTCPSCAQHQKREHL EGGEGGGAQSLTAPSSATSSQDPISAH AVEDKLSIRLETDLKTKS/WPGAUGHT CNPSTLGRRRQANHLRPGVVDQPGLVIC RPRPPKVMGLQA
2377	16278	A	2394	3	396	QLLERLKQEDRLSTGSQGCSELRSHHCT PAWATEP\DSVSK
2378	16279	A	2395	273	416	FFYSFLIKIRWKKQPGMVAQACNPSTLG GQGGRI/TLRTGVRDQPGQHG
2379	16280	A	2396	329	76	FIPIESACSQECLKENLRQEW/YIFGTL KLIFPETESHPTQ/DWSAGELL\DPRG RGCELSRCHCTPAWATRACLCLKHTHK IKK
2380	16281	A	2397	210	7	GGKKMYCRKPGGGGFFAAVWSPKGLFS/ RIWKEAPILSPQKKKKTNPIKKWAND ANRHFSKEGTQQ
2381	16282	A	2398	48	393	SILKTRKPLKKGRRRKEKESVVRTHV FFSYQSNAPSKPLNNSMTLGRLLSFSF FLVHFFFTDGIILCCPGWSRTPLGLKGS SHLSFPKCWDYIHEPPHPAYS/LFCR
2382	16283	A	2399	128	383	EEAPKHFPKPNLH/QKKVLVTAWWAAAG LIHCSFLNPWETITPEKYAQQTNEHQK LQCLQLALVNRKGPILLHHNVRHLHITTH AS
2383	16284	A	2400	54	384	LFTFILNSVFHTYMCLYFWTLFFSVNPF VSMPIQCLDSSFIISLDSEINENIYS QLIFDKKTQRGKNSLPDRWCWENCIFTY KRMKWDPYL/SPYTKIISNWMKDLNIK
2384	16285	A	2401	393	1	HRGENTHQGGGLSRWRRHSRQRTSRW IRHTRQWGPSRWITPSRQRGSSRWKRKRS RAGDIEVEKTQQSEGALEVRIRSRQRT SRWRSFSRQVRSFRWRICSRQRCSS/KV RRRSRQRTSRWRRHSRQR
2385	16286	A	2402	1	330	RPPPPPHCWDYR/HEPPR\QPTLWVIFK LSVETRLCYVAQIGLELLGSSKESSRLD LPKCWDYRHLLCWMVIFQEKLV\SGFL FKIPRFFKAGMEIFKQIEGFWSHPLAT
2386	16287	A	2403	3	407	ADAWGLRGTHGPWEQAGISGISPSNSFL FVCFRQSVLVSOAGEQWRRLGSLQPPP PGCGRESC\PSFQGGITPSCFFVFLEKM GLHRVGQAGLQLLMSGEPPALCSQRRGI TGVSHHARPPSKGFIWHTGAPAM
2387	16288	A	2404	239	573	VCPGVFSLSHFFESEFSSITQAGVQWLN LGSLLQPPSRGFKQFLCLSLPSS\YWFTG TPPLVGGGSAGLRGG
2388	16289	A	2405	1	122	PTFRGRCGCELRSCHSTLAW/VNSETTS QKKQRKEKKLPLL
2389	16290	A	2406	417	130	QALRVKHVQLVPSSDFLAKTRAQSVNNL LRHSSSSSSSSSSS/SSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSFLFLFFFFG LRGAFLGRFCPIRR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2390	16291	A	2407	327	3	RQSQSLRYMAHQPVCCFTCSILTRAEIN EI/ETKNKKIEKINET/RKSWFFEKINK MGAITPDATERONI IQGYEQLYMONLE NLEYMDKFLGRFKPPSLNQBEELDTLNR
2391	16292	A	2408	178	404	AAVRINSLQEVQHPTRKHSQPRKQSKLR EGNAQRNNIRRGPGMVAHACNPSTLGGQ GGQV/TLRSGVRDQPGQHG
2392	16293	A	2409	94	386	TSFALVALGGRSCSEPRSCHCFPAWVS\ SETLSQWKRKTPTLNNAKYWGGRFRLRF FLTRGGGGRFFFFGGTATKSLGAGFKKG GGGKPGGPPNKGGLG
2393	16294	A	2410	1	384	PTQRVRIKLPRIYVHTRKRLKNYIGNT ETFITQPFKNHVSQWLIRNNRRAKQEN VAHNEEKNNKQSIETN\QKYTHNKNLDT TKKKKKKKKKGGGPKKTIKARGGEN NFFFLGPKLNSGAGF
2394	16295	A	2411	423	2	FFFFPPPPQKSLFPFFPFCGPKIFSSPP VFLTPPQKIFFCPPKKKKYFPFPRGKIF FFLK\PPPPPPPPPPPPPPPPPPPPPP FIFPPPPFLGFLLSLLIGVPLLNNAN IMILLQKKILKDEVQIISSFPSTKNRNV L
2395	16296	A	2412	218	112	LKKENNTKCYVWGTTGTLIHC\WW\KL IQVLWKTD
2396	16297	A	2413	64	403	LKNFFFFFPPKKKGGPPGAPGGSKPRGLG EPPPPPPQGGNTGGGPGARPKKNGGGF FFWRRGEP/PPPPAKGGGQDLGPGPFG REETNNFPAPPPGPKNNLGPRAQKIL CF
2397	16298	A	2414	217	409	VKYLSSVLLTIICTVQACYQELRPGAM AHTCNPSTLGGHGRI/TLRSGVRDQPD QHG
2398	16299	A	2415	416	0	ERPPSSFFPPLAPGVQOFFYKGWP EKSKKKNRFWGTPFPPEGGGPPPPNS PPGGGEKSLPFFPGGKNPTWSPGPKFL KKRVIKGPLHPGGKGYKTRFGLKPGP PPPKFFLGGG/PGFQWNEKPPQP
2399	16300	A	2416	277	0	PFVLLSSSSSSSSSSSSSSSSSSSSCS LLVRYLCKVKHKSLLCAHPGTVPFLELI HDTDSFAH/VFPADLL
2400	16301	A	2417	205	486	RHGYGFGFWKNTCMQHRHSYRRVYIHRH IHLTFLAYVHRESPEAMSALLTQILLFF KLLSFLRCLA/SVTQAVVQWCSLGLSLR PRPPGFKRFWC
2401	16302	A	2418	364	1	KESLGDVPKDTVILFATRNPMQMSNYQ FFIYLCILTHLLSRSYCNFGCKMLQ/PLW KTVWQFLKKNLNAEFPPYDPAIPL/DICIP VFTASLFI AQRWBQPKCASTDEWINQM WHMHTIEHYPR
2402	16303	A	2419	281	492	LFPPSLPASHPKLSTQQPERSHVSHTCG /VDRRGDLGLLQPRPRLKPSRLSLW SSWDYRAPP RPANSC
2403	16304	A	2420	63	465	RLQRFLLSF\VCLCPADTGGAYRGRQAS LSCGGLRPVRASLLCLPKQAWAMAGAP PPASLPCLISDCCASNQRDSVGVGPS NPGAGYYLVARFSLPLEKRSIQVGVTL FSRCRLSPLSLTRKGNLSLTPCAS
2404	16305	A	2421	61	482	QRARITGVSHHAQ/LRFCLFDMRSHSVA

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						QAGVQWCDNSSLQPPPSGLKML/STSAFQSL/WDYRCEPQHPIHY
2405	16306	A	2422	90	444	YCFSECESEKCRCPGHDLQLSPGLCHHGVSGLAKPLLCFWPWIIWKQPLCSPPTSLPFLPLPPFSQCQGPAPWLELEGRPSLWKQGGQLSLAKR/REGSRAQWLTPVIPALWEAEAGG
2406	16307	A	2423	1	444	PGPGPGCGPVATLGSFSPARTDSFSLP PHSQLEAEARNRDIEAHVRQLQERMELQAEAGTGESLMCLPRTT/WEEVGRLL
2407	16308	A	2424	189	418	SRRAEPGSFRGCLRVGVPSCTCV\SLWVCVCVWG/VCVVCVCVCVCARA/CLCLCANFSL/CSHVSLCLSLSL
2408	16309	A	2425	30	895	LDEQCTSEIHRRGATARPRAPEHPAPPATAVRGRDAASQNLKRRPGSGTDGLRLQGAEP SRLRLTYAGGAVIPRGTPERAQPPPPQDPLGRRRWLSRNTWGPWPQTTPPSQOLLRNWDGSCGFMPAARGKVFDQSQEGAHIRRET VSKSVCAEPWRHQARDPAPTNPLKCKQKRGASTSSGQHGDVRNLVFFIDDDYSPESKR/EKTNEFPQPPVPEPANAGERKMRFPNSGPHNPVEETKLICLCPSGHASCQVHLWTGAMLLGFQSWRKLPGSGLKARILQ
2409	16310	A	2426	494	154	SSRVRCCCA LLGGASQLGCSGVDRDPLEEAVCPFSDLPFRAGRTTALFKAQMEMQKSPVFCVAHAGSCRLFLFLGHLGSSLHG LWN
2410	16311	A	2427	416	1	PORGPLLALFPGRQGAAPVEDLPQGPDKPPPPPLPQPFRRARTVVTAAVPRHPPPVACHPPQPLAASKWP/SVAGGDLPLPGPERPVHAFFIGFIFVHLGLGGVSGRGAVAPARSGPVPRPPSSSTRFSLFLHE
2411	16312	A	2428	84	409	DYKHAPTMPRIONFVYHSPQPPRCENRINFTPKKKKKKKKKKKKKKKKK\KIFWGG
2412	16313	A	2429	1	389	LRDLSSDRSNPGRFLSTSNSSLY/EKDKRNKAYFTK/RPSPVNDIIST
2413	16314	A	2430	456	0	PGWPGRGAP\PSQTGWPGRGAPHIPDDGQPGRGAP\PSQTGWPGRGAP\PSQTGWPGRGAPHLPDNGWPGRGAPYIPDDGQPGRGTP\PSQTGRPGRGAPHIPDDGRPGRD/GSSLPRRGGSRAEALLTSQTGWPGRGAPP
2414	16315	A	2431	3	344	CRERRSCHCTPAWAT\SETPSQKKKKKIFFGNGPPGGPQAGLKLRAWGFFQKRGTMGPGTKNHPPGQGEPLQLKQKQITRPGGGPGGAPPQGGGAGKSFNPGGGMFQGGGIP
2415	16316	A	2432	1	109	RPLRRLRQENRLNRSGRCSEPKLC/HLCTPAWAT
2416	16317	A	2433	1	239	QSFVLPRLVSNWAKVICL/PSVSONAEIT
2417	16318	A	2434	3	464	DWLQLEMQGEI VALVHSHHGGLPWLSSEARRLQVQSDLPWWLVCRGTIHKFRCPVHLTGRRFEHGVTDCTYTLFRDAYHLAGIEMPDFHRENDWWRNGQNLVLDILOAPGLYPVPLSAAQPGDVIMCCFGSSVPNHAAY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CGDGELLPHIPK
2418	16319	A	2435	3	427	EGARTSSERHPCNKYLLHLSLAHLFINA LNLVLKGLSPSPFPALPISFPFFSPH FLGTPTLEGGRADLPFLQPPGAPG/QPA PLNYGPGPYRNPCP/RLPQLKPAQPGHG LLKSPPPNPNGRNWPLLSLDFDFKKRTS IPLP
2419	16320	A	2436	238	400	QFRWKRGAIFFFFLRQSPSVTHAGMQ WSNLSSVQPPPPGFKQFLC/PSVPSS
2420	16321	A	2437	11	442	LGTRPRATDWGVRELSRACPVIGHPAK HPRPQRWCKVNFYSPEQADELKLQAGE IVEMIKEA/CGNPDMPSVSPGPQRPPT TEDKGWWECECGRRGVFPDNFVLPPPP IKDAQPLLLFGIDQEAGPTESGISGIRF RRLSC
2421	16322	A	2438	411	80	PQAEAGAPTSGSENFNPPPPRGGAPPP PQKNFFPPRGVNPGGGGQKRPKPKGG /SPKKNPGGDKNPPPKKKKNIGGGGFI GAPRGTPKKTTPPRDGYFQVFFIVSLK
2422	16323	A	2439	290	1	QLNKIKKTPLLFLPWANEKVPKIPPNYP RGPKKKGYPPIFFFFFLRQGL/NSVTR AGVQWRDLSSLQPPPPGFKRFSCQKPNS AFPHASADAWDP
2423	16324	A	2440	440	213	PFSRPLFFFSPPPKKRASPPFFFCFPR VFFPPPPF/SKPPPKFFFPKPKKKKIS PPPPKKIFFFSPPP
2424	16325	A	2441	131	408	GCVPEPEAFLCFVLEIVSSVAQAGVQR NLSSLQSPSPGLKRFYRPLPSS/QDYR RAPPLA
2425	16326	A	2442	102	351	QASSSVLKLVCVVRARLCV/CACVCACV CVC/VVCVCEVCVC
2426	16327	A	2443	190	3	PQGAAREKSHRPGPIGRRLKL/DPPFLSP HVKINPRWIKDLNVKPTTIKTLEGNLGN TLLDTCPG
2427	16328	A	2444	410	30	VCVAPPLCVCIGTLCVRTHQTQFCVCVHT HSLCVCV/CQFLCVCVQ/VAVSVCVCRA SLCVCV\ALCVCVCV/TVCVCVHSTVCV CVCVDSFCMCVCAGAVCVCVCVCV/C LCVCVASAQLLGRGFCSSVNIKAGAP
2428	16329	A	2445	243	1	KVMVQNKGFPSNLFFFGPTINFFTPQFK QGGGQNPFPFLFFFFFMROGL/DSVTQA GMQWCHAGSLQHLPPGLKQFSLLP
2429	16330	A	2446	276	408	MLKNCAFWEPTVAHACNPSTLGGQGGRI /TLRSGVRDQPDQHG
2430	16331	A	2447	24	405	LGDVCAFFFFFYLNQNLNPGGKLLPVG PAGENQRWEQFDKLQKGGIKMNPRLGGI SVPLTKKKNQ/WARGE
2431	16332	A	2448	239	3	SPLCGNNVYKPS'TVEKTNQVEKMPPSQ IWELCVELLWQ/SNRGIAGSGAHACNPG TLGGQGWIRIMRSGDRDHFGQGETP
2432	16333	A	2449	406	144	GCSEPRSRPCTPAWVTSETLS/RKKRKR RKKKSCLLRILSTSPELTHFTLTPLF SRYNDYPHFRDEKTEARRVYATCSGSHS WKRLG
2433	16334	A	2450	349	1	GGAIFLTTPRKVPLTPITPLAFNPGHQE EIPLPKKKKIVRAIYDKPTANIILHQ KVEVFPLKTS'TROGCPLSSLLYQHKTRM PSL\PLLFNIVLDVLAIRAQKEKEIKGI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QIR
2434	16335	A	2451	382	19	DLGRMTAGSGDQRCAGVGVKLLSFLGAA GKGPKEHSEAEASLPRNPGSYNRQAQWPQ SSLHLKGTIPDTSNTLTPWKMLSSLKVP SWQGAHAHDCNHSSTLGG\RGGWITRSRV RDQPGQHG
2435	16336	A	2452	3	396	FKLLKMLIYHSENPRALKNYTKSTLSML YKWNNAWMAHVFTTWFTYFKPIAET YFWGKKKITLKLPLVDNAPGHPALME MYKEINV/VQICILQPMQGVISTLSR R\KNTFCCKDLAIDGSSDRT
2436	16337	A	2453	115	411	KGGNFPFPPGGGGGKKIW/PNGGPPPRGK RKPPPPPPGGGGGKGGHPPPGPIFFFEK KKKGLFGG/PGGAPNSHPKRNPPWPPE GGELTNPPTFFFEFGAF
2437	16338	A	2454	3	114	HHV/GQAGLELLTSDPPASVFQSAGIT GVSHRIRSVS
2438	16339	A	2455	397	1	WSWQK\NRRIDQRSNIESPEMNPRMYGQ VIFDKIAKNTIEWEKDSLFNKWCWNWI/ LKRMLDHPHLP/KQSKWMKDLIRPE TEKLPEETGGNPHD\IGLSNDF\LDLTPK AQGAKVNTDKWDNIKLNFPTRP
2439	16340	A	2456	424	3	PKKKKIFFPPPGFKIFFFLRAPPPFFFL CLSHFLNRSRSLSCCTTSCCVSTIPTSL CNKSSGV\CGLHCSLLAI/CSLIHLTLC PFCVLLVCMCDTVCVCVCVCVCDTVCVC PCPYGTLDIAFKHFFSRWSLTLVAQAGV QR
2440	16341	A	2457	266	379	HWFGAMAHTCNPSTLRGQSGRI/TLRSG VRDQPDQHG
2441	16342	A	2458	10	409	SRTGPNPRAQTDRPVVCVAFACFELPLW RSVDSATREAEAGGL\DPGGRGCSELO LCHCTPAWV/TSETL
2442	16343	A	2459	184	387	IVHFQMHKMINVAYIIPQFYFILEIQS HSVTQAQVQWHSLSLLPLPPGLKQSSH /LSLPSSWDY
2443	16344	A	2460	110	1	KNRVSFFF/CSFETESRSVQAGVQWCN LGSLQPPTP
2444	16345	A	2461	380	2	FFFFFSETESRSVAQAGLRT\QWCNLS LQAPLPG
2445	16346	A	2462	382	29	NGPGHGGPPVIPGTWGGQGGGFPRF/GS KPGFTWGNPPFLKNHKNYPGGGPPPVIP NFLGKPGNFFYPGGGGFQ/SGPGAVFP PPPGQRRSIFLPKKKKERKILFFPSLEQ RLQNCDA
2446	16347	A	2463	228	1	KKGTLPKPPPPGGRRFFFFFETQSRSA VTQATVQ/WMP SRLTANPTFRTQGILLP PGLKGSSCLSLPSSWDYRHV
2447	16348	A	2464	395	1	RLRENHLNPGGGGCSEPRS/HPAWQSS ETTSQKTKTKQKALASDTVLSPRQSS EERFHLSLFHSSFTVPGIFSLTTSPL PILPVWLAPQLPAICYGDSVIKSNFQL WLSKELQESLSRLLWTOAFS
2448	16349	A	2465	29	299	ETPNEASPKTSWDYRHVLPCLANFFIFF VKTGL/HRAGLELLTSSDLLCFPKCDY RH\DRSTWPLSSVFGSIFLVVYWPPLYI ETNMLTTL
2449	16350	A	2466	1266	1473	YFVPQSTQNHAHVFRVGSLLQEGCGKIS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KLYGDLKHLKT\FDRGMVWNTDLVETLE LQNLMLCALQTVNG
2450	16351	A	2467	49	356	VQVILLPQLLRRLRQENCLNPGGGGCSE PRWSHCCP/PAWVTEQDSISKTKK
2451	16352	A	2468	115	3	LSHTKWSAWPGAVA/STLGGRRQITRS GVQDQPDQHG
2452	16353	A	2469	3	404	FVAPGGGQGTFFPGSLQWPWPGRPGASGS PSRAPLIFGFFGGKGVSPVPGGFLLP SRD/SGPPGPPKGWGS/GLOPAPGP
2453	16354	A	2470	404	218	FAQVVIKYGALSSPKPPFPFGKLFSSRPS PPSYWDYR/RRPRPRLFFFFFLRQGLA LLPRLE
2454	16355	A	2471	386	258	AGGLSPGVQGYNKLLSCFCRPAWTT\B ETLSQKKKKKLPFY
2455	16356	A	2472	2	364	HHTQITIFVFLVETGFHHVGOAGVELLTS GDPPASWDYGR\GHRTWPYSHIFNNL
2456	16357	A	2473	1	292	DRGCSEPTSCHCTPVWAT\SETVSQKKK KKKKKTPLLRGPEKKNNGPPFRGFFRKN PGFKRKKGGAPPPGLFKIGRKKSPVGGH RHTFILGGPLPRF
2457	16358	A	2474	1	307	SLSCSSIVRRACFPFTFYHDCKFPEA/S PVMLEPVKVEL
2458	16359	A	2475	2	596	MKNABDILTMEVLKSTMKQLEAA\OKK HSLWELLRIPNICKRICFLSFVSSSSSS SSSSSSSSSSSSSSSSSSSTKITAW/LP PLEASFYRSTCLMPARALLFASTIPFWG LTLHLQHLGNNVLLQTLFGAVTLLANC VAPWALNHSRRLSQMLLMFLLATCLLA IIFVPQGEKSSQVEERKCLSLFSQGLEW SHLS
2459	16360	A	2476	367	44	YQEDITIMN/TYALNIGVPTYLANI/DL NREIBSNIIIVEYFNTSLSKMDRYRSSR QNIDKETVDLKYSI/HINQMDLTDYRT FHPTATERDSISKRIKIKIKINKSLT
2460	16361	A	2477	12	362	HHEPG/GGGCSELRLCHCTPAWTELD VSKKKKKKSKKK
2461	16362	A	2478	401	1	FFFFFSETRSHPA\RLCSGATSAHCN QCI
2462	16363	A	2479	3	353	YMCVCVCACVCICVLPWMLCVC/CYCV CVCWYLCVCLCVSLCGHQHLAVSGKRSQ PPSHESFKTSLLLWVFNLPPLCAWVP QVSQNMPLDGTRTLNNVSLPDEKVHDL LPLTAA
2463	16364	A	2480	57	361	MNESLSCRWSSLLAFSHI/CVFCILCS TDISALCVTVACMHVCGCRVCVCLCV CLCLCVCRMYGRVCPMCLCVCVHCVL ARMCACGCGCVYKAECPI
2464	16365	A	2481	3	381	YMCACGYICMHA/CVPVCMCVCTCLCAH VCL/CCMCVCTFVPVCMCVICVCLCVC TPIITLPLSQERISFCTDLRSFRATAK RSHEEVKNCVYLQTIWNQYLIIFYLQNP NFGWAQWMLVIPAVWE
2465	16366	A	2482	2	380	IHLGNCLYFSEPOFPHQQRITRSFLE GYGENLMRLHMSYIHMCLHICAYICI/C /LCVYICVLLCAYICVCVYLCVICMCI FVYLCTHICVFVCLVCIYLCV/C/VCV CICVCI
2466	16367	A	2483	296	1	NGTITRRMLPIFSRYRPGMPGLVQCTIQ

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						SCTANSVPYSHGFIYFFIYLLRDRVWLC YSGWSAVAPSWLTITSN\YRLKPSSCLD LLGSWNRYQMPPCI
2467	16368	A	2484	1	319	NTVGLCVCV/CLFVCVLSLCV/CLSCLV /CLCVCVSLCVC/VSLCM/CVSHCVCL CVYLWLCVSVCSLCSLVCVCVYECVIS STKRSIGAPSRAEAALPRNWAQAKQSH
2468	16369	A	2485	3	334	NHFIISIDI/DKHFRKIHPFPVKAITK LGIKGNFLNLLRGTSVKSTGNINM\NGE KPNLPLRLVIQGDVLFHLLLEVLASAV KKKKKKKKKKKKKKKKKKKKKKKKKKKK
2469	16370	A	2486	17	409	CLDNKKPRKEYCQKTHLYKKNPLLSRIC KELLKLYDKRMINPIKKWABALYRCLSK GDV/HEMASKHMKRCSIS/L/SIRKMQM KMTL
2470	16371	A	2487	410	165	LECNVTIMAHCNLRNLGSSDPPTSAS\Q TAGIHHSLOHFFFLFFVBTGFCYTOAGL ELGSSDLPTLASQSVGTGTGHGTWP
2471	16372	A	2488	142	417	VEQLLEGYRTKSLYLSFFLFVCMFLRW SL/DSVSPGLTNCHHLGSLYPPPPGPKQ FSCIS\LWAWRRT
2472	16373	A	2489	1	404	KAGAQMGIKHPQHSSRLRLRRSPRLPS SQKPLNTHYFSPSFCAHRHTHTHTHTH THTHTGTG/HLPHT
2473	16374	A	2490	373	146	YGLEEKISFKIL/LFVGKSPSYPRALME MCKINVVMHANTTPTLQPIDQEVILGP GTVAHACNPNLRGQSGRNA
2474	16375	A	2491	427	85	KTPPPP\RGFFFFYFFFFFKAKNFFPP PPTPPLGKKKNP\PPPEKKISPPPGFPP PPFKKGPPKTLFKTPLKKKKGPGAPQKK PFFFKTPPPPPFFFF
2475	16376	A	2492	443	240	FLFFFFFFXFXFFFFFFXFFXFFXFFXFF FFFFFFXXXXXXXXXXXXXKFFXFFXFFX FFXGCLFIYLF
2476	16377	A	2493	3	135	ISAHCCR\LLPGSSNSTASAPVAET GACNNNRQDFSFIILQI
2477	16378	A	2494	37	420	AHVCVCTCVCVCICLSRRVVVCAHSHVC AGIFLHLINQTFTHL/CVCKVMALRVT PSPCLQGA\QTLAGQCMCAKVMNFM YIFIEGHICPQTCSCLGEPGRGLSPLVC IC/MCAGFFVSFC
2478	16379	A	2495	402	178	RQNKTPFGVKQITGGGGGRVSYFLRG VSQENPLNPGGGGCSEP\RPPGWGTKNP LFQKKKKSSKQGEGRGED
2479	16380	A	2496	138	439	RTFILGDHHPHPSAVHFLPRRKLCTHE TGAAPPPALGATVPPSVSVCLTGGGPQ ITPPPALGARDLPSVSVRLTMGGPQIT PPHPDQQL/SPPSVSVC
2480	16381	A	2497	118	382	VKSCASMRACVCEVVMCVSMCVVCV CVSACLICVCLCQ/CDLINKCV
2481	16382	A	2498	164	439	VKSCASMRACVCEVVMCVSMCVVCV CVSACLICVCLCQ/CDLINKCV
2482	16383	A	2499	1	411	ISTSFYTDITNRTALHFAVGRNHLSAVD FLKKHARVDVADKGMNALHATQSNH VRIVEYLIQDLHLKDLNQFDEPKESPLH LVVINNHITVVNSLLSAQHDIDIL\IRS SKPLHVAADRGNVCLVE/LLKAGCD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2483	16384	A	2500	80	404	RTAAAVSTVSFPQDFEGQSPKCTQGVRE ALRQIK/RLVPTGSLRH/WPAGSLA/LC QPLSDEKDLTQLFMFARNAFTALAMMDY PYPTDFLGLPLPANPVKGRRRLPRRRRP
2484	16385	A	2501	215	1	AAIQQGS LACSHSVPPATTPRAYTPVPP QLLV RN F\YPK TLE LRSQ LRCARRFPRE TGADCRHAGAGRQTK
2485	16386	A	2502	423	214	WQAVQVGG LLEP\GGRGCCCLRSCHCTPA WVT\GEILSQNNPKRQKNKTKQRMGPV PGSWGSPRAGGLTV
2486	16387	A	2503	294	1	LHWNQRQRCPPPPPPPLPPPPPLPPPPPL PLR\HRIAGAGQTGAKIRVVGVRVVG GLGVAAA/DSRESCPDGAAAGGGGGGD SAATAGPGGGGGGGTK
2487	16388	A	2504	331	411	PFLKTGNKGAPPPTKIFLFFKKGG/W PGAVAHACNPSTLGGRRGRTIRSGDRER
2488	16389	A	2505	407	195	GGRGCSELRSCTPAWVT\GEVLSQKK RKSSNKSRCLDQAEVGGERQLVQVSV PSTCQRRVGAWFIYL
2489	16390	A	2506	1	468	RQGS MNKLETERQIKKAPARNPERERER ERESKKGEDRHTDICRP/RERERQNYRD RQ
2490	16391	A	2507	27	380	FVCLCPAPRGGAYRGRQASLSCGGLHPV RASWLLCLPNQAWAMAGAPPASLLPCS LISDCCASNQRDSVGVGPSRPGVGYNLM VRRFLSRSEKRNIRVGVTFRSVCVCHPF L*LGKG
2491	16392	A	2508	396	234	RQENCLNPGGGASSEPRSLCTPAWATE RDSISN/QNKQTNKSHILRAAFSRPSY
2492	16393	A	2509	1	421	AKKIKPPFPLKKKKKPGRGPPPPPP/ AKFGRETPLNPGGKGSIKPKLGPPPPPP GGPPNLPKKKKKKKAIK/PLVP SHVKS TGFP PSCS/RSALLRAFTQ
2493	16394	A	2510	197	3	TGPPDFNFFFPLEMKSHSVAQAGVQWRD LGS LQPPSPQFKQFYWGLQGA/LPPCL NKICIFSRGGV
2494	16395	A	2511	114	454	QGPLEKKGAPFKNKFFKTGVLFSGQNI PPWVFKKGFSRTPFEIKKNPPGILGGS PKKFFFFFEMVLLHHPGWSALAQSL TTASDF/LRLKQSSHLSSL
2495	16396	A	2512	3	495	FFLSRGLFIHLSAPAFIQCLLFVVVLV FVATGSHYVPQAGLKLASNEPPASNSP KCWVYRHEYPAKCLCFGLCLF/AFLP
2496	16397	A	2513	25	437	PLLFSPAGHAMEEDILPPAPSF LFYFF FYWLWVKIITYLVLAQAATTNYHRLSG LNNKHLFLTILEPRMP/SIKVPA
2497	16398	A	2514	2	256	QAPSAEGEMTSYVLLAYLTAQAPTS LTSATNIAKWITKHS\NAQGGFYINQDN LPYSLCSGRNESTAFGTNGQDIHPVHS S
2498	16399	A	2515	2	284	KCQCDELCSYYQSCCTDYTAECKPQVTR GDVFTMPEDYTDYDDGEENNAIRHEQ A\GFTSVISDLQAQIIWISSEKHAMSFV EEMTVLEVL
2499	16400	A	2516	2	432	RDCESSRAAEYTSALKASCWMDLAR SPSLDPQVAMGTPPAGPCGWSVGTRSP FPRGFSRGPCCVSPPSWTPEPGTGQ/CG EGGGRWSQVPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2500	16401	A	2517	401	2	GGEAAIRGQTKPQLEGKAPCECECKKI VRS\PRLIRRQRTPTGEKPYECECGKS FSRRYRLAQHOR\TRAGEKTYECNEOGR GFSESDLINHYRVHTGERPYKCDECGK NFSQNSDLVRHHRHTGEKPC
2501	16402	A	2518	398	1	ETFGK\SGGRSIVPGQFLAVGPKGRAVM ISAEKQKLVYILNRDAAARLTISSPVE AHKASALVYHVGVGVDFENPMFACLEM DYEEADNGSTGEAAGNTQQTLLTYELDL GLNHVVRKYKEPLEEHGNCI
2502	16403	A	2519	384	3	GGGID\SDASLVIAGVRLDEGRYRCBL INGIEDESVALTSLGEALPLPPHSCV AAGPRLGLPGLLPSISSAPLGTAPSP RPRRPSSPSAPIRWSPSPGSPPPRCGVS VPTQPGVPVQLLRGVY
2503	16404	A	2520	1	426	GDRQMITALLRKLKQSSRESVEENRRL LKALKELGDFYLBELHWDQSWVPLLSRI LPSDACKIYKQGINIRLDTTLDFTDMK CQRGDLSTFINGDAAPSESVVVLNNEPK VYQRLRHEES/QEKNRTQVDCLT
2504	16405	A	2521	2	425	ALPIGRMPIMVRSSR\CVLTGKTPAEFA KLINECPDPGGYFIVKGVEKVILIQEQL SKNRIIVEADRKGAVGASVTSSTHEKKS RTNMAVKQGRFYLRHNTLSEDIPIVIIS KPMGVESAQEKIQTVPQEPWR
2505	16406	A	2522	2	376	IQSFSVVYGYHLCSQGILSERVSASKFP LLFFFFFKGGPPFMP/QGGKTKGPKLP GDPQSPGIKGFPCLAPPNKGKGGPPPP RGNFLGFKKKRFPQVGGGSKPPREGK PPPLAPQGGNRRG
2506	16407	A	2523	403	3	GAPRSLSEKERQLMGMINQLSSFREQLL HAHYEQKLAASQIEKQRMKLGKQ/Q QEQTARQQRLIQQHKINLLQQQIQVQ GHLPLMIPVFPRDQRQLDALAQGFLL PPGFSYKAGCSDPYPVQVPLPY
2507	16408	A	2524	2	369	NARCLILRAAEYMAACVVICISVFACMC FCVRVCPVVCVSGCLCVCSMNHLSLC /VEQCACLWMCVSLHVCLYTACLCVSV CEAVCLHLESHCRGSRPFPVVGPAFSL SSCLILAPPSVT
2508	16409	A	2525	59	380	RNRNFKNNSFFFFFKGPGWGGPGGK GPKQRQGEF\NHWGQKNFPQTRKPRKP TPGPPPPKKIFFFFKPLEKKPGQGPQG QKPGGQKKPPGGAQKRGKTGGET
2509	16410	A	2526	1	371	VMPLSRKHPKGFSSNHTLVLHVARSEMD KERVQATRKSSP/CFVPLLPWPT
2510	16411	A	2527	445	3	RWLGLALIALKRELKKGDL\PEMRNWD SIIIPNG\FDLTEETPKREDYFGIANLVE HPAQLNPPVDNDTPVTLGVYLTKEQKK LRRQTRREAQKELQEKVRLGLMPPPEPK VRISNLMRVLGTEAVQDPTKVEAHVRAQ MAKROKAHV
2511	16412	A	2528	1	478	RPTRPKRKLKSHRLQSRQESKKVRVL/T NARDNEMEEETDDGPLLVRVKVAEDGS IILDEESLTVEVLRTKGPCVVEENDPIF ERGSTTTYSSFRKNYSPKWSNKETDMF FLAISMVGTDFSMIGQLFPHRARIETKN KFKREYASAIEDQATSVHT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2512	16413	A	2529	385	1	QKKCEDLK\DQDNPIVRPPPTPGSCGHG GVVNI SKPYVVQLNWRGFYLYGAWGRD YSPQHPNKGLYWVAPLNTDGRLLLEYRL CNTLDDFLYINAREIRITYVQSGIAV NYNNKYVSMYNTVNV
2513	16414	A	2530	1	1228	FRATLRPETMFGQTNCWVRPDMKYIGFE TVNGDIFICTQKAARNMSYQGFTKONGV VPVVKELMGEEILGASLSAPLTSYKVIY VLPMLTIKEDKGTGVVTSVPSDSPDDIA ALRDLKKKQALRAKYGIRDMLVLPFEPV PVIHPIPGFNL SAVTICDELKIQSQNDR EKLAEAKEKIYLGKGYEGIMLVDGFKGO KVQDVKKTIQKKMIDAGDALIYM\EPK QVMSRSSDECVVALCDQWYLDYGEENWK KQTSQCLKNLETFCEETRNFEATLGWL QEHACSRTYGLGTHLPWDEQWLIESLSD STIYMAFYTVAHLLQGGNLEHQAESPLG IRPQQMTKEVWG\YVFFKEAPFPKTQIA KEKLDQLKQEFEFWYPVDLRSVGRDLVP NHL SYYLYNHVAMWPEQR
2514	16415	A	2531	335	2	KKKALFFIHPPPFVNGRPHKNPKIKSLG SPTFFSLIFLKKKFCFVNQDGVRLYFG SLQSLPSRPPPPFCNLNLSWEYRGLPP RPGKYFFPFIFFYFLVEM\GFTVLARMY
2515	16416	A	2532	3	380	AINSYIRGDDPSSYPEVVQSASRSSK\W SPLPRALHLTDAK
2516	16417	A	2533	3	2083	SSEGYLRGNMSENEEEISQEGSGDYE VEEIPFGLPEQSPGFEPQSPFEFQSPR FEPESPGFESRSPGLVPPSPFAPRSPE SDSQSPFESQSPRYEPQSPGYEPRSPG YEPRSPGYESESRYESQNTLKTQSP FEAQSSKFQEGAEMLLNPEEKSPNLISV GVHPLDSFTQGFGEQFTGDLPIGPPFEM PTGALLSTPQFEMLQNLPLGTALRGPG RRGGRARGGQGRPNICGICGKSPGRGS TLIQHQRIHTGEKPYKCEVCSKAFSQSS DLIKHQRTHTGERPYKCPRCGKAFADSS YLLRHQRTHSQGKPYKCPHCGKAFGDSS YLLRHQRTHSHERPYSCTECGKCYSONS SLRSHQRTHTGQRPFCGICGKSFSQRS ALIPHARSHAREKPFKCPBCGKRFQSS VLAIHARTHLPGRTYSCPDGKTFNRSS TLIQHQRSHTGERPYRCVCGKGFRCSS TLLQHRHVH\SGERPDKCDDCGKAFS\R ASDLIRHQRTHT
2517	16418	A	2534	434	3	APLHSGKRSPTKCN\ECG\GAWNRSLL DRHKI IHSEENPNKCEECGKAFKQASRL TIHKI IHAGEKPYKYECCGKVFSQSSHL TTQKILHSGENLYKCKECCGKACNLFSNL TNHKRIHAGEKPYKCKECCGRAFNISNL NKQECI
2518	16419	A	2535	46	454	PSTFSSKVMKQTLCSQATSNTSRYAA ALYRQGSIVPKEMKTCVHTKPYTVVHSS IFMIKKWKQPRCPSPA\DSWRNRMWSIH AMGYLTMEKNEAVMLPRR/WSLENIVL SERSH
2519	16420	A	2536	13	476	ALKTYKYSHKKAFFNPKKVYGKCSQKDPF PINHCLPTEKLHLCDKIGBGVFGKVFQT

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						IADHTPVAIKI\IAIEGPDLVNGSHQRTF EEILPEIIISKELSLSGEVCNRTBGFI GLNSVHCVQGSYPPLLLKAWDHYNSTKG SANDRP/DFPKDDQLY
2520	16421	A	2537	162	296	YVCQRYKL\NFFLPSTYKINCKWVTDIN VKPTSVKLLQEKRRKSL
2521	16422	A	2538	495	348	FGW\HAFIVKEPRVEKLCASARAKPQP PAIIAKTFKAGGITGQYAQAAL
2522	16423	A	2539	480	63	ARSEAWISADAYMASPGDRIAQLLLLP YIKVGNSEIKRTGGFGSTDPTGKAAYWA SRVSENRPACKAIIQGGQFEGLVDTGAD VSIIALNQW/PKNWPKLKAVTGLVSVGT ASEVYQSTVILHCLGPDNRDSTSHYSKT R
2523	16424	A	2540	2	509	NVDADDVRLAIQCRADQSFTSPPPRDFL LDIARQXNQTPLPLIKPYAGPRLPPDRY CLTAPNYRLKSLIKGPNQGRLLVPRLSV GAVSSKPTTPTIATPQTVSPNKVATPM SVTSQRFTVQIPPSQSTPVKVPVATTAV QNVLINPSMIGHKNILI/TNMVSSQNT A
2524	16425	A	2541	501	1	QWQVVEDPGGPRPREEASSYKCELREQ \LPQYVRDFFRKKAE\SGMDSSRNLEKL AERFLAKTCTKDDQFKKQNVLSFVNC CHILLTQVKRESRAHTTLDIYLNIIIP RFVQVSEDSGLFKKVQRYFFTEVRGWS NDTIFKILLDIMLITWVTQLSVHQTPEV
2525	16426	A	2542	473	287	EKDFNLPPKDLRL/KTSDV/TSTKENEF EDYCLKRELLMGICEMGWKPSPIQVC
2526	16427	A	2543	268	482	KKKAWGLQGGKNFPKAEPLTHGIIQI NSCSVRL/VDIKKEKPPSILKVEGQAQA RTHLNRAFDIIVLTRGG
2527	16428	A	2544	407	1	CKKICYLIHYWEYKMIQPLWKTWQFL \KKLNILYDPAVILYDIYPEELY
2528	16429	A	2545	28	399	FRHSSFQSRGRGSQLMVHFLSL/SVMPK IGSVAGINYGLVAPPATTGETLDVQM/K GEADTENH
2529	16430	A	2546	2	365	FVVNVDEVGGEALGRLLVVYPWTQRPYE SFGDLSTPDVAMGNHVKVAKGKKVLGAF SDGLALLDNLKGSPATLSELHCDKLHVD PENFRLLGNVLVCLAHH/FDKEFAPP
2530	16431	A	2547	375	1	GFACRRMQKRVREVSHAEESAASKKVR ANGSGKQNEGMNVTWTATLALSQAVISS ATYTQMOPHSLIQQQQIHLQKQVVIQ QQLAIHHQQQFQHRQSLLHTATHLQGA \QKQKQQQHEWR
2531	16432	A	2548	3	376	ELGSDVA\GABALVDRRQERKGEIDAHE DSFKSADESGQALLAAGQYASDEVREKL AVLSEERAALLELWELRRQQYEQCMDLQ LFFRDTEQVDNWMKQEAFLNEDLGDA VDS/IKEILKKHE
2532	16433	A	2549	360	1	RGEMLWTV\NNRPLKNFVPGKIEPFKSH SLYPPCYVHDVSFWDQKGFDELEFHT VGRAVSQDTIISIQLSRFQHPKTQQVS LCYRLTCQTCDKALTQQQVASMRSQIRK BIQQHQY
2533	16434	A	2550	2	403	VVAEDTELRLDLLVQTLNLSGVLNRIKA ELRAGVFLALEEQEVENKTPLVNESLK

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						KFLNTKD\LQGLEGRENLARDLGIIIEAE GTVGGPLLELVIRRCQKQKGPPTTGBGA LDLSDVHSPPKSPGKTSAQTT
2534	16435	A	2551	1	409	VPRNPTPLGGPGGPIILRSREGGPPGLPR EPSPVLKKREPPTRGGGRPPGFLPRV RPEKWNPPGGQTFPEPKLRPRG/HHPGG QTKNPFKKK
2535	16436	A	2552	256	1	HEMDGTLGGFPFPPGSSKGPSTLGPPII FQSPGP/APHTPSSSPANLKT/CTPVCP SHLPW/CCPLCLPMLPWSVPVPSKSS PPALY
2536	16437	A	2553	398	3	ARQQQLLQQQHKI/NWLQQQIQVQGG PPLMIPVFPDQRPALAAAQGGFLLPG FSYKAGCSDPYPVQMIPTTMAGAAAATP GLGPLQLQQLYAAQLAAMQVSPGGKLP IPQGNLGAASVPTSHTDKRCI
2537	16438	A	2554	20	517	DRPESTKRRDTPQLRGADLSRGPAPV PECPEH/SPRKTSACRPLPLRPSHSS PLP/SPQPSHSTPQASCPLPEALSPPAP FRSPQSYLRAPSWPVVPEEHSSFPADS SAFPATPRTTEFEAWGTDTPATHRSS WPMRPPSPD
2538	16439	A	2555	361	3	KSSQEALEELRQRLEELKCLREGEL PGKLPVEYRLDPGEDPPIVRRRIGP\AF KLDEQKILPKGEEAELERLEREFQISQ ITEADRRLASDPNVSKLKKQKTKYIN AVKKLQVY
2539	16440	A	2556	470	2	LKAAVTAGLEVPSDVSDRAFE\WLSAPP L\DSPYSIHHPRIQVSSEKBAAPDAGA ERITADSDLAYSSKVLSSPGLEELYR CCMLFVDDTAPRETPEHPVKQIKFLLG RKEEPPVLVGGWSPSLDGLGPQADPQV KVSNAIRCAQAQTGT
2540	16441	A	2557	2	315	VVAEDTELRLVQTLNLSGVLNRIKA ELRAAVFLALEEQEKVENKTPLVNESLK KFLNTKDGKMFSLFLFIYL\EFNLDTI WEKSGISGLFFVENCYRSSF
2541	16442	A	2558	372	3	CNISSHFANKKQDVIVAARNVMTSQIH HAV\KIIPGFNINVPGLPPPPDETELEV QKVSNPQYHEVMNLELENTLDQHSYSLP TCRISEYVKLMELAYHSLLEAASSDQ CADQLFYSVRCI
2542	16443	A	2559	64	435	WGDASCTGRAQLGIAHKSVLPTLTOKFN TIPAKTPMSFPKEPKLTPKFT/WKNRT PRTVK
2543	16444	A	2560	113	375	VPGPARDSTQRAVKNKKELMSIPGIP GPVQVPGGLST\GMRGFPGSSLGFLTI PGGALIPFSPAFFSRVGGDLSRNTGPG QKPG
2544	16445	A	2561	431	51	RKIYRVYERENFRVEIMFRSHTSKKVC KGNV/DVAKFIKLRDGHVNLNVQCACH QKGGIYWFRIHVELIGYPPRSSHNIK IGDKVRVKASVTPKYKNGSVTHQSVGV VKGNIWVIKFLMLTFH
2545	16446	A	2562	1	455	PEGIALEVVTSTGKEREHTFQPGDNVE VCEGELINLQGRILSDGNKITIMHKHE DLKDMLEFPAQELRKYFKMGDHVKVLAG RFEGDTGLIVRVEENFVILFSLAMHGL

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						KVLPPPLQLCSETAS/SIN/VGGQHEW
2546	16447	A	2563	407	1	KWDHPLSKCEVPCGSSIISNGFVSYPG FPSPY\TSSQDCVWMITVPSGHVRLNL SLLQTEPSGDFIAIWDPQQTAPRLGVF LRSMVKKSVQSSSIQVLLKFHRDAATGG IFAIALSAYPNTKCPPPTIHPCI
2547	16448	A	2564	382	1	TQEVAVSLDRAPAFQSGCQSETLSQN SNSSNKTWILDHFLSDFLDQRFSACTV FTPREQVSSHTRMFIAALFTIAKTWSQP /KYPPVIGWIKK\MWHIYTMYYAAIKK DEFMSFAGTWMKLEAMY
2548	16449	A	2565	429	0	PLQSSCQTSCHQNCRRKTSLHFGDVL TPEQVGGSPAQVPIPYLDDDIPLLEVQ EPVSLELGDVSLVSVSRBGLQPASITGS RGHLIVQLQELLHHWLVSAVKSRRWIV GLFVSLILSLVFAIRL\SASRAPVLL RP
2549	16450	A	2566	464	1	VINGVI\NPFVHGDQYKKKFPPLK\FYQE IYESPFVTETGYYKQEASNLLQESNCS QYMEKVLGRKDEEIRCQKYLHPSSYTK VIHECHQRMVADHLQFLHABCHNIIRQE KKNDMANMPVLLRAVSKGLLHMIOEHVL RALGRIPTSYVRMQS
2550	16451	A	2567	3	178	YNPGGGVCSDLISSHCTPVWVT\SETLS QKKKKKKKKKNFLPETRERALPGKKKG GGG
2551	16452	A	2568	215	411	IHLIFIHLVFIIDYLSVRHSSKILGYISE QIRKRN/SWLVVAHTCNPSTLGGGGGQ ITRSGVQDQPG
2552	16453	A	2569	170	430	TSSQLAPQCLAV/VSGPLAACPELTSAT SPWLQVRTNAMASPLLKFSAEILLFKAA LSQFCVIMLNALSVQKYEK\LISAFSD SR
2553	16454	A	2570	3	463	CRFFGYSTAAAPMTSSGGSTLSGITAP AVENIPSPIGVNGFTGLFPQANGQPAE AVFANGMHPYPAQSPTVADPLQAYAGV QQYAGPAAYPAAYGQISQAFPPQPPAMIP QQREWPEGCNLSIYHLPQEFGDS\ELM QMVLPFGNVISSKV
2554	16455	A	2571	3	424	LKTMKGGTGNGLIIMLDIQDEYLPVWG ETGTSPTSGAPLHGSRPQP/PARGFLGF TVRPG
2555	16456	A	2572	1667	2046	YIFFFTAFLWAALTFOVTTTLAPLALLV RSKMMRASHDKPTANITLN\GKTGRAS KQRREERNRQEVKLSLFTDDMFYLESP IVLAPKLLLLINFSKVLAYKINVQKLLA VLYIKSSRESNEEHN
2556	16457	A	2573	1	399	FAISQDHPALPSRPPSLHHPKPGTLTFH PDLPHQATCSRPIRHQRTWPEADPLAKA DTVSPAHEPPAAATKAP/TR/PAPDKPG GTSDPQTGPAP\FASPPCSGP/APQVPV RKPSRAAPSKVSVTVPRVPRTFPP
2557	16458	A	2574	2	452	AKVNMKSPMRKHTLLKNKEEKLNQLE SSLWEASDEGSLGGSPTKAVTFDLSD MDSLSESSSESFPPLDSTPSLTSRKI HGLSHSLRQISSQMSSVLSILDSLNPQS PTILLASMPAQLPP/RDPKSTPTP/SYC GRCRGFSITS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2558	16459	A	2575	2	369	TLVYPATTFILLSTICYWIVTAVFLTT SGVPVYKVIAPGGHCIHENQTCDEIFN TPEIAKACPGALCNFAFYGEKSLYHQYI PTFHVYNLFVFLWLNLFVIALGQCALA/ GAFATYYWA
2559	16460	A	2576	406	1	RQEGTGPSYLLLVGITPRSFWGFSPPLG PSGKNPIKTFGGPLQGFVQVQMGVLLP LPGPSGN/CSIKVSALNSSFSPPGVNPG EASLPWF/CFFEMESRSVAQAGVQVQPP PPGFKRFSCLSLGSGWGYRRPPLV
2560	16461	A	2577	3	410	YISPFYITHMRAHTNLGPF/KLNQRAD ALVSAAFADAQTFHSLTHLNAAGLRKRY GLSWKQVKEIVKHFSAGEVLHLPHQGAG VNPRGLSPNSIWQMDITHIPTFGKLSFV HVSVDIYSHFIWATYQTGEATAHVK
2561	16462	A	2578	386	1	TERIRQRQYQRETEKDKRYTERQRKTER IRESDRDRERONQIERDRRAT\REDRRE KQRESRETYRERENQIETERDRKQSD RDRETQRETGRIRYRERERQHQTESDRD RERESDRETQRHRECI
2562	16463	A	2579	2	432	LLYFAKRYGAAPGECQADKAACLLPK LDELDEGKASSAKQRLKASLQKFGER AFKAWAAARLSQRFPA*FAEVSKLVT LT*VHTECCGDDLLEACADRSDLAMYIC ENQDSNFSKLNCECKPLLEKFHCIAEV END
2563	16464	A	2580	3	426	NLLNDALAIREKTLGKDHPAGAATLNNL AVLYGKRGKYKRAKPMKRALEIRKKVL GKQHPDVKQLNNLALLCQNGKTEQGE YYYPRALHIYHTKLGPDDPNAANTKNDL VACYLKHGTVKQA*SLNKENL TSAHEWD V
2564	16465	A	2581	10	389	KLAG*GLWGHTLITNPLTEPLTYPFLGL YL*SIITSSICLLQTDL*ALIAYSSII HIALVITAILIQT*P*STGAVILIIAHG LTSSLLFCLTNSNYERTHSRIILFQGL QTLRELIAL**LLA
2565	16466	A	2582	1	192	LIPTLATYTR*GGQPERLNAGTYFLFYT LVGSLPLLIALLYTHNTLGSLNILLTL TAQELSNS*ANNLI*LAYTIAFIVKIPL YGLHL*LPKAHVEAPIAGSIVLAIVLLK LGGYGIIRLTLILNPLTKHIAYPFLGLS L*GGQPERLNAGTYFLFYTLVGSLPLLI ALIYTHNTLGSLNILLTLTAQELSNS
2566	16467	A	2583	2	438	QAHGFLAGCRLRPRSPSPVLWRRRRRW RQRRKWKTKTATAAAGMYASWTKACRGL EELINLTRLNVSYNHIDDLGSLIPLHGI KHKLRVIDLHNSNRIDSIHLL*CMVGLH FLTNLILEKDGDDNPFVCRPLPGYRASIFQ TFAQL
2567	16468	A	2584	3	415	GRAILLLEAIQVLSGIEIDLIDTRGE WDSLTPQARR*KEAGLQMFVQLARFHNI VCKEAFGTLAFLTSEIKSLFGHPFLAER IISMLNYFLQHLIGPKMGALVKDFSEF DF*POOHVSDSGAIYLDLGDDEENFC
2568	16469	A	2585	2	453	DAKMYLSKYATVIRNLRGTCPPEAPSD ECKPEKRCALSHQRLKCEWSDISVGK IKCVSAETTEYCLA*IMNG*ADAMSLDG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine : C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Value, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						GFVYISGKCGLMPVLAENYNKSDNCDT PEAGYFAVAVVKKASDLTWDNLKGGKS CHTAVGRNAC
2569	16470	A	2586	3	413	MAVESRVTOEETIGKEP*KPIDR*KTCPL MLRVFTTNNGRHHRMDEYSR*NVPSSSEL QIYTWMDATLKELTSLVREVYP*ARKKG THFNFAIDFTDVKRPGYRVKEIGSTMSG RKGTDSSMTLQSQKFQIGDYLDIAI
2570	16471	A	2587	1	798	LEVMMLVKAGADQRAKNQDGMNALHFA TQSNHVRIVEYLIQDLHLKDLNQDDEK RKPFLAAERGHVEMIEKLTFLNLHTSE KDKGNTALHLAAKHGHS PAVQVLLAQW QDINEMNELNISSLQIATRNGHASLVNF LLSENVDLHQAEPKESPLHLVDINNHI TVVNSLLSAQHDIDILNQKQOTPLHVAA DRGNVELVETLLKAGCDLKAVDKQG*TA LAVASRSNHSLVVDMLIKAERYYAWREE HHESIRDPSTGFTL
2571	16472	A	2588	2	285	AWSTAPSHPHSKVPPGPRRGKABGRPGA AAQAAEQAEVHPSPSGPSPLPARQPPVW QIPPTPSLKTTRRGAQPQHSRKRLA*S RSVSVLFRKM
2572	16473	A	2589	11	438	AYYGLNWHLGATLSQKKKKKKKKKNFP RGGGPPRNPHFWGIGGRPGTGPPRGEKN GLKNQKKEKFLAPR*KKSTGKPLKPPQG KGWGGGPKFPKKRPPRAGGSLKPKGK NREPFALAKSLPGVFLGGFGGNPGMGLK NQ
2573	16474	A	2590	313	391	VHLVRVKLGL*SRIYKELLQLNNTT*DN PI*KWATDLDRHFSKYTQMVDRLMEKC STS
2574	16475	A	2591	62	616	EVHQGTEVRDSEVRRRPQARGPLMPAER AGRQRLVLPALQPRRGLRR*RGAVRQH GAHPHGLLLQDQKI PALPGRKQAGSLHA PGTEGEPDHGGDPVLDAGIQHHRQQRHP TADHLNPGEHRRGEAHVRAAV*PAAGAE GAAKERRAHQANTALQVHRR*LGSPAEI RLLRKPGRTSVWPSPM
2575	16476	A	2592	345	438	HKRWLFPVFIYQHLF*VFGHPVEVYILIL PGF
2576	16477	A	2593	479	313	QDGLDLLTS*STRFSLPKCDYRREPPL KLINLQSSGVGLEHVQLFPSPFCFDQLL
2577	16478	A	2594	3	419	LTLHSNTLPPPEMSGTL*PPATNAYWTF LPSAIRLFPEIFFIAVLLSVSLFDETET LSDAHSWRLTFKYERDANYHLLMSAQER LERLFGLHGGTIPIVPTADFHDSSISGAS DTDIAHSGLAYTMERSARQIMRTAMKY
2578	16479	A	2595	1	419	HKCEGRYRGKTYGGYWSLCATVNKALDE RIPITSASYATVLDHVRNLSGDDTDV SMPLL*ERHRILNETGKFLVDKFGGSFI NCVR*RDNIHKLMLLVESFPSYRDVT LFEQN*VAFYTRAQILVTDGTGTLEGK
2579	16480	A	2596	199	397	SPTALNTDDVNFPMGSSSRGHRQFOTG IVSDHPAEAGPIS*DEQELPYAVLHFHK VQPLEPKVTD
2580	16481	A	2597	154	3	MLSIRGFFCLFVCFETGS*YAAQAGLKL LGSGSPPISSFSQARITGVSHL
2581	16482	A	2598	425	223	QITGHGGKCL*SQLGKFGQENFLNLGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RSFN*PKLLPGTSGWVTMLNSLGKKKKV TAYLNKWMPTP
2582	16483	A	2599	3	441	QGFSRDLVSELYQINAFDTPESLLMIGK DHSDPIHHTFDHMRWTKHNEAGWLLLR SVDKVMKENDELGDSISQLQKQILSLKY AKIALTERLISCPV*TEIVLNYT*SLIM LLTDLL*KVHAQSHHAHSGQASNCNVM LIGLOH
2583	16484	A	2600	131	423	GPAPMVLFLHGTGFLLAFLPLSHLLTSY LVPWILSGTDGHTFRSACLPRWLEAWI FGGVKYQYGGNQEGK*CFGTG*SYVYNG SSGKVPWETFSRT
2584	16485	A	2601	222	447	SGIPSFGL*VVEQNRPGRLNAQILKDLG VSPGSDYGLKNGISSGLDNGVTSDHD VLKMAIVGRKIWILGDWSG
2585	16486	A	2602	2	457	FICDPLIKAIGTEGDTDLSEIMNSFAK SIEVMGDGCLNDEHLEELGGILKAKLEG HFKNQELRQVKRQEDNYDQQVEMSLQDE DECVDYILTKVSDILHSLFSTYKEQILP WFEQLPLIVNLICSSRPWPY*QWGLCI FDDIVKHCSPSL
2586	16487	A	2603	1	297	DHRQKLYAHTCECGKALLWKSVCVHQY LEBEKPCGCTKYDNIFSNRGCPVPRMV HAVEIPCK*TECEKATGVHGPGRASEFL PERPTGMNMAKCESR
2587	16488	A	2604	1	405	RFDVSDGLELRPKYNGIAHRLTTIWL GLRGLYKGVTPIIWSAGLSWGLYFVFN AIKSYITEGSSERLKASEYLASTAEPGP MTLCITNPLWVTGTGLMLQYDAVNSPH *QYKGMSDTLVKIYKHGGVQGLY
2588	16489	A	2605	165	3	PEELLLVFFVFLKNTGIRPGAVHTCNP STLGGRI TRTGD*DHFGQHGETLSL
2589	16490	A	2606	3	455	KRYGCFSKRMNKR SATNVFFCARKGEVL GLLGHNGAGKSSSIKVITGDT*PTAGQV LLKSGSGWDALEFLGYCPHENALWPNLT VROHL*VYAAVKGLRKGDAEVAITRLVD ALKLHDQLNSPVKTLSQLKIKLGFCLS ILGKPSCGILA
2590	16491	A	2607	1	429	VDYTVRKFCIQQEGDMINRKPQLITQF HFTSWPDLGVPIPTIGMLKILQKEKACN PQYAGAIVDHCKA*VGRGTGFDIEAML DMMHT*RKVDVNGFESRNRAQSCQKVQT DMQYVFIYQALLEHYLGDTELEVTCLE TPW
2591	16492	A	2608	166	435	KFLSNNYVHFQKQNFKKVLKFIKHLVLNY FKNIVLGQV*RATPGIPALWEAETGESL EPRSSRP TWAMWRNSISTKNAQIKNIVL RILDPG
2592	16493	A	2609	228	431	IFSKICIFNGFNYPFIVGHIGRIYLFIE TGSCHCVTQAGVQWCDYGS LQP*TPGLK* SSHLRLPSSWDH
2593	16494	A	2610	439	175	RNGGLHLWSQLRLRLRWYHSPGSQGC SKS*SYHCTPAWVTQGDSSSLKKQKRKIS TYTSLSVLNETVYIIIVYTKKLDTSFK RKKL
2594	16495	A	2611	1	439	LLGSLSSMQKPRGLVDQETLRKAR*QA ARLNKLQEHKQKQVEFRIRMEKESVHV V*DSGHITT*VQSMNSIERSILHEVVEV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DGLTSFYFGEDDCRYGMIFTKDAAPSD EELDSYRRAEWDPHMADDKRKLTELAQ RPDDDA
2595	16496	A	2612	1	439	VIRKVTGTGSSSTVLDTTIPSSSTGGMP VRKSEDQTDTKRTVIKTMEDYNDNTAP AEDVIIMIQVPQSIWDQDDFESEDQDDK STQPISSVGKPAIVIKNVRTKPSAIVKY PEKSEPFKILKFTMDVSHEVIPHEVK SS*YSA
2596	16497	A	2613	2	453	EKPEKEECNLWTEWQENVPFGSFGGIRL YLQELMTITOKALHSQPKMKQAQGAIAM ASMALQTNLSLVPYLGMLTALVEGLAG RTWALKEELLKAIACVETARSDEL*KS V PNQPSSTHEIIQADLKECKENGYPYKI*P VICAADILHA
2597	16498	A	2614	2	441	LEPALPGRWGGRSAESPSPSGSVKTRQN KQKTPGNGDGGSTS*APQPPRKRARAD PTVESEAFKNIMEVVKIPEELKPWLD EDWDLVTRQQLFQLPKKNVDAIL*EY ANCKKSHGNVDNTEYAVNEDVAGIKEYF NEMLGT
2598	16499	A	2615	1	430	RGDRDLHCTESQSEASTEEGHDSLSVGI FEEDSQLFILDPPKSKPAWLNGIMTC *DFELLNPRVRFLLEVKDLALTRRQIL LHKGLSDYEKSTTLQELVLKSSRSRSGPP LSIEDLGLNFQL*PSSRVYGFATAEELKP SGE
2599	16500	A	2616	373	552	ICKIKYKLFNSALLFFROGLALLPRMEC SGAIKVHCSLDPLGSSNPL*RKIKESTL NLEKSLCTRGIPLCKYBEVPKQFLKICF QIFLETGSRSVSQAEVQWHDQNSLQPR PGLKSFSCNLNPKCWDYRCEPPRRALCS
2600	16501	A	2617	498	157	QLIGSSTHQAALRSRSLFFPAGFGTFHF HYQKAWVVKGGTSPDSLPSLLGRGVS V QLHPRGKEQRGASDT*HKCPVKLWTIGG KYRVSETSRIFSLPPTTLQAGLDSSG SL
2601	16502	A	2618	255	389	LSEFYTYEGPSTRPPIGS*GTNLPLPLS YIPRSPSAVDENLLDE
2602	16503	A	2619	3	207	QHSSLIIIRATAIKLGIAFFHF*VP*VA QGTPLTSGLLLLT*HKLAPISIIYQISP SLNVSLLLSGT
2603	16504	A	2620	3	207	QYSSLIIIMGVGIKLGIAFFHF*VPEVA QGTPLTSGLLLLT*QTLTPISMIYQISA SLNVSLLLSGT
2604	16505	A	2621	45	447	WRRIDCRNLCTTASLKHFFSIAHKEH LHNGSHLQSQHSCBAQLRRARFIICCL PYGESGQSWPTTLERANLNWLTIVYFNN WKDWEYDSQYMSNFRSSEMNIIVW* RSIDNLPHIICSTLINTKNSPL
2605	16506	A	2622	3	142	GNQATPKTAPATMSTPTILVATAVHAYR **VAEKEHPLKFGGRACS
2606	16507	A	2623	2	453	HGPGGLLDYIDKERIRDFLNGECMCCEVP DGGLVPKSLYRTA*DLNEDLKLWTDTI YQSASVFKGAPHEILIQIVDASTVITWD YHVCKGDIVFNHYHRSRSPLPNPKDYLI AHSITFPDGNVHLNNKVVWMLGPDYIMW ITTLITNNEN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2607	16508	A	2624	1	315	EEKQAPGFTTGRGKLTPLPCAHAVRFII STSLIYKGAYP*ALKGKEKY*LAVFWVY NKKGLNNNNLFLDGVHLCFVPEVRKYLA GKGLPFSIGLYHLILLFFFF
2608	16509	A	2625	232	478	LDCGNYFTV*MYIKTSHCIF*IVYILNF HLYNFRYNLDYNGEIVSEVMAQRQPMK PTYAIPPIITNSSQFKHQEAMDVKE
2609	16510	A	2626	3	430	TSTPNVHMGSTSLPGDSTTIEDAQSHS ESASPSALSSHPNNLSPTGWSQKTPVP AQRERAPVSGTTPDRDKLRPCGQRD*GY WEIBASEVMLATRIVSGSPGTIVYQSKWH GDVALAILQVVDSTPEQFQGRNDVAGL RI
2610	16511	A	2627	2	341	ALQKHEDTDCPCVVVSCPHKCSVQTLR SE*SAHLSERVIA PSTCSFKRYGCVFKG TYQQIKAHEASFVQHVNLKKEWSNSLK KKGSSFDKECVDKNKSIHCWHIQCSSV I
2611	16512	A	2628	2	179	RHTGLWVTSPLPAVFPQVVRTLFTITGLP RDARKETVESHFRAHVLVGFDFSPCCIS RTGEADPVHRTPTQRCEGDCGEPLPVS RWVGSFLIHYIQEHCL
2612	16513	A	2629	1	418	GFSPCHPVPVKWRHRDSDQP*TPGLK*S CLGLPKCWDYRHEPLRPANISY
2613	16514	A	2630	3	442	FTCGTIIIAIPNGVKEFT*LATLHGSNM K*SAAVL*ALGYIFLFTVGGTLGIVLSN SSLDIVLHDTYYMVAHFHYALSIRAVFA IIEGFIH*FPLFSGYTLHQAYA*IHFTI IFIGVNLTLFPQHFVGLFGMPRQYSDYP DAYTTR
2614	16515	A	2631	2	454	AAPMELICWGGWGLPSVDLDSLAVLTY ARFTGAPLVHKIINPW*SPSGTLPALR TSHGEVISVPHKII THLLKBYNADYDL SARQGADTLAFMSLLEKLLPGLVHTFW IDTKNYLEVTRKWYAEAMPFSLNFFLPG RMQRQYM*RLP
2615	16516	A	2632	131	410	WMWSSKAPHCFLRLPSIGDADTVHQCAMS FQKGHSALEGVHLVFKPDLVYQTLLOM PPRKCLWP GAVTHACNSMTLGGRSR*F TRSGVQDQP
2616	16517	A	2633	2	230	FFSETSSLEIQGIARHGGTWRRLRQENN LNPGGGGCSELRCSCAPAVTVRLDLR KKRNRNP*KILKNYLKIFVI
2617	16518	A	2634	2	370	GTSSSDPAQPGDDKEFIDASRLVYDGIR DIRKAVLMIRTPBELDDSDFETEDFVR SRTSVQTEDDQLIAGQSARAIMAQLPQE QKAKIAEQVASFQEE*SKLDAEVSKWDD SGNDIIVLAKQ
2618	16519	A	2635	2	376	MTDIDALY*RELFDPADKDKMDHSRRGI ALVFNHERFFWHLSLPERRCTCSDRDNL TRRFSDLGFEGKCFNDLKAEBLLKIH VSTVIHSDADCFVCFVLSHGERNHYYAY DAKIEIQTTLTALF
2619	16520	A	2636	1	461	DMAFLILTERKILGYGQGRIGPNVACPY GLLPFGDAI*LFTKEPLKPVSTITLY ITAPTALTIALL*TPLPINPLGNLN LGLLFILATSSLAVYSIL*SR*ASNSNY ALIGALRAVQATISYEVTLTIIILLSTLL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IKGSFNLRSLITT
2620	16521	A	2637	2	384	ENFKALAMIAFGQYRQKRPFDHVKLAN D*LNFAKTCVAESAENCDKSLHTLFGD KLFPATLRETYLEBLADCCAKQ*PDIEH CFLQLKYDNPYLPRLVKNVDVMCTAFH DTETFLK*LYEIA
2621	16522	A	2638	1	373	TFIYLLFLFSSAYSRGVFGRAHAKSEVA HRFKDLGDNFKALVLIAPAYLQQCPF EDHVKLANEVTEFAKTCVAESPEN*DK SLYTLFGDKLCTVATLRETYGEMADCCA KQEPDRNECFLO
2622	16523	A	2639	2	375	KGPCYRLVSTGTQRRHPGAVYLNKHL* CNVGA*GPCEKCTLPCTFNEEPLKAL TFFREHGP*VSDPEVATAPTEKEIPSLD QETTKLEPGQQLSPGISTIHLPQFPV VIEKTSPPVPEI
2623	16524	A	2640	215	478	KYFLASHTSLFTICCTAHLTCTIAPKQ IESHFGKRLDADLVF*KSDSTVVDVIP SKPV*TSGLFSGKCL*HIVEGITRAVD RKLY
2624	16525	A	2641	208	376	ILRNLIKHFPGVVAHACDPNTLEAM* GQITRSRDWDHPDRHGEAPSVLRIRLA
2625	16526	A	2642	424	2	KGEPLPPLGCKT*GPRAPQAQIPHAG FKTRGCPPLPQGRNKAQVNPFCPRER FLPGKSGSRVAPLKNQAQLGGPPFYPHP FGGPSRPVPLGFGVQTHLGNKPKPPFP KKKGGTGC SVGNWGPSSQTLPSPOAS
2626	16527	A	2643	190	3	ELSTRGFQGPHRRIAGLKQCLVMFPELE RSGGLSEH*HLHLPGSSDSRASAS*IAG ITSVCH
2627	16528	A	2644	2	339	CCEKPLLEKSHCIAEVENDEMPADLPSL AADFVESKDVRNRYAEAKDVFLGMFLYE YARRHPDYSVLLLRRLAKTY*TTLEKCC AAADPHECYAKEFHEFKPLVEEPQNLK
2628	16529	A	2645	81	369	VEVTGQPQNASFVKRNRWLLPLAALA SGSFVWFRTPDG*TSVVR*IHNHTQLI NNHLRA*YSYRDIYFLWIAI**SS*PA SVLLFTADYCP
2629	16530	A	2646	1	348	DMDMNLPRPQNYRFG*ELKADIDYHKE DNDEDDHQLSLRTVSLWAGAKDD*HIVE SEAMNYEGCPIKVTLATLKMSVQATVTL GGFEITPPGDLRMKCGSGPVHIMGLHLV AGEE
2630	16531	A	2647	1	178	GYTDTILDVRSQRVRSLLGLSNSEPNGS VETKNL*QILNGGESPKQKQEI KRYDL YLT
2631	16532	A	2648	181	244	TIKRYKNVMIFYFYFNFF*R*GLNSLAQA AAQWCNHGSLQNPPLKGSCLSLPCS *GYTIFYLSIHQLIDIWVSTFSKLFLH VSAYSSIKMS
2632	16533	A	2649	2	369	KWITFISLLFLFRSVYGFELLDAPKN DVAHRFIDFGEQHFALAEIADFHYFLH CPFEDLVTLVNE*TEFA*TCLADESA*N CDKSLHTLFGDKLCTVATLR*TYGEMAD CCAKLEPERI
2633	16534	A	2650	1	349	VTFISLLFLFSSGYSRGVFRDLDAKSEV AHRFKDLGEENFKALVLIAPAYLQQCP FEDHVKLVNEVTEFA*TCVAESAENCD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RSLHTLFGDTLCTVATLRETYGFTADCCAKQD
2634	16535	A	2651	21	403	CVCCVCVRESRTESLPGDNEDFNVKNASVKDVRCVHFDCDSQNDPPMEATGFTAQV TIYSLINLLHRLKYFETLDLH*IAIFFS KVSILNHPGQI LADYAPALDCHTCHIA KYAELKEMIDRRSVK
2635	16536	A	2652	1	355	ARMSITDTYGQHLIAGGLMTQEDVSEIK SSYYAKSNDHLNNMAHYRPTALNLQAHW HGLAQAEAQITTWSSGVFPDLLLLVMGMM TVQVP*ELQMHSHLLKTHDQSRMENMMY GIKLDW
2636	16537	A	2653	2	360	LFEHLG*YKFNALLRLRYTMKVPQVLT TLVKVSRNL*KVGIKCKKHPEAKRMPCA QDYL SVVLNQLCVLHEKTPVSDRVAKCC TESLVNRRPCFSALEVDETYVPKEFNAR TFTFHAD
2637	16538	A	2654	360	314	YTCAIVPCKLFWCCDRVSLCCLYWSQ TPELK*SSCLSFPKC*NYGHEHTWPAR IFLNLYNKSQ*TATRKCPPTKVTPSSHQ Q*HCTWPYFYFK
2638	16539	A	2655	1	353	NWTL*TLKKIFSLKDAIKRIKIQSVRWK KIFAKHTSDRGVESKYI*RTLINQ*ENN SIKNWSKNLNRFTKDIQKANKHMLSAT SLVH*ESKLK*Q*YHYTSIRVAKMKKTD YVTSW
2639	16540	A	2656	340	10	GREDKSEKCYLKPGRSQPDGAPKSSPG VP*PPAPPALPGPGRSSPFPQGS LAGKD LRPRQPSQPGGPGELIFPVKTKKKIK RKTLTAWTRSNRPEIAQREGGCLRQ
2640	16541	A	2657	509	261	IPYFKIHCLHSA LGVAETEKETA EHLDL AGASSRPKDSQRNSPFQIPPPSPDSKKK SRGIMKCLFGK*VKQ*TSGMGPVLHVA
2641	16542	A	2658	345	3	SAHLSHPKCWDYRREPLHLARISFLFKA SSPLYGRATFYLTSTPPLMDGRWVASIFW LL*IVLP*AWVYKYLSETPLSIF*KTGS LSVAQA AVQWHNHGSLQPQTPGLKRSSH L
2642	16543	A	2659	271	56	VILYIVMPIPRPCPHPHYIHTHTHTHT HTHTHTRLGKREF*LYSW*LPGYSTNGN KIFLEIYLLPILLKM
2643	16544	A	2660	366	68	PGQOSKIMPQTERKKGRKEEREEREKE EREGRKEGRKNEGTEIVIEGSSKTQEQ TRIKAS*LNSLYTTVKPQRLKGGKKHP KDSNFKD*RNISPHR
2644	16545	A	2661	351	199	LLRRLRQENLLNPEGRGFSEPRSHYISP DWATE*DFWSNKKIK*QKVQYSKY
2645	16546	A	2662	1	160	ERAWLHLSPGDGVCEPRSHHCTPTWVT E*DSVANQPGWDRVRLCLKPTWVTE
2646	16547	A	2663	233	3	GRDNWLKTVAKPESLSGKROPSLLRKVF NPFVYIILFLPOAPKGKWLSPFPFFFF FFFLRGLSLAM*PGCSAVAQS
2647	16548	A	2664	96	349	QMPSSVLTRVANAYSGFFFWFLKQKFC FVTQAEVQGRSIS*PGPLVPGFKRFLGL TLLSTWNCRRAPGLVIACGFKMSLLTL
2648	16549	A	2665	322	74	DTYTLPRNLQVESLNRPTGSEIEAIIIN RPPTKKS PGDRFKAKFYQRYKEELVSF LLKLFQ*IEKGGIGWARNLMPVIPVL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2649	16550	A	2666	2	228	NLALSPRLECKSQGFTMLIRLVSVS*PC DLPASASQSAGIMGVSHHAQPFLLHSYLR PLILIKGDQFKYAFNLFSC
2650	16551	A	2667	129	301	VRPLAGLGSPLIFFFFFEKSLAFVAQAG GQRHNLG*LLPLPPGLKGFSCNLNPSTW D
2651	16552	A	2668	318	21	FSLLVKDFQNDLAVNSSSIFPSTFLFLV RS*LDFVNLNFFNFYLFDRDFSLCCPGW TRIPRLKQSSRLRLSSWGKCVPLHPA INRFL*CDFSIGY
2652	16553	A	2669	2	322	QDGLDLTS*STRGLGPKCWDYRREPFR PAPINKCLLSIYHGPGPSLGTEGEGKQD YIPALIEQLTDQWRRLTWGTCYCAVAED SMGVVWPLLPGYEAEKEAGRPH
2653	16554	A	2670	29	261	EFNTLSKCVWIY*LFSLSLSLSLCVCVC VCVCVCVCLCVSVCLFYGPSICLHFMHP DTLSEESFHLQIISKELLKC
2654	16555	A	2671	5	224	GSAWWLTPVIPALWECKAGRSPEVGSRL PA*PRDPPALASESAGITGVKKNLIAL WEVKSCILLIFISLDKV
2655	16556	A	2672	126	321	WGRRGARARRDSHRALRVSPELALLELR PSTMAHICNPSSALGGRGGWIT*DQEFET NLANLEKPC
2656	16557	A	2673	360	74	SRLRLKLRQEVGLNLGGRGCSGPRLHHC TLAWATERDPSKNTKQKQRR**TL PETNSLLAWEPDCVCKTNKLATRLTMA QKSCSQRPQYH
2657	16558	A	2674	192	357	RIRKWLYYYYYYLLRWSLALSPRLECRG TILAQCNFHL*SSSRSPASASPVAGIT
2658	16559	A	2675	236	375	EEVLYSRKDRHVASYSRK*W*RSQAAH ACNPSTLGGRGGWITRSG
2659	16560	A	2676	236	2	ATKVSINSIGTLGVKVGGLLEGRRRLRPG PKQSSCLGLQSSWDHR*VQPHGNNFTL FVETRSMLARLVSNWPQAIQ
2660	16561	A	2677	164	389	LTQVHGLRGLRKLTVMVESEGQASHLLH KAAGRRSECQGNQMLIKSSYQPCAEA HACNPSTVGG*GERITRSG
2661	16562	A	2678	208	1	CSVYEGSCFCILRVRRVCVCVCVCVCVC VCARSCIYVRSENH*KQLPSSSILT*RF *IQSTFRSNKRLR
2662	16563	A	2679	159	382	RWLKKNHPTQARIQVRGLLDRDCQTQTW LWESGVQPLATTPRRHSEMGGWPGAVAH ACNPSTLGGRGG*ITPPRPESKLEDCLT GTARHRLGCGSQGCSLNLPPPGGIQKWG VGRAQWLTVPVIPALWVAEAGRSLEVR
2663	16564	A	2680	29	367	DCQSEQLRKLWEHHSQGV*GCSQP*S HHWTPAWVTEQDPQNKQTKNYNTHQRA GEVWREINCLSTEQLTELYSEITQILAL SVRN*KLL*YVKSSVISAETQISGGKIF
2664	16565	A	2681	256	1	ENIVPVRFLCIHRLFAILIMVQ*LERKR DHIVIHNLTLTETVYLKKWQTRPNAVAH ACNPSTLGGQGRITRSRARDYPGQHGE T
2665	16566	A	2682	1	395	LLIEHILIAMALLITERKILGCIQLRK GPNVVGPGYLLRPFDAIKLFAREPLQP VTSTITLYMTAPTAVTMAVLL*TPLR PNPLVNHDLGLLCILATSSLADY*IL*S R*ASHSNYALIGALRACPH

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2666	16567	A	2683	3	349	VRIDNAAVCLLY*AWAEFIWALANLIIR PDLDPGNLLGNDHIYVIVTAHAFVII FFIGIPIIYGGFGN*LVPLIIGAPDMAF ARITNIRF*LLPPSLLLLASAIVEAGA AGT
2667	16568	A	2684	99	2	LTVAHACNPSTLGGQSG*ITRSGVREQP GQHG
2668	16569	A	2685	325	4	SSFMSFIINSFIIIFLYTTIFLIYDV VYSPEFKP*VCFCLTECWDYRREFQCSF LPCKRV*VLAPFIKNFFFFFLRWNF FVAQAGVQWRHLGSLQPPPPNFK
2669	16570	A	2686	382	269	MGFHHVAQADLELLGTNDPPALASQSAG ITGVSHHAQPKLTF*TFSY*ACVGGSSP QFILVVOHGLAGNSFCCF
2670	16571	A	2687	3	381	GHLIALTFEFNSQICLFPRITYKCKKSF WLPFLNLVSLCAIEGYTKKVPNSV*KG IFIHHQTGFILRMQGWLNI*TSINGIYH ISRIEDKNHKTMPIDAEKWFHNI*HPFI IENIRPGVVAHICN
2671	16572	A	2688	289	91	IKYKELGVACSKTSRNVSYCYHHHHH RCHHYHHHS*RLAALCEESGWRKALGST SMGRVAFHRH
2672	16573	A	2689	3	211	LHHVQDGLDLLTL*SAPLGLPKCWDYR TEPPFPAPNEFLHLSLSKHYALGRPH TPRERKKASGILR
2673	16574	A	2690	2	197	DLTTS*SAHFGLEPCWDYRREPPRPASY AFIKYFCPALSCFWCIETGPYLIFAYLR ERSFVRSRT
2674	16575	A	2691	253	356	AVPVKMAIVKKTRNNRCW*GCGEIGTFL HCWVEC
2675	16576	A	2692	211	339	PGHPLSIIQLWIWGEDTRRGPMHEALH* PCCSELRSCHCTPAWPT*NSIF*KKKK KWLGELEKQKNMACANDP*PGHPLSII LQWIWGEDTRRGPMHEALHGKSGDGYVA VRLLTAY
2676	16577	A	2693	1	175	RHEGLNLGGRGCGEPSSCHCTPAWVTE* DSVSKKKRKGKKKSALILIFSNGVLFCH LG
2677	16578	A	2694	234	13	KTSREPWSEFLSIKGEQQCSFGLLYVFC FQMESHYAAQAGV*WCNLG*LQPPPTGF KQFSCLSPSPSPASAS
2678	16579	A	2695	149	2	SQGEDFTKTRALQWRSRRSVVAHACNPS TLGGRGWWT*QGEFKTSLAN
2679	16580	A	2696	2	194	CIGLGVVAGACSSRLRQENDMNLGGGAC SETRSHCTPAWVTE*DSISKKRKRNR WGTTRFSN
2680	16581	A	2697	338	357	YLIRKKISNSKS*FSWPGVVAYACNPS TLGGRGRRITRSVRNQPGQHGDPKFLL VSS
2681	16582	A	2698	53	293	TISIKSKWKNKQGEYNKWCMENWLAI RRLKLCPPVVLVHSCIAIKNYLRLGNL*R KEV*LAHSSGTCTGNMAEKPHRR
2682	16583	A	2699	2	335	LYAAKVPLQKACIRTFYSIFIFIFIFIF FFGKQSSFGPPGLKARGGTPLGTPLG VKRNFLPQFSGKPGITGCPPLPQKFWFF KKKRGLIF*PGGVPSNDPKGIGPPNPP
2683	16584	A	2700	166	3	DYRRVPPRLVVR*GFTVV*AGV*WRNHG SLQTQTIGLKQSSHLSLATCWDYRYE

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2684	16585	A	2701	209	340	YRMTVPFARHGGSHTCNPS TLGGRGGWM T*CHEIETTLGNMVKP
2685	16586	A	2702	78	341	EVACNCLLP AIGCFASVTYV*SSVLL*F EL*VLNENSS F*NFH*FF*NRVLICCP DWSVMA*S*FTEALTSQTIRSSHVSLPS SWDY
2686	16587	A	2703	258	185	TMIAPVHSS L GDRARPYLFKQKR*GLAL SPRLEWTGAIIVHRNLEFLCSSNPPTS A SGVTGITEMEVE RHGWIQETFWK
2687	16588	A	2704	361	41	NFGPVYKTNPGPSRPGWGLGKPGFPQK FFPFGVPPSPFPKKGSVFSPGQKGP FKGVPWGF*PRGKKTPTQPGSPKVP NWDFFKGGFKKKKKKKRILRN
2688	16589	A	2705	12	329	SCTLQLTTPRLK*SSRPSLPNN*DYRHV PPHASFP*FSEMF*DSQIFLNSLKFS S*YYLVIFFFKMRPCSI TDGVQWCDLS SLQPLPPRFKRFSCLSLPSTRP
2689	16590	A	2706	232	1	KRKRKSFKTYKKFFLNSSFKNQCPYAI GHIPRSIIFFFLRQSPGLVA*AGVQWQ DLGSPQPPPPGFKPFSHLRLR
2690	16591	A	2707	135	1	CFFLIFFFFSSDTQAGV*WQPPGIKRS SQLSSPRSDYRRISPR
2691	16592	A	2708	1	157	LDLLTS*SARLHHPKCWDYRREPPRPAD YKYFLKEVASLIVKLYLPCKLNFE
2692	16593	A	2709	88	344	MQEHYYFIKRGKMKIRKYVQLHANKLD SLDKIDKFQVKNHQN*L*KK*KS WPGAV AHACNPSTLGGRGGWITKS*DRDHPWLT C
2693	16594	A	2710	1	383	LHKVTIVLRFLSKPHILVLYFYVTCVHV SVSDMNCWFLY*IFD MYNAVQ*LDFF KLSIKFLRCIC*CVY*IFIPVFIYCFEL YLICLFLSYFLFNIYVMLLFYILCIIYF YVIFSSSSIF
2694	16595	A	2711	227	1	IFFFSNSFLKISLGFFLNFAFF*KPKFF PFLSPKINQNEFFGFNFNLKIFKFFP NKFFKF*IYLTFFKTKPK
2695	16596	A	2712	1	136	KNTKISQGWPTPVIPATQBEAGGSLE RGRQLQ*RNLSLQPLPPTFKRSSCLR LLSSWDYRRPPPLANFCIF
2696	16597	A	2713	3	349	LIPRGQGSTVVL PYNPATSI FGNLNEY KMYGHAKTCIWMFTSSFIIDTRKRQ* CSSVREWINKQ*CIQTMELVFGRNFFFF FFFFFFFFPGGPPPKIQIFKBI NPQ
2697	16598	A	2714	181	342	TSQLNLNLPPIKA*AIRQEKEIKGIQL GKREVKLFLFAHDTIVYP
2698	16599	A	2715	3	205	FRHVAQAGLELLSASSLP TLASRSAGIT GVSHCVQ*TVSSLRLGFYDTSFKIADI QSCFSWVLYCLQSAEL
2699	16600	A	2716	388	23	ASNQSKNSFEKGEKNQQSMVKTSQQAL NKRAFFDMIRSVYQKTYK*RNA**ERQS FSLKVENKKEYPSSLLLFNIVLKVLVNT GHKEK*KAHRFDRNIIQFANDMIVYVEN PKDSTKRLS
2700	16601	A	2717	4	194	FSCLSLSSWDYRSMPPHEANFLYF**R RGFTMLARLVLSNPHSAGITGVSHHAQ PFNYFFI
2701	16602	A	2718	1	212	LCCPGWETARLKRSSRLSLPKWDYRH

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						ESLHLAFGFLL*YFGPYLMVYVFSFNL YDFSLVYSLYGTSL
2702	16603	A	2719	53	299	KAVHVNIFFTITKVHLMETQIVLSLFP FPSFLHPSLSLSSFL*RDRLVLLCYPG*S AVVQS*FTWQIPGLR*ASCISLVSS
2703	16604	A	2720	139	320	QPTMRHSFSF*KQEISIFLKVSSSLHHT LRFLFFPFLDRVSLCHPGWSTVALS*L TVAV
2704	16605	A	2721	1	99	IILAYSSITHIG*IIAVLPYNPNITILN LTIYM
2705	16606	A	2722	215	361	LTFFFFFERRSNFVTQAEQQGNLV*L KPRPPGLKHFYLLSQSTGNY
2706	16607	A	2723	335	24	AIPLRPEF*THPGQNGKTRFPLKPNLT GVGNARYSQFPKRLRLKIPNPEVGPS INPNFHPGIPFWAQENFFPKKKKKKEI IMLNFLICYNLFFLYICY
2707	16608	A	2724	27	314	WKQLKYPSPDEWINKMWCIHAMEYLAIK RNKVLQCVT*RWRWLMDTKKK
2708	16609	A	2726	1	112	GFHHVSQDGLNLLTL*STHLSLPKCWDY RHEPLCOAR
2709	16610	A	2727	271	3	RSPMLKNQAIKSVIMVYIGTIWRSAGPF AIFPIAEYTNIIIIITLTITIFLGTTVD ALSHELYTTYFVTKAVLLTSLFL*IRTA YPRFR
2710	16611	A	2728	121	1	ENKYRPGAVAQAYIPNTLGG*GGWIT*G REFETSLTNVEK
2711	16612	A	2729	2	290	NRHFTKENIQMPTRHKKRDPQSSLVIRE MQTKTKVRYFYLIRMAVKKIDNTTC* *GYEKLNSPKLQTTKCPFEWVNKLWHS QIVEYFSGIQHA
2712	16613	A	2730	98	264	LVSSE***IYQILFFPPEMECHSVSQV VRGSNLC*LHPLPDPFKRFSFCSYWE
2713	16614	A	2731	2	286	PFYKATVIRTVWY*KN*QIDOWNRKES PEIDLHK*SLLI FAKGAKAIQWRKDSLF NKWC*NRWISTCKNESMLGVVAETCNPS TSGQGGR IA
2714	16615	A	2732	323	181	RDFVLLVETITMLARLVNS*PCDLPASA AQSGITGVSHRAPFLDL
2715	16616	A	2733	272	131	GRVDRINPGGGGCS*LGSCQCTPAWVKE TPSQKKKNKIICFYAFLFI
2716	16617	A	2734	227	87	AASTLTLSLIPFILTTLVNPKNKNSYP HYVKSIVASTFIIISLFPITIFNCLDQEV IISN*H*ATMDFT
2717	16618	A	2736	25	415	FSKYLLDHQLSAGLLVEQHRGSLCPLSL LHSDSSLSFAVSGKVS LAASIRNKLELP ET*RALMM*NHGHPLFEGM**PWT*EP GS*RC*ELGQPGQARRLACNPSTLGGRG GWIMRSGVRDQPGQDVET
2718	16619	A	2737	390	1	KGFFLETKRKFFFTNGFFPLLGGKGVFP PGKRLGPPILGFYPPQRFVFPFKPPFP PGPFKRGQKPPGGGKNF*RGPPGPPKKG GAPTGKKKKKEERKEKEKTPRNISKP LSHPFPNFFFCATVRGFS
2719	16620	A	2738	96	331	QFTYTHGLFPFNRLCVFFFS*KLVGG V*LCCPGWL*TPGLKQSSCLSLSTWDY KGVPCLAEHFFFEKKSPLSL
2720	16621	A	2739	379	14	LREVFPPFPSPKIKCFSKNSPKYFPPF VVFKTPTPTPPFFFPPLFGKNFFPPLFN

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						FCPPRGFF*RPPLFFFFFFFFFFFFFFFF FFFFFFFFKVYFSLLLLYFLILK*MLTF KTSISTQCY
2721	16622	A	2740	198	38	ANPLFFFFFFFFLRDGVLYVRPGWSAVVQS *LTADSTPWAQVILQPQRNPIEHDF
2722	16623	A	2741	290	39	MSKVGPLLGVLGTSFRVLLKGPEIKGDP LLANPLFFLFFFLRDGVLYVRPGWSAVV QS*LTADSTPWAQVILQPQRNPIEHDF
2723	16624	A	2742	1	399	ILIRKHSDIGTLYLLFDA*TGITDLS VLNRTELEPDQATLLGNPDVHEVIDTAH ALGIIFIVIPILIGGFGN*LVPLIIGA PDMAFARINNISP*LLPTSLLLLASAI EEAVPGTG*TVYPSLA*NYCR
2724	16625	A	2743	398	2	SPPPLIFFLWGFYSIFPPPKFFFLINP PPKFSPPPPFFKPPPPPPPPPP*EBKK NECSPPPPSPPPPFFLLPPLFFFFFFFF LKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKRARSRSRTSPTRP
2725	16626	A	2744	295	185	FFFFFFFFFFFFFFFFFFFFFFFFFLF FFLFXFFXF
2726	16627	A	2745	374	4	LKKHKSTRVP*NVKSGK*NFSPPFKIRP WAQKRAKKGAREKKAD*EKGEFGKLLK KKSFRRPGKKV*G*PKGFQRNFEKKPVKS QGPVNMGVIPAFEEKPRIPPVAKIPI*G AQKKKGRPLAI
2727	16628	A	2746	2	382	QDATAPIIDELISFHDHALIICLICFL ILDALFLTLTAKLTNTNISDAQBIETV* TILPATILDLIALPSLRILYITDEVNDA SLTIKSIHQWY*TYEYTDYGLVFNSY ILPPLFLEPRDLGLL
2728	16629	A	2747	2	374	DWPPTVKRKTNPRAQSTAADRIFLLFTV RGLTGIGLANSSLDIVLHDTYYVVAHFH YVLSLGAVFAIIGGFIH*FPLFSGYTLD QTYAKIHFTIIFIGVHLTFPQHFLGLS GMPRRYSYDYPDA
2729	16630	A	2748	55	230	QIPAK*INKYLQ*KKKKKKKKKKKKKK KKKGACLKKPHGGAKEKSWGRQKLFSPK GG
2730	16631	A	2749	161	3	NGNYTLVKKCFNTKEKIKWVK*IFFFF MRWSFTLVAQAGVQWCKLGSLOPL
2731	16632	A	2750	362	1	PEKKSFAIKGVKKAGKQCFCDAPKKGN PPKKKNPTGTPKRVLLK*PPREEKKNSP QRKKKNTAKNKEKEAPQEEI*KGPPRYI FFFISFFFFFFFFFFFFSIVINLEGT FIATTLA
2732	16633	A	2751	311	110	ITLPRHGGPHVQSOLFRLRWKDHMSLG DRGCSELSSCHCTPVWRQSKTFSKIKYG RNGTDKAATCNPGRFRSWGRKVA*QGBS ETSLSNSRTRL*KNKIWSKRDRGGYL
2733	16634	A	2752	223	16	KKTPQKKNTGEGKGPVKSPQKFLKST PP*IFFYVCFFFFLFYIYLLFRIFS FFILFVYLFILP
2734	16635	A	2753	367	10	PAPRGGVYRGRQASLSCSLHPLRASWP LCSPTQA*AMAGAPPPASLPPCGLISDC CASNERGSGVVALS*SGAGDNLVCRLL SGKCRNHPSSASLTLAAVDWSCSYSAI APPLKNS
2735	16636	A	2754	14	341	PGPNF*FGGQNSPGKNQNSLPT*KGNG

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						PGNPKNGGPTVPGTPPETRGSLRLTLQG PLRPSGTPPTRRAPGTPVGNPGF*PRDF FAQKGPVNVREGLKQGNPKGLNPPP
2736	16637	A	2755	15	172	HSWWECKLVQPL*KTVRRFLKCLKIDPP YYPALPLGLIYSEERKSUVKQSRRG
2737	16638	A	2756	263	2	QKPLPPRNDFVPFKGPERTPRPTWGFI GGVPLGKFFTLVSPFFFFFFSPSNLFF F*NRVSLCRPGWSAVV*SWLTAASTSQA QAI
2738	16639	A	2757	311	106	FVCFRLRQLALLPLECSCVILAHCNRL LCSSDSPG*QSETVSKKKKKRKKKKEK GNL*RSMDMKGR
2739	16640	A	2758	23	328	NITYYT*LFVLYFYVPGHTVVFVFXFXF FFFFFFFFFFFFFFFFFXFXFXFXFXFXF FXFXFXFXFXFXFXFXFXFXFXFXFXFX FXFXFXFXFXFXFXFXFXFXFXFXFXFX
2740	16641	A	2759	1	338	DR*LFSTNHGYIGTLVLLPGA*AGALGT ALSLLMRAELQPGNLLGLDHTYNGIDT AHAFAILFMSLAIIIRSPGN*LVTLII GAPVLAAPRITDISW*L*PHSVLLLLA
2741	16642	A	2760	120	2	INKYAWLGTVAHACNPSTLGGRWTA*GQ EFKTSLANMVK
2742	16643	A	2761	251	3	CRQIGTPTLHYSSSSSKWIKDLNVRV KTIKLSNTGVLNRELELGDCLDDTKS KNSTRKIR*SLKLETFFLGGTR
2743	16644	A	2762	11	303	ALVLKRSSCLDLKCDYRHEPLHLALS EILMYRFL*IPDIFPYWYSREIDLIFV Y*FFFFFFLETGFWFLPRGDIG*WEPPP PGYKGSSCLGLPR
2744	16645	A	2763	236	356	DWLIFVFSVERGFCHVAQVGL*LLGSGD PPASAQAGIT
2745	16646	A	2764	2	332	LTQTPGLK*SACLCLPECWNRYCEPPHP AGFLF*RHFDKGV*LLIYPGTGWS
2746	16647	A	2765	297	19	KKKSWF*FKKKKCGWATKFKN*RGFFL KFVYFFFFIG*GVFFFFFFLISIIFFF FFFFFFFFFFFFVFFVFFVFFVFFVFFFL FAMKINVFY
2747	16648	A	2766	1	147	QILRLRWENCNVNLGGGCGSEPLRHCT PAWVTV*NSVSKKKKNPLLPF
2748	16649	A	2767	357	183	NNDYRPLSPRPGKFLDF*VNRGFPLLT LVSNF*PCNLPPSTSPKAGISGFNPRAQ P
2749	16650	A	2768	2	193	RWESCLNPGGGGYSEPRSCHCTPSWVTE *DSVSTTTTKEKERQNRWSESNSLQK YKDTNHF
2750	16651	A	2769	333	173	VSQDGLDLLTS*STHLGLPKCWNRYREP PRPAQKLLMVIWLGFMSSPKSPLEL
2751	16652	A	2770	3	331	CMENCMVIPPKKVHKHNYHMIQKPYFWK AVQQLSTELNLL*PYDPAITLLGIYPKE LKTSFRKTCT*MLTASLFVIKTKWQK RCPSVGE*LSNL*YVQTMCCYSVLK
2752	16653	A	2771	209	55	RPGRPQVLRVRPQNRNLNPGGGGFSEPK *GPCPPAWGAQRDFISKKKTTIT
2753	16654	A	2772	213	57	RPGRPQLLRRLQNRNLNPGGGGCGSEPR *GPCPPAWVTORDFISSKKKTIT
2754	16655	A	2773	148	1	KATGRKTWVKSRCVGTVHTCNPSTLG GRGR*TAQAQEFKNSLRLTAK
2755	16656	A	2774	2	364	WSAVRRDWITALQPERQRETPSQKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKKKKKKKKGGVRRHGVKSRKP*TSGR PGRKNHWRQIQGQPKTPRERAEALKNRV GLKKLFKTPGHVNGAGNPKFRNGKSGKP PEVHLNGAW
2756	16657	A	2775	121	2	HLRSGVSDQPGRHGKAPSLLKIEKLAGS GGTCL*SQLLG
2757	16658	A	2776	195	3	GRVDINTLLALLLIITF*LPQLIGYIE KSTPYECGFDPISPARVPSIKFFLAAL PFLLEDL
2758	16659	A	2777	3	285	FLNIRNKVSLCCPS*A*TPGLKQSCCLG LPKC*DVR
2759	16660	A	2778	135	379	HWSATVKLYAILLGLLKWESGTLCSKD VLFFL*G*SSAYSIESVIMQIKAT*VKG KARVQLGAKKLKAYWQRKSPGIPAG
2760	16661	A	2779	364	1	GSFTGAVILYIAHGLTSSLLFCLANSNY ERTHSRIILSQGLPTLLPLAF*LLA SLANLPLEPTINLLGELSVLVTTF*SN ITLLLTGLNLTALYSLYIFTTQWGS LTHHINIK
2761	16662	A	2780	356	1	GCLRAHIWPKGNHEGQVHLFDKVCRO PMTEDCINEITQVAQIFLVHFLLRQSL TLSEKRRKKRKKRKRNRIESPEINTHI YQQLIFNKGAKKIK*G*NSLFNKTYLDP WISTCK
2762	16663	A	2781	1	204	AQVGLQDASSPRIELITFDHALIITF LICFLVLYALFLTLT*LTNTNISDAQD SETDCYSQSYIL
2763	16664	A	2782	1	522	YKNECGKVFNQQAHLAQHQRVHTGEKP YKNECGKTFQSQMSNLVYHRLHSGEKP *KNECGKTFQSQMSKLVYHRLHSGEKP *KNECGNTFHHNSTLVSHKAIHTGEKL YKNECGKVFNQKTTLARHHRHTAEKL YK*EECDKVFGCKSNLETHKKMQFSKTD SAFSLQ
2764	16665	A	2783	1	327	ENRLNSGGGGCSEPRSHCTPAWATERD SVSEKEKEQKQNFHLNAQSNCOQLKSP* KYLKHPEKTDILSKASQYNNQLTADQSI LKFKTKTFDQKGRPKGHGMTYSNS
2765	16666	A	2784	335	128	FSLIFCRAGILPCCPGWS*TPVLKQSSC SSLPKCSDYKQBPPYLACATLKCYQIPN FYCWPHIFKRMFY
2766	16667	A	2785	208	3	RPICPLSLWGVSLFFFFFLDRVLICH TGSAVAQYCNTAHCYSPRLK*SSCLSL PSSWNHNLIPPR
2767	16668	A	2786	49	332	VEMGNSPINRKYVPKSYNRCLKNTEB GVLNDLGIAEFNTCSKSLLLIFFKGRI LLCCPGWIEVVQSLTASSTLGLK*TFH LSLFGSWDHR
2768	16669	A	2787	331	187	GCSEPRSPPCNAAWATKGDVSKKKKN KKREEKKH*HNTSGEKNLI
2769	16670	A	2788	325	34	RSQRLGLPSMSIS*I*NSRLR*LRPRRL FIFCRDRVSLCCSGWSQTPGFKQSTHRS LPKCWDYRREPSPLAQIRYLGLFFSQGL SSAFICYVAMVSGF
2770	16671	A	2789	3	150	AASTRQLIFHFTSKHHFGFEAAA*YWHF VDVV*LFYVSIYWL
2771	16672	A	2790	86	311	NIHPLNDIFTRLKNGFKKKEISLVKNP NKGT*SLISIKVLFHT*K*FIRPGVAAH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						T*NPSTLGGQGGWIT*SQE
2772	16673	A	2791	2	123	GGGACSEPRSHLCTPAWETE*DSISEKK EEKK*LQIYTN
2773	16674	A	2792	302	162	PLLRRLRPENCNLLGGGFN*PRSRNCP PAWATKRDSLLKKNLKNF
2774	16675	A	2793	1	258	GGCSQLRLCHCTPAWETD*DPVSKKKKK KNFTRAKLLIFGTLVLGKVKRGGPFKPR ILKLPWETWQNLVFTKKKKIFFLKNRGG GE
2775	16676	A	2794	199	3	VGPIFRHDKPPHSKQLCTYSPAFTQLFS SGKILKNIHLWPGTVAHACNPSTLGG*A RWITRSGDR
2776	16677	A	2795	1	302	GGCSEPRSCHCIPAWATEPDSI*KINK* INK*K**KINRNKKGKHFLLSSST**PQ VASSFLTQGHRYTKL*SSQKVLLDSATL QSKSNAEVKRVNRTD
2777	16678	A	2796	228	326	NDNGQSGVVVAHACNPSTLGGQGGWIT*G REFKT
2778	16679	A	2797	270	1	KFGISAPFAPSPKV*KRGFF*NFLGNP PVKIPPF*TPL*NFSKPGKNFPFF*KT RFSKIPNGFFFFFFFFFFEGVLLCCPGWS ALTRSW
2779	16680	A	2798	307	36	FKNFCG*EVSLLCCPGWSQAPGVK*PSC LGFPKCWDYRCCLPCLASCSL*CDRNQT RISAVVLWIEFHLSPILPVLPLFLKKPQ AGLLCF
2780	16681	A	2799	132	5	IFEVTV*CTK*HKRNMQPGVVGHACNPS TLGGQGGWIMRSGV
2781	16682	A	2800	32	314	KQHPGNGPNPSCGKPGGRASRLKKNPF F*KTPPKKHTPCPKSPKGGPERLEWH FFNQKFGPLPMGPNPDQAGFCLRDP*G GGKNRSPPTL
2782	16683	A	2801	139	3	AASTFYIFFETTLIPTLAITR*GNQPE RLNAGTYFLFYTLVGE
2783	16684	A	2802	238	3	AASTSHVISSMYNIYIIQPKTFPVFFF RDKVSLCHTGWSAVAQS*LTAAASALTS CVQGIPLTPQPEYHTRPLRLFL
2784	16685	A	2803	110	291	KKLGVFVGFGFGFKTSNFMQAKGQLPN LG*LKPLPRGFPQFSGLSLSTWDYKHT PATR
2785	16686	A	2804	97	2	SYNNQDSVVLEKEKTNRSVKQN*APIPE KKKKKNKVGGLTLPNCRTYYKATIIKTV WYWRKKRQIQQ*NRIESPEIDPHKY
2786	16687	A	2805	268	1	ATFLLFYVFRPQIPYVL*IFILSLF*Y RHSGPPYVGPQQYPVQPPGPGPFYPGP GPGDFPCRLPIRKWWLVWMLPQLNPTVW PTIIT
2787	16688	A	2806	153	3	IFLEKGLLVPLFGVFLKVVFFFFFFF*D RVSPCRPDWSAVAQSRLTASS
2788	16689	A	2807	3	216	NAARDHIVKPS*PLTGALSALVMTSGL AM*CHSHSISLLILSLTSTLTIIYQ*RR NVTR*TSYQGHHTPTDQGLRYGIIIFI TSEAFFLS*FF*AFYHSSLSPTQLRGH WPPTGLSPNLPLEVPLNTSELLAS*VM PLSLHIASNTKPTNQHTNHIPKAQCNT INLIPRPHTN
2789	16690	A	2808	168	354	FLERESGFVAQEGQGNLS*WKPFPP LKHFSCLLLRSWNYGPTSPVPAKVGGF

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						WRNKIY
2790	16691	A	2809	61	360	YVNSKSCSNHRK*SLFFFFFFERESSFV PQVELHGRDLG*LQLWLPFGKFPGLTP LRNGDDGPRPQPANLGLLVKTGFSPVA HLGVNLGTLGDCPALP
2791	16692	A	2810	236	3	KMFFQMRVTMLKK*QATPGFIALKKNVL KTFLAPIFFFLRRNSALVAQAGVQWRDL GPLPLP3GLKRF3CLSLPSC
2792	16693	A	2811	140	210	NAKITKC*KGYGKRGTLMHCCQFKMGQ LLWKTGYQFLKKLKLELSNVPIPYL*I WKKGNPYALLAI
2793	16694	A	2812	230	1	VKLCPSVSLKTGVRPLTSSSEVIFILNCK FNIGV*LLPGSLLLLASAIVEAGAGSG *TVYPPLAGNYSHAEPYALV
2794	16695	A	2813	3	345	HEVRIDVHTRTCTFTGTIIIAIPTGVKV FS*LATLHGSNMK*SAAVL*ALRFTFLF TVGGLTGIVLSNSSLDIVLHDTYYVVAH FHYVLSIGTVFAIIGGFH*PPLFSGYT LD
2795	16696	A	2814	2	184	ARVGFHHIDQAGLKLTL*SAYFGFPKC WDYRHEPPRLALKFNNIKKKKKKKKTP GEKI
2796	16697	A	2815	276	3	ARVHRIDHGLM*HQPLGLK*SLCLSLPS SWD*SMQPCDDYGRSDQKKPTFKSP YVSQTGLEHLGSSDLPASASQRAKITGM SHHALV
2797	16698	A	2816	3	94	HENQYSSLIIMAIKIGIAPFHF*VP EV
2798	16699	A	2817	93	1	GGGGCSEPRLHCTPVWVTE*NPVSKKK TRA
2799	16700	A	2818	1	197	GTRAQSLLLGLRLRQKNQLNGRGCSBP KSGHLTPAWAT*PDLVSTKSCTLIYLV TQALHITLLP
2800	16701	A	2819	109	2	GVF*GVFLAQGLTLVAQAEVQWHDLSL QPCPPRLKRLV
2801	16702	A	2820	2	347	ARAPGFAENEVVFSSCFVWVPGGKGE NAELMQPSSY*BSQHFFAPPCCSSCV* LCSLGP3LLGTLIFCQFTLSELPRFRKG *FSSSLKKVFCFGDRVLLCHPGWSAVVQ TQL
2802	16703	A	2821	1	353	CTRRDVTRESTYGGHRRPPVQKGLPYGI ILFITSQVFFFT*FF*TFYHSTLTPTPQ L*GHWPPGTITPLNPLKVPLLNLSVLLP SRVSIT*AHHILI*NNRNQIISSLLITI LLGLY
2803	16704	A	2822	261	400	VEHSNSNKENFLGQGTGCHACNLNLGG RGGRITWRSGV*DQLDQH
2804	16705	A	2823	273	97	LNTFRMQRLTQLATVILRFHKDQGFAML PRQVNS*QAACHLGLPKC*DYRREPP GQK
2805	16706	A	2824	159	355	KKFFSIFFFFFFF*DRISLCHLGSASV VQSWLTAAS
2806	16707	A	2825	67	338	LSPEL*LY*IF*KPFS*QLSLTSHSPSL FSALLLSISPPTWLHSQSDKNLHLSF LFRDSVLLCCLGYSAVT*SWFTVASNSW AQVVL
2807	16708	A	2826	3	359	HEQKYSFLHDSQTLFCF*DSIPTPSNMD ETQQKSRLVLVRISLLIEFWLEPERLL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						RSMVANNLVYDTSDDYHLLKDLQEGI QTLMGRLEYGSRRTGQMLKQTYSKFDTN SHNHDAI
2808	16709	A	2827	3	338	LERNLDTTFLDPAGGGDPILYQHLP*FF GHPEAYILILPRFGIVSHIVSYFFGRLE PSGYLRMG*PIISVGLLGPIV*SHHIFS VGVDIHARAYSIFGSLVMAIPCTLEVFT
2809	16710	A	2828	1	406	RHEGEKLRRTFGPRHRGAGTAKMSASL VRATVRAVSKRKLOPTRAALTLPASVN KIKQLLKDKPEHVGKVGVRTGRCNGLS YTLEYTKTKGDSDEEVIQDGVRFIEKK AQLTLLGTEM DYVED*LSSEFVF
2810	16711	A	2829	332	3	GIIVMQATIATALIGYVLPGLQISL*GA TVIAYILAAIPFIGTDLVQ*I*VGCSVD SPTVTGFLAPFFVLAFIIAAVAALLLRF LQGTGSPNPLGGASQSDKIAFQFSC
2811	16712	A	2830	186	349	YSEREVAFFFFGNGFCF*TAEWNGGNL G*LNLLPPR*KEFSCKIFPRTWYNSP
2812	16713	A	2831	303	590	NILTTLLNKQSKSNQLQNKIHTVYIKI KIFFFFLRQSLSVTQADVQWHCLCSLQ PPPGFK*FSCCLLSSWDYKHAPLHPAN FCIFSRDGISPS
2813	16714	A	2832	1	370	EELITFRDHAVIISFLICFLVLYALFLT LTTKLNTNILDADQDIQT*TIIPAILL VLIGLPFLRILYITDEVDDPSLTIX*NG HQWD*TY*YTDYGGILFNSYILRPILLE PGELRLROVDN
2814	16715	A	2833	207	1	QFFIFLRHSFTLFAQAGMQWRDLGSLQ SPPGFK*FSYLSLTLRGLARKITLAQEFQ TSLGNMGGPHRA
2815	16716	A	2834	223	1	DNLAHKGKTRVYLKSRNKLKGGGAGNL VSLDSIGSRDRHRAPPANFVFLV*M GFPHVGDGPPELLTSCSC
2816	16717	A	2835	1	321	GTRKPS*PVTGALSALLMTSGLTM*LH FHSITLLILGLLTNTLTIYQ*WRDVARE STYQGHHTPPVQKGLRYGILFITSEGG LFAGFF*AFYHSSLDRTPLQGGQ
2817	16718	A	2836	57	370	IWMGRVLWKDRLYGVFCRAFNRVTSRV WARDPWRVPKTLSDVPRKLPPFS*ISVR GQIYFT*FFFFFETESHTVAQAGVQWWG DLG*LQSPSPGFKRCLSLP
2818	16719	A	2837	2	345	ARAHQQLDEF*L*RRPGERHPSW*SEET VERQRTKT*SESSQTGTSITSSRNARRR ESEKSLHLETNLNKEEDCHSPTFKPSTPD HPLKVMPPAPSPKENAWKRSSNPARSQ SS
2819	16720	A	2838	15	376	AKIEPLYSSLGKSETPSQKGGKKKKKK KGKGGGEGKKKKKTEGGTRGLTQETQFF GNPKGPKHLGARN*KHRAKQAKRGNQPR EYRFTEEKKEKLFNPGGGRSQKPKTGQ WNSAGGKK
2820	16721	A	2839	3	336	HELLASILLIY**CRDVTREIRIPLAHH TPPVQKGLRYGIIIFITS*VCFLAGLF* YLYHSSLPSTAQLRGHWPTGITPLNPL EVPLLITSVLLASLCSFI*AHHSLEIH
2821	16722	A	2840	338	3	KIIFLYFLRSIAFLAQIBGHWAFFSS KLWPPGFKHFSASTFLVNRVFKGGPRAR VNFGEFFIKSGFFPIF*VGF*LFFFFFFE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M. eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TESRSVAQAGVQWHDLCSLQAPPSSC
2822	16723	A	2841	2	149	ARGCSEPTLHPCTPAWVTE*DSISKKKK KKVECSNGNVCRTMCILCCFW
2823	16724	A	2842	348	175	SACKVVSITGMHCHA*VIVSVLLV*TGS LHVGVQVGLERTSDDMHTLASVSGGITG MS
2824	16725	A	2843	338	118	DPGGGACSEPRLRHCTPAWVTKRDFVSK KKKK*NIKC*HAKSGTVLSFLYLFYS* YFLMRVVSVHIPGPSTK
2825	16726	A	2844	189	47	KCVALLLSLFLSCSVM*RNACFRFAFCH DCKFLEASPAMPLIQSVEL
2826	16727	A	2845	335	139	EVSPSWFG*SQTPDLKRSACLSLSKCD YRPGVSHRARLNGSFLTQLYEMLYTFPI IWTLOQVER
2827	16728	A	2846	3	352	HEQRLTPEWCKAATALGDVVVKVGAVDAD KHHSLGGQYGVQGFPTIKIFGSNKNRP* DYQGGITGGAIVDAALSALRQLVKDRLG GRSGGYRSGLQGTSYRSSKKDVIETND SFDN
2828	16729	A	2847	2	269	ARGLFSTNHKDIGTLYGLFGA*AGVLGT ALSLLIRAE LGOPGHLGRDDISRIHVK RIIPGCGTLDGISVGRECACLWTEACSR KCARG
2829	16730	A	2848	317	28	SFLPN*KLAGHGGRL*FQVLRVRLEG CFSLEG*GCSEPWSCPCPLTWATETDPF SREKKRRRRREEKAEKRRENNRVPVSLSV FLEEVVELTLIL
2830	16731	A	2849	326	107	FHHVQDGLDLLPS*SAHLGFPCWD*R CKPPCPASRNFKTLKLYHIFSNLIE*N *KSI TRGTLETVQLPGN
2831	16732	A	2850	224	3	SILQANLKVSPPPGNPLGLLQSQVDFFF *RQGLALSPGLDCSGMIMAHCSLKLGS TDPPTLAS*VAGTPSSC
2832	16733	A	2851	27	329	VRTAAINRPGFLLPCFIGQNFFFY*RFE TYRLGV*MILTPH*YLLSSLSGLD CVIF FSFILEFFYWFIVYCHVMVYLFPLFVI LFVLCVFVVCYFLLFV
2833	16734	A	2852	351	60	NLLSSLQGGRLPRPPGLSPHPQIFTPHG GVPL*LPGPWKSREASLNPRS*PPPGQ PRGNFPFPKKNFFFTVLLCRPGWSAV AQFQKKKNLLIC
2834	16735	A	2853	186	365	LTQLLNLI*YONQIEYPQPYAQCGPRSG NAQQIGHSFNG*QVPASGMHGLPWTHQ GLKK
2835	16736	A	2854	17	239	HFTTLQISMSLLTETLARHDSHLWSQL L*RLRRNDLLKSGAGGCSELGLHCTPT WTTEQDPVSRPGAVASEH
2836	16737	A	2855	325	140	GFHYVSQDGLDLTTS*SACLAFFPKWDY RHKPPCLAAYIFIQSRVFLAVISISTHS SFQLL
2837	16738	A	2856	1	157	GTRGFHHVGQAGLEVLTSDNLPVSASQS AGITGESH*AHERSDGYANTNSPG
2838	16739	A	2857	157	361	LLLRIVSLFWRKSSPLGVQAEMYRPDLF VTKPPPPD*DKDSCSLSLITWYRLAPP LPANLEF*I*TG
2839	16740	A	2858	3	346	HEGNHKKFIINVHLR*LNQNL*SGLEGD KVIWRNI*TSVTFLEFC*MNGKMNPD LFR QFTYEVGRIFFFSLKD*VWLCCLSSTV

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						DLGSLQPPPLGFKQFSCSLSPSSWEPPC PA
2840	16741	A	2859	18	233	KNPTILCCKGGGAQA*KRLLGLRLRQEK GLTPGGEGCRDLKSLGIPPWATRPKLL LKKKKKKGGKKTLF
2841	16742	A	2860	356	3	RVNFKIFGKKGFPCGGPGGFVLTPGDL GPLFFQKGGDSPSKPLKPPFFCFALKST TLNYFQFAFCVLRPTPN*SVTOAGMQ*H DHSSLQPPPSLK*SSQLGFPSSWVYRH APESC
2842	16743	A	2861	115	374	IVCGKILNV*YTO*HNKLNKNKVD*PT IKMLISQSLGILIFIQKRDFFVNYGMI LKKRGWPGVPVAYVCNSKTLGGQGGQIT
2843	16744	A	2862	163	360	LKRIWLLILHSHPTSPHGRGVTOLEAY GPRWY*TYEYTDYGGLIIFNSYILPPLFL EPGDLRLDDA
2844	16745	A	2863	1	236	GTSEFFSFFFLSFFPSFLFFLFFNPTT LLLSLHSNIS*KKVLPSEFEMESHVNRL ECGTISAHCSPAATGTDSSIS
2845	16746	A	2864	67	364	VVCVCVCVSVSVVCVCVCVYICTYICMY VCA*YRIRRYIMLPTLVNNSCPEIHDSK SCALHTGAITRATR*PCLCIHIPVCLTV CLTVWLHICLSVCM
2846	16747	A	2865	2	155	ARGLTQENRLNLGGGGCSELRSHHCIPA WATE*DALSQKRKKKGTYRGII
2847	16748	A	2866	344	81	IQPNSFIFLKIFISRDGALLCCPGWSPN SWAQSSRLNLPKCWDYRHEPPLVQF L*KHYMYKWKVHCVFVSHYKIFTGQTK TEN
2848	16749	A	2867	217	340	RVFSDPYMNLKWSLRKRRTWPGLVAHAC NPSTLAG*RGQIT
2849	16750	A	2868	3	349	HEATSPITIELITFDHALIIITILICYL LLYALYLTTLTKLITITMSDAHEIHTA* TILPAIILDLDLPCLRLIYVTDEVNDP YLTITSIGHQWY*TYEDTDYGGLIIFNSY ILT
2850	16751	A	2869	1	352	GTRIDVYTRAYFTSATIGIAIPTGVKVF S*LATLHGSNMK*SAAAL*ALGFIFLFT VSGLTGIVLANSGLDIVLHDTYVVAHF HYVLSIGAVFAIIRGFIH*FPLFSGYTL DQTYA
2851	16752	A	2870	2	342	ARARFRTSLLLAFAFALL*LPWLQEAGAAQ TVPLTTLFDHTMLQDHRHQLAIDTYQE FRETYIPKDQKDSFLHDSQTSFCYSDSI PTSPNMEETOQKSNLELLRIFLLIESR L
2852	16753	A	2871	254	2	YPGYQAISQSDMQSYAYRHL*LQPPGVK *SSIVSLSS*DRPVPPCLANEKNFFF *RQLAMLQSRVLVNSWLLLYSHAEPRA
2853	16754	A	2872	282	3	HTHILHYIYIHGHIST*HLSPPPTNIYS LCNIKILIYTPYDH*IIIRIPLHQEHAVH RRRLIHIIHTSVCCVCVCVSVCCVACVCV CVCVWVLV
2854	16755	A	2873	278	3	LWPLKNSGPPQWPQMDLGKPOVKTPVVY YKGP*KKFFRKF*KWPGFFFFFLRQS HSIABAGVQWRDLGSLQPLPPGFKRFSC LNQISSC
2855	16756	A	2874	2	348	ARA*SLYLVSLIYPNATSNLLGLLPYSF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TPTTQLSINLAMD IPL*AGTMVIGYSSK IRHALAHFLPRGTPTHLIPILAMIESMS LLIQPIAMAVRVTDNITAGHLTMPLTGS PTV
2856	16757	A	2875	1	260	GTRENHLDPA GRGCSKSRSHHCIPAWVT D*DSLKKKKKKKQIILGNNGGTEGNQK* RGNPFGRGPGPSRQKIKELGPGGKHGKS KF
2857	16758	A	2876	176	1	EHLFCCKLLGEEKGSLSKFEGKCVNPR *KWN SRPGVVAHTCNPSTLGGRGQITR SG
2858	16759	A	2877	168	1	GVRVFGFSSVPEPSFDT CAGAQWRNLGS LQPLPPGFK*FSCLSLLSSWDYKRTPA
2859	16760	A	2878	67	333	WQGLGRAVARVPRS YEITWAGNLKGAA* FQQLFFFFFFFFHLLFFFFFFFFFFFFFFF FFFFFFFFFFFFLSFFFLFFFFFFFFFFFFF FFFFL
2860	16761	A	2879	335	1	GRKEGRREKEKBRKKKKERKKERTIP KKHIPSPLAFPRKAWKLEIQIKLVAH* KINRQAIRGCPPNKRPHFPQNMKPGRE EGGGLET SRDGERNLWIFGPSVGPLR
2861	16762	A	2880	3	345	HERHETASILLIAILFNILSGQ*YIT NTTNQYSSLIIMAJIAIKLGIAPFHF*V PEVAQGTPLTSGLLLLT*QKLAPISIIY QISPSLNVSLLLTSLISIIAGS*GGLN QT
2862	16763	A	2881	347	156	WLIFVLLVEMGFHSGOAVLKLLASSDP ASMTSQSSGITGLRHCAQPR*AFLLALC LPPSAKI
2863	16764	A	2882	338	2	IKKAL*HE*LREKKKSPIRTSQSSKAP* NLPRSKKKKESNNYQLL*AHKLQKVKE MGKLLLETPNLPLLSQKVAEPLNQPIISS KIETLIKPPYHPEKSYGHDEVTAKFSSRA
2864	16765	A	2883	206	1	IRTRPFTPMFIFYMFVYLATRSCPTLA GVQWHNHGSLQL*PPGLKESSCLSLSS WDYYACLHAELV
2865	16766	A	2884	341	140	DGGCREPRSRHCS PANVTE*DSKQNKTK QKQKRYTNISSPQTSPLCYFSAYTPLH NMPGNIMFSSL
2866	16767	A	2885	360	247	FHRVSQDGLDLLTS*SAHLSLPKCWDYR REPPRRPKAL
2867	16768	A	2886	229	351	KLNNRPGVVAHA FNPSL*KLNNRPGVV AHA FNPSLGG*GGWIMRSGVRDQPNQH GETP
2868	16769	A	2887	359	2	FYSSSSSSSELVPCRQDVQVPHYLEGLF LRSCFMEIKYDT*KRKIYTHVHTHTHT HTHTHTQREKEDFPRFTAKWKNLEAG SGYATASSIRAVLWTTITLV
2869	16770	A	2888	4	305	ADSHMWKYKAPGITKILLKSKI*GYHQ DWISSRYQDLFHKDMIFKIMSYWYKKRQ VDHWDRIESPETSSQMYEHLIYNKONIA EW*EKDSFSLKWCWDN
2870	16771	A	2889	1	436	IAILT*YDYTLL*RVGPRGQEGFTRATV ITNLLSAIPYIGADVVK*G*GGYSLDSP TLTRFFTFHFILFFIIASLATLHLLFLH *TLSNIPLRITSHSHQITFHPYYTDQYS LRLLFFLLSFTTLLLLILNFFLYPP*TT LTFFP

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2871	16772	A	2890	1	218	RKISPLIKLINHSFIDLPSPNISA**N FGSLGACILILQITGLFLAMHYSPDAS TAFSSIAHITRDVNYG*IIIRYHANGAS IFFICLFLHIGRGLYGSFLYSET*NIG IILLATIATAFIGYVLP*GSLGACIL LQITGLFLAMHYSPDASTAFSSIAHIT RDVNYG
2872	16773	A	2891	3	368	LSNS*ANNLI*LAYTIAFIVKIPLYGLH L*LPKAHVEAPIAGSIVLAAVLLKGGY GIIRLTLILNPLTKHIAYPFLVLSL*GI IITSSICLRQTDLSLIAYSSISHIALV VTAILIQT
2873	16774	A	2892	3	342	HENLI*LAYTIAFIVKIPLYGLHL*LPK AHVEAPIAGSIVLAAVLLRLRGYGIIRL TLILNPLTKHIAYPFLVLSL*GIITSS ICLRQTDLSLIAYSSISHIALVVTAIL I
2874	16775	A	2893	2	361	ARVCLRQTDLSLIAYSSISHIALVVTAIL ILIQTP*SFTGAVILIIAHGLTSSLLFC LANSNYERTHSRIIILSQGLQTLPLIA F**LLASLANLALPPTINLIGELSVLVT TFS*SNIT
2875	16776	A	2894	229	3	YTFVQSFI FSVVLFICKVCLL*PAHSMV CACECMVCVCLCVCLSSLKIIPLLECL IYLQILVLSSAIYNSRFE
2876	16777	A	2895	3	391	GFLITNNISFASPFQTTIPLYLKLTLALA DTFLGLLTALDLNLTNKLKIKSPLCTF YFSNIGFYPSTHRTIPYGLLTSQNL PLLLDLT*LEKLLPKTISQHQISTSI TSTQKGIILYFLSFFF
2877	16778	A	2896	381	2	GRCRVSGSIIIDHRMAPQKWRYYTKGGPHQ WHNFCFF*KKGVPYGPVKVFLFRAPVFS PPGPPKRWEIKV*TPPPALFFFFFFV EMGSHCVAQAGLKLGSSTPPTSASQGA EIAGVSHRAQPHAS
2878	16779	A	2897	324	1	LYTNNTKHINPQONNTK*YQRNTKNRRK KEQTKNNIKRHI TESARKNS**HRNIQ KANKSQSNKHYRARSRHNNNNNNNNN KKKKIENSHAASD*ITSSGGRSRA
2879	16780	A	2898	120	345	PPAPSS*YTTSLIQDRFLMMAVLSSAS LMRGNVGSNIMNALSHFLPQGTATLFI VLDIMEAISLLIQPIALAV
2880	16781	A	2899	381	219	CVSQDGLDLTS*STRLSLPKSWDYRCE PPRPAGSGHLYSSFKKQTGDTHNF
2881	16782	A	2900	1	224	LSWCLTYFAYLLALFYFYLKILDLAI LPRLVPYSWP*ASSPASASQSSGITGMS HYTWLPQTLNPLFFVP
2882	16783	A	2901	1	228	KYLINNRLITTOQ*LIKLTSKQMITIHN T*GY*YNRSGSSFNGVYDYLRLSESEH PMMIVDNTYEDEIYTRGGIE
2883	16784	A	2902	2	332	LPPSFSLLLAPSPSSSLPSPSSSLPSP SSSLPSPSSSLTSHSSTLTSPASCT LTITESTQRLAQSYITILP*ASRTIMQ LLKYRTLQTRNTHSMTRPKALTKI
2884	16785	A	2903	3	243	DIGFGTDFSDMTPKAQTKQVDQLDFIKI *NFWPGTVAHTCNPSTLGGGRM*ITKLG V*DQPGQGETTQKLGHGGVDAV
2885	16786	A	2904	179	2	CGYFNAYICYSLLCFLYLSLCNQPFWRK

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						IFLPLFGLVFFFF*NRV*FCCPGWSA VSQ
2886	16787	A	2905	108	2	GRVDIKLTSKQMITIHNTKGR*SLILV SLIIFIA
2887	16788	A	2906	318	2	YKESNSKNNEKKKITRQRKQKKNRPSM MVHTCNPSPMAGRDGQIPSILFNQPHSP RIIRLTLILNPLTKHIAYPFLVLSL*GI IITSSIGLRQTDLOSLIAYSS
2888	16789	A	2907	17	308	KLAGYGGMCLWSKLLERPTRMNHLSPRS EGLMEP*SHNCIPDWTP*QNPVSVQITG FCFLTFLNLAAMPRLNLSGPICCQLSLRL LGPRLFAASVSGV
2889	16790	A	2908	378	1	RSLHSTETAAKTHGHQTHPGLSTFSK*T PTPIASIPINPHNCLPAFNSTTSASYF SECVLTSSFKI IADFR*KYSSTN*HPY HLFLLKFVFFCSRDSLTMLPIRPGINS RSQAILPPWPVKVL
2890	16791	A	2909	1	129	HLFGTNHRDIGTLCLLFGA*AGVLGTAL SLLIRAEIGQPSTRP
2891	16792	A	2910	1	323	CVCWGYPRIPCNIGHHLKFFFSLEFFF FGKYNVFCSEG*RAGDQLIMEPLASGF KGIFFLNLPQWE*RVSPKLPKFWIF* LKTGFPLVAQVVFELRTSGDOMA
2892	16793	A	2911	367	136	ETPGNHLSPGV*GCSEL*SCLCPTAWAT EQDPISKQKRTKSKTLLKNTKADLTRW KHIHKSACVCICLCMYMCLRE
2893	16794	A	2912	258	140	FLIFCLDCFLNLIKVLGVGFPFSLKKK QT*RGGLALSPRLCGLI IAHCTLEPL GSRNPLTLAPQIAGATGMSH*VQYNEL
2894	16795	A	2913	48	242	YSMIFCVLILPVSFTSSDGIPLLINLFL FY*STYPLAFFKTESHSVTQAGVRWHHL GSLQPPPPR
2895	16796	A	2914	309	76	GPIICVCVCVCVCVCVCVFIFTEYSPH SLFC*IRCCVFFLALSLLIGFYLFWNR YLEVYNISFEVWASLFNRELLL
2896	16797	A	2915	1	122	FSVETGFHHVGQPGI*PPTSGDPPSLAS QSAGITGMSHHA
2897	16798	A	2916	167	1	GNMCSKESVSGTNINRKPD*YNPRLGT VAHAYNPSTLGGQGRWITGGQBEFKTSL
2898	16799	A	2917	2	356	ARGILLRLIMLTTLTRY*RDVTRST YQGHHTPPVQKGLRYGIILFITSEAFFL PRFLPPFLSSSFPTPSLLKPPPPSSFP SLPSFFPPFLPSSFL
2899	16800	A	2918	2	351	AREYTSLLQLQMTFIMAPTCTDRTLYE LAPEC*LMRTLDIITR*GNQP*RENAGS YWLFYTLGLPLLIALLYTHNTLGSLN ILLLTTLTAQELSNS*ANNLI*LAXTIAF IVKI
2900	16801	A	2919	32	321	ALMGITFFFFLGKGVLAAPRGGRGNGP LWGGPPPGLPFG*SLQGGGA*GPPPG AGANFGFLILRKTRGSPGCPGGFWIPGP GDRPAGAPQGGG
2901	16802	A	2920	1	361	GTSTRIGVLLLSLHAGSINPLGITLHS DKVTLHPYTIKDALGLLLFLLSLMTLT LFSPDLLGDENYTLANPLNTPPHIKPE *YFLFAYTILRSVFNKLGGLVALLLSIL ILAIIPII
2902	16803	A	2921	3	152	HERLYSVPLRILRLPDELSPQGWHRV

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						<p>IRESAYKSHLTLPARRGLODGIILFITS</p> <p>EVVFFAGFF*AFYHSSLCPTPQL*GHWP</p> <p>PTGITPLNPPESPLLNTSVLLASGVVIT</p> <p>*AHTKAISHYLREEAFKTG</p>
2903	16804	A	2922	410	1	<p>RAGYRQKWGSLATVIGQLGPFVERGWYG</p> <p>PSGGGTQQRHCSELVLDLHVITONRA</p> <p>NHRPRCGGSLSELKFAPLALQGRQSK</p> <p>TLSQKKNKQTTTKKNTKKQPGSVAHACN</p> <p>PSTLGG*GRQITLPSGVRDQPGQR</p>
2904	16805	A	2923	2	145	<p>ARAARGDVI*SPHFVAQRDLNLLSSRD</p> <p>PALASQSTGITGMSHQCPG</p>
2905	16806	A	2924	29	340	<p>EMNEVERRGRK*LPHDSIQSR*EYRCAP</p> <p>QCPANSCVLM*RWGFAMLPKLVSSDLPA</p> <p>LASQSAGITGVSHCAWLVLPLSTSF</p> <p>SQRHLYLPRA</p>
2906	16807	A	2925	2	337	<p>ARVLILPGFGIISHIVTYISGKKEPFGY</p> <p>IGMD*AMISIGFLGFIV*AHHIFTVGID</p> <p>VDTRAYFTCATIIIAIPTGVKVFN*LAR</p> <p>LHGCNMI*SAAVL*SLGFIFVFI VSGQA</p>
2907	16808	A	2926	76	388	<p>RYCTPAWATETPSQKKEKKKQCQTFEPE</p> <p>SSFPVCLENGCGGNFISLFFFLIILSL</p> <p>FFYFY*FFFIIFVYSYYFYFCLPSYFF</p> <p>FYFFINLIIFLLNYFFFFFI</p>
2908	16809	A	2927	48	374	<p>KDQBPTDMGSAHFQVFKGWRQVGGANED</p> <p>RINSHGGPVMFSGQYQGLVRFIVY*II</p> <p>IFFMLLFFSLFYSYFLFISIFFVLVFC</p> <p>LFIFLFYFSFFFIFVFFFYFIVIF</p>
2909	16810	A	2928	3	294	<p>HEGFHYISQDGLDLTS* SARLGLPKCW</p> <p>DYREPPRPARFPPTLRILWLYLKALYTV</p> <p>LGCYREYBAYRPWCWTHRMDGGQEVEGR</p> <p>REGTGGGHILGF</p>
2910	16811	A	2929	7	420	<p>IRRRDVLLLTLTSLSPTAARICYNGRR</p> <p>GNRLNSLAYLSKELLAAWSLRKPSHGLL</p> <p>TPIRCPLYIRGHF*LLPPSHLLLLASA</p> <p>IMGAAGGTG*TV*PTLARNYSQPGVCVN</p> <p>LAMVSLHLSGVSSILGATFITAIMNME</p> <p>APAITQYQTPLEFV*YGLITADLLVLSLP</p> <p>DLTAGITILLTDRKLSTFFDPAGGGDP</p> <p>ILY</p>
2911	16812	A	2930	11	253	<p>GLLHKAPSP*KFFFSKPFNFNFKFSP</p> <p>FSPPKKKFLSKNPHIVFKFPFKGIPT</p> <p>FPPPLKFGPPRVFFKAPPPPPPPPPPP</p> <p>FFFFF</p>
2912	16813	A	2931	70	341	<p>DSSFFS*LATLHGSNMK*SAAVL*ALGF</p> <p>IFLFTVCGLTDLALPNSSLDIALLDITY</p> <p>VVAHFHYVLSLGAVFAIRGLIH*FPLF</p> <p>SGYTLDS*AKIHCAIIFIGVYITFFPH</p> <p>HSLGL</p>
2913	16814	A	2932	3	340	<p>NYSHFGASVNLIIFTVHLAGVSCILRAI</p> <p>NFITTIINIKPPAITQYQTPLEFV*SVLI</p> <p>TGVLVLSIPVLSAGITILLTDRNLNTT</p> <p>FFDPAGGGDHILYQLLF*LFGEPEAYIL</p>
2914	16815	A	2933	2	364	<p>RVQGLRYWIIISITSEVLLFAGYF*AL</p> <p>YHSSLAPTQPLGGHWPPSGITPLNPLEV</p> <p>PLLYTYVLLASRVST*AHRLIQNNRN</p> <p>HIIQALLITILLGLYCTLLQAS*NFEPP</p> <p>FTISDGIYG</p>
2915	16816	A	2934	2	367	<p>PRVRPRVRYLLFGA*AGVLGTALSLLR</p>

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						AELGQPGNLLGNDHIYNVIGTAHAFVII FFIVIPIIIGGFGN*LGPLIIGAPDMAF PRINNISF*LLPPSLLLLLASAIVEAGA RTG*TVYPPL
2916	16817	A	2935	3	365	YHIV*PNP*PLTWALSALLMTSGLTM*F HFHSITLVILGLLTNTLTIIYQ*WRDVSR *STYQGHHTPPVQKGLRYGIMLFIT*DR FFFAGVF*ALYHSSLAPT*PHLGGHWPPT GITPLNPLE
2917	16818	A	2936	3	144	DSHGRHIVING*TCVTICFIRQLIGHFTS KHFGFEAAA*YWHKKKKK
2918	16819	A	2937	3	422	QRLATNHHDIGTLYLSFGA*PGALGTD LSLLIRAEALGQPRDLLGNDHIYNEI*TG HALGILFFIGLPIIIEGFGN*LHALIIG APDMALPRINNISF*LLPPYLLLLLASA IVEAGAGTG*TVYPPLAGNYSHPGASVE
2919	16820	A	2938	3	382	RTRGLFSTNHIDILTLYLLEGA*AGVLG AALSLLIRAEALGQPCNLLCNDHIYNVIV TAHAFVIIFFIVIPIII*CFGN*LLPLI IGAPDMAFFPRINNISL*LLPTSLLLLLA SAILEA*SGTG*TV
2920	16821	A	2939	225	3	NISWRMKQIVPKGEPYNGVPVFSVLWFH KMFIFETGSHSVYQAGVQ*RHLGSLHPH PPGIKQFYLSLPSSWDY
2921	16822	A	2940	1	247	PTREPPVIYSTIFAGTLITALSSH*FFT* VGLEINMLAFIPVLTKKINPRSTEAARK YFLTQATASIIILLIAILENNIKKKKK
2922	16823	A	2941	3	369	TRDSTYLGHHTPPVHTGLRYWRILFITS DAFFFAGFF*AFYHSSLAPT*PLGGHWP PTGITPLNPLEVPLLYTSVLLASGVSVT *AHSLSVEDDRYQIIQALLITILLGLYF TLLQASEDFE
2923	16824	A	2942	3	401	LTVCVIVLRRLKTLFFFFNKPFLOTQGY FNTPEEGFFKKPNRRVGPSPMTDPTML TNLIKGVKPKAPPRILMGGGINMTF*GF VTPRAPFPLTLRLNPMQLQGGIDLLTLKA SGGSPASGNFLKELGLRSINF
2924	16825	A	2943	189	348	RNARGWVTDKEKRLRLGMVAHACNSSTL GGDGR*IA*GQEFETSLANMVKPCL
2925	16826	A	2944	2	349	ANSNYERTHSRIIILSQGLQTLPLIAF **LVASLANLALPPTINLLGELSVLVT FS*SNITLLLTGLIILVTALYSLYIFTT SQWGSLSLTHINNIPKSFRENTLMFILL SPIL
2926	16827	A	2945	621	929	GCSSGTGCCFILCDLPRPWSRCRGVGGSP SSTAHLCPRGWRSGRCFLPPLSAS*VDS AMSLIQAAKNLMNAVQTVKASYVASTK YQKSQGMASLNLPAVSWKM
2927	16828	A	2946	379	395	SQHFGRLRREDHEVRSS*FRDPFALTSQ SAGITGMSHCARPLVATSIHKIDNRYID DRS*NINIGTIFINLLIFYLSIYLSIYL SIYLSIMYSFTVAQAGVQWRDYGSLQPE SPGPK*SSCISLSSSRNHSHTPPHGWD PKIP
2928	16829	A	2947	2	357	HTYDIRKPRR*TLACALSALLTTSGLAM TDCFHYITLLILCLLTNTLTIIYQ*WRDE TRESTYQGHHTPPVQKGLRYGIIILFITS EAYFFAGFF*AFYHSSLAPT*PLGGHWP

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						PTGITP
2929	16830	A	2948	2	357	PRVRYSTDHSDIGTLYLLFGA*AGVLGT AISLLIRAE LGHPGNLLGNDHIYNVIGT AHAFV I IFFIVIP I IIGGCGN*LGPLII GAPDMAFPRINNISF*LLPASVLLLLAS AIVEAG
2930	16831	A	2949	2	217	KNLRIVQV GDMCLWSQLLRELWEDRLS SGG*GCSELCSCHCTPAWTTQQDCLKKK KNFWPVGEVKGRHML
2931	16832	A	2950	2	354	AIPMTTARLTIEAYLIILERTTTT KD VKNPRRIAAITASCLGGLED AISCQY GIATKDRPTGLGTPEVLLGALPGAGGTQ RLPKMVVPAALDMRLTGRSIRAHRA LK M*LVD
2932	16833	A	2951	3	150	LFSCSPTFSSDPLTTPLLIIT*LLPLT IMASQRHLSSEPLSRKKKKKK
2933	16834	A	2952	283	344	EKKKKKKKKKKKKKKKKKKKK*KLKKKK KKKKKKKKKKKKKKKK
2934	16835	A	2953	3	378	DAWADAWNQTPLFN*SVLITAVLLLLSL RVLAAGITILLDRNLNTLFD PAGGGH PILYQHLF*CFGHPVYILILPLGLIY RIVTDYYGTKEPPGYIGMV*AMRSIGFL RFIVRAHHIVTVG
2935	16836	A	2954	3	387	ILYQHL*FFGHLEGYIILPGPGIISH MVTYYSKGEEPPGYIGM*AMISIGFLG FIGRAHHIFTVGIDVDTRAYFTYATIII AIP TGKVF*LATLHGSNMK*SAAVL* ALGFIFLFTVCGLTGI
2936	16837	A	2955	2	432	PRVRPRVRKHIAYPFLVLSL*GIITSS ICLRQTDLSLIAYSSISHIALVVTAIL IQTP*SFTGAVILIAHGLTSSLLFCLA NSNYERTHSRIIILSQGLQTLPLKKKK KKKKKKKKKKKKGGGLLRESLGFPNLTG EGK
2937	16838	A	2956	12	391	SYFISSSKPHLSPWLSSPDEATSKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KGGGFK*KRIGGSFKKGGGEKKI FFFKG GKKKKTGGFFEKKF FLGGEKY*DNLPKK NKTVGEKKNFLGGG
2938	16839	A	2957	1	352	PTRPYFPVDAGEAQHHPRTCRRLRALW SSHHERWKVTLCTHCSLGVFFLYCCTYY IFVLFI P*SSCGLTLIFITCIILFGSIS FFLFFTYIVFSIIIVTTFKFRLLYSIIFL SYLLC
2939	16840	A	2958	1	243	NLPRLNPKETELNRSIICNKIKAIKS LLSKKSSGHNDVTAEFY*TFKEELITIL LKFYLT PKKKKKKKKKKKKKGGPF
2940	16841	A	2959	373	3	FSSLKKRVTPPPPKTGFSLGLHLKK NFPQKPPPKKFSQKNPPPKKPPF* KKKPPPPPI*HPPPKILQPPPPPPFF FFFFFFFFFFFFFFFFFFFFFFFFTDMR GFIVRKFRTRG
2941	16842	A	2960	2	136	PRVRSTLPISYKWNRMALKAHLIMK*F TEYFKTTDELYLHDNT
2942	16843	A	2962	1	358	HTPPVRKGL*YGIILFTSKVFFVPRFI *AVYHSSLCP TLQGLW PATGMTWLNLP L*VPLCTTFVLLA*VSIT*AHNLDL NRCHVIYALVITILLRLYFTLLPASEYF

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						EAPLTIS
2943	16844	A	2963	2	373	RAYDIVRPRP*PLLGALSALLMTYGLAM *VHWDCTILLILGLLINTLAIYQ*WRDV SRSTYQGHHTPPVQKGLRYGIILFITS EODVFAGIV*AFYHSLAPTPQLGGHWP PTGITPLNPLEV
2944	16845	A	2964	403	61	LEFPLEKNFLPPGFSAFFSPFSP*KFFF SPKALIFWGNFSPFFPPPKIRFLPKIPP WVFFSPFFWEKLFSSPPLNFGPPRVLF KGPPLFFFFFFFFFFFFFFFFFREGBCW RL
2945	16846	A	2965	2	360	LIPNLAMVTR*GNHPQRLNAGTYLLFDT LDGSLALLIGLTYTRNTLGSINVLITI TAQELSNS*ANLV*LAYTLAFIEKIPL YGLHL*LPKAHREAPIAGSIVLA AVL SK LGGSGKN
2946	16847	A	2966	321	2	STGMHFFPHINMAINPPPPRPPPLFPP NPRTKPNPTQ*KGGFPPLGPF*KKLSPP LTLFFFFFFFFFGHHPGPWQKKKKKVF FFCVCFSFQRVHNIKNTHQQQ
2947	16848	A	2967	200	1	RRTYTSHLLACLQGLAFSPRLECGGKI RAHCSLQLYGSSDPPT*APQTAGTKQHN ORIAQCNDN
2948	16849	A	2968	2	354	LLTASSSEIAPLQSSLDRLCLIK*K EGLVNSI*SGNQKSYANVYRLYLDPI PKIYAEAYTP*NVNSTNLETSPKTIQK FPEDREFKNDPFEKTKNGDRETGAFFP LLFLV
2949	16850	A	2969	99	400	ALGIHFIFTVSGLTGIGLANSSLIHVLH DTYYVVAHFHYVLSLGAFAIIGGFH* IPLYSCYTLDTQYAKIHFTIIFIGVNL FFPQHFLGLSGMPRRY
2950	16851	A	2970	2	377	NILLTLTAQELSNS*ANLI*LAYTIA FIVKIPLYGLHL*LPKAHVEAPIAGSIV LAAVLKLLGGYGIIRLTLILNPLTKHIA YPFLVLSL*GIIITSSICLKKKKKKKK KKKKKKKKRGGPF
2951	16852	A	2971	1	407	GTRSYTHLYRVFLELIKMSVYDLNHTVI MVISGHVRLAFYGIHVLTLILNLLTDHI LYPFLVLSLGVIISSIFLRRTDLSL IAYSSISHIALVVTAILIQT*STTGAD ILIIHGLTSSLLCCLANSNYER
2952	16853	A	2972	10	259	SRSVAIYFKGMASA*RMFSSKKKKKK KKKKKKKKKKKKKTAITKTTAKWKN *RTEKIRHTRLPLISSRDAKCVDFLYT
2953	16854	A	2973	12	400	LNCRTPSLYLQAGELLSENPHIWCQK CVRKNNFFLFFFFFFKTLYCHICIAL SITCFLAISISGLFAFFLLNSFNHYFII VP*NFSLSIYLCCLHSLFYVGFSSFDM IFSILT*TLFFCLLFLH
2954	16855	A	2974	125	3	RPRRPAQVGQV*KNLSSLPVPPGFKL FFPLSLLSSWAS
2955	16856	A	2975	2	332	RECTINYPAQPPPPLEAEEGFQPLPPTD TG*LECLPPLGGGQHRALGLGATWHLEN ACALVLADLTGTPKPSGPFSGQACGASG RLPILLSGPIPLPGQGHLSAUGHHA
2956	16857	A	2976	7	329	SRDILVMTEDGEFF*GHV*P*DRSRRAD TPRLGGHWPPTGITPLNPL*VPLNLSV

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						LLASGGST*THRLIEYIREQTIHALL ITILLGLYFTLLQASEYFESSFT
2957	16858	A	2977	2	339	AHHIFTARIDVDTRAYFTSATIIIAIPT GDKAFS*LATLHGSNMK*SAAVL*ALGF IFLFTVRGLTGIVLADSSLDIVLHDTYY VGAHFHYGLSIGAVFAIIGGFH*CPFL
2958	16859	A	2978	394	0	QGCSEL*SCHCTPAWVTE*PPVSKKKKQ RK
2959	16860	A	2979	149	383	PLCFPSQHWGKSSNCLSSLYFPSSGLP LRCKAELDDVKQKADKELDVVAHACNPS TLVGQGGRTILRSGV*DQPGQH
2960	16861	A	2980	2	378	ARVSIQFLGLIVGAHDMFTGRMDLYTRT YCTPATILIAHTGVVPFI*LATLHGCN MK*SAAVL*ALRFIFISTVCGLTGIVLP N*SLDIVLHYMYAVAHLYVLSIGAVF AILGRFIHRLPVF
2961	16862	A	2982	2	409	PAVAEAYLKPVVDDSKGSFLWGKPDLDG IRECCQRNFGWNRTRTDESFPVLKQLD AQQTQLRIDSFPFLAQQEKDDAKRIKSO RLNRAVTCMLRIEIEAASSEIEAVSD* QKELELIDKAVACHLEYMYETDP
2962	16863	A	2983	3	453	HASAHASAHASGQRKGAAPAEKKCGAEA QHEGLELRVENLQAVQDFSSDPLQKV CPNHDNTLLATGGTGDYVRVWVKNLEK VLESKAHDGEIEDLVLPPEGL*IVCPD HYSFVGINDFMWLL*LNWGNRLYPPIHS VYLMFHFRTF
2963	16864	A	2984	3	417	LILPGFGIISHIVTYYSKGKEGFGYICM V*AMISIGFLGLIVRAHHIFTVGIDVYS RAYFTSATIIIAIPTGVKVS*LSLHGS NMK*SAAVL*ALRFIFLFTVSGLTGIV LANSSLDIALHDTYYV*THFYVLSI
2964	16865	A	2985	273	408	MKIFIF*VSPPLFFFFFFFFFFF FFFFFFFFFFFFFFFFFLAVFTFI
2965	16866	A	2986	176	335	TFQPSLWRTALLPRLECSGLIAHCSL ELGSSSPLAS*IAGTGSILRY
2966	16867	A	2987	65	398	KKEFKIGRKAEEKMTNRINNAPGPGTAN ECTVQWPKFKCKGNKSLDEBCSGRPL EDDNDQWRAIIEADPLTTREVAEELSV NHSMAVQHLK*VGKVKLNKWPHEL
2967	16868	A	2988	2	158	PGWSLTPDLR*STCLSLPKCDYRHKRP SPTSRTQFDHAPKNSSHSPIYM
2968	16869	A	2989	435	23	GVVPPNPQKSFYFPQRLKIWGGGRKRP PPKKKGFSQKTPEGF*KPPPKRRKKIFH DPGKKGPPKGIKRGPPPLFFFFFFF FFFFFFFFITIECLHSRFPHRHNKFP PNPPSPRFWPOHLNTSLPNPKNEP
2969	16870	A	2990	410	3	GGRGHFFSGAFFIKFPWNKKGISQPLCF PRGGSPPLGVPVGGGPPCWGLCHKG PVKKTGAPRGKNGISPPFCFPLGSPNR SGFFWALLGSPPLFFFFFF*DRVSLHHP GWNVAQS*LTKTSTSWQVILL
2970	16871	A	2991	371	132	KQSLPFRVKGFFFPPEVENAIYPSHTA FYSW*KRSTFSKKKKKKKKRKRKKEE RKEGRKEGRKRRKKKKKEIENA
2971	16872	A	2992	336	1	CPRWSRTAGLK*STCFGLPKCWDNRHES PCPASSVLND*QLSTVQRAT*WQTKSLV LKAPPARGALPVSRVSPPPSSHHFAYF

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						LHMI*QVSCLEFLR*SLALVPQAGVQ*RD
2972	16873	A	2993	317	440	HLGRLRQEHLSLPG*LRKFFFFFGRDGV LMLSMVLVFNSTQVMLLPQPPQVLGLR
2973	16874	A	2994	2	181	FHHVGLDLLTL*SACLGLPKCWDYRREP LCPALVILLTAKFTNFRYRVKNVCTPHV ESN
2974	16875	A	2995	1	165	GFHCISRDLGLDLTS*YARLGLSNCWDY RHEPPSPAPLFISYSICLFLSKLIQFL
2975	16876	A	2996	405	2	KKGPFIFSRMPFLYKHIEKPLASQKFG DPKWSPPHPRPIFFFLKKGVLYVWREGF KFHPP*FPPPGPPKRW*RVKPPHPPPP FFFFFLYVEMGSHCVAQAGLKLGSSTP PTSASQGAELAGVSHRAQPHAS
2976	16877	A	2997	2	415	CLFTGGGLTGIGSAGSSLDIVLHDTYYV VAHFHYDLSIGAGFAICGLIH*FPLFS GYALDQTYARIHFTIIFIGVNLTFLLPQH FLGLSGMPRRCS*PDAYTT*SMSSVG SVITLTAVIVLIIMIREAFDSKRTVL
2977	16878	A	2998	349	370	HHFY*SIATFRPFQHMELRNFFFFFLFF FFFFFFFFVFLFIFLFLFYFLFYIYL ILFL*HHFYSAV
2978	16879	A	2999	36	139	LCHCTPAWETFSKEKKKKKKKKKKKK KKKKKKKPGGS*KTALSHDCATVLQPG RLFQKKKKKKKKKKKKKKKKKKKK
2979	16880	A	3000	104	373	SADREXXSKTDNLGH*TNVNCKVPRV IQSVFSSHSLKLEINNRMKEKSLNT* KINNISYWQCSLYNLKNSYTKSSDNT TTQYMY
2980	16881	A	3001	1	396	LDCSKISSYLQKSSSHVLFFSFSFFFFP GGGGGFALENPYPPAGLGPQKKTLSP WLVGGPPFPEKAPP*GGHFLGKKPQKNP GGQNPKRPSGEGNPFQPPGGEKKQIGP PTGFGGKPFSS*PREPPGP
2981	16882	A	3002	412	104	FFFFFLPVRQTFYPQPFVSFFFLPFFKF FFFP*AFNFFWGFPIFSPPKGFFFSKI SRLVFFSLPFWKFFFLPFPFAPLRF FFKGPPXFFFFFFFFFFX
2982	16883	A	3003	400	46	LFFFFFFYKLFPFPAFGGFPPFPL*NFF FPPGPFLLGGFPFPPPK*VFFPKIP PGFFPPPP*KKFFSPPPFLLPPPGGF FNDPPPPFFFFFFFFFFFFFFFFFLCVV VQVEAY
2983	16884	A	3004	411	69	YSLPPLFFSSPPSKFPWPFFSLFFLTR VYKGGFFFFFFFFFELFGPPGLSLGSKPP PVFLGGDPAFFSIPHRVGSLLPPPNWP FIGPSFW*ALFPAPPLFFFFFLSSFFFF F
2984	16885	A	3005	3	200	DAWG*LFSTNHKDIGTLYLLFGA*AGVL GTALSLILRAELGQPGNLLGNHINVI VTAHAFVII
2985	16886	A	3006	259	146	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFGLNDILL
2986	16887	A	3007	118	414	QNQPQNKATHTVKIEKKEKPKTKTVAK EHNKAKTAEKSE*TKKEVKGGKQKVN HTAAKVKEVQKTPSKPKKEDNKAAS KHEQKDQYAFRLYMI
2987	16888	A	3008	427	111	FFFFSPVGNFSPQQFPPPPPPPPPKIF FFPPPL*FFWGGFPFPPPPPKVFFPKS

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						PPGFFFFPPF*GKKFIFPPPP*FCPPPGF FLSPPPPPPPPPPPPPPPPPPP
2988	16889	A	3009	3	302	SLASCLSVLVCVIFLGQPKPTI*LQNST PHKK*NPTEYVKTCTQIFIALLFKKEK QPRCPSAGEWINKMLYACTIEYWLAIKR YEILYATV*MYLEKI
2989	16890	A	3010	1	409	RLHDATFPIIEELITFHDHALVITFLIW LLVLCALFLTLTKLTNTNISHAQEIET V*TLAAAILALMVLPSLRILYITDEDN DPSLTIKSIGHQWY*TYEYTDYGLMFN SYILAPLFLFPGDLRLLDVDNRVV
2990	16891	A	3011	157	2	GRVDLKIQLKARCGGACLSQHTQONHL NPGEKGCSES*LPPCPD*VTKQ
2991	16892	A	3012	2	423	ARARAHIVTYISGKKEPFYIGMG*AM ISIGFLGFIGRAHIPT**IDGHTRAYF TSATIIIAIPTGVKVF*IATLHGSNMK *SAAVL*ALGFILFTECGLTGIVLANS SLYIVLHDTYVVAHFHYVLSIGAVFAI
2992	16893	A	3013	2	140	ARANILLTLTAQELWDPRANNLI*LAY TLAFIVKKPLYGLHL*LPAHVETPMDG PILLAALKLKGSGIIRLTILNPMTK HIAVPLGLSL*GIITRSICLRQTEK WLIAYS*ISHIALVVTDLIQTP*SKHF TTNSHCPRMTGPOSQQLNMTSLHTSFYS KETSRLTPLMTP
2993	16894	A	3014	2	420	PVLAAGISILLTDRDLLTLFDPGGGGD PILYQHLF*FFGHDDYILILPGFGIIS HIVTDYGRKEPSGYIGMV*AMTPVGFL GFIE*AHHIFTVGIDAHTRAYLTSVSL IVIPTWRQVFS*LATLHGSNMT*YAALF
2994	16895	A	3015	6	292	AHHIFTV*IDVYTRAYFTSATVIAIPT GVKVS*LATLHGSNMK*SAAVL*ALGF I*LFTVGGLNGIV*SY*LLDIELHDTY* FVMGCPKRVYP
2995	16896	A	3016	3	422	TPIIIGGFGN*LFPLIISAPDMEFPRIS NISL*LLPPSILLLLASAIVEAGT*TD* TVYPLAGNYSHPGASVDLTIFSLHLTG VSSILGAINFITPIINIRPPAITQYQTP LCA*CDLMTAVLLLLSLPDLAGITILL
2996	16897	A	3017	21	490	TPFPGRHLTMFSLHLAGGCSILGAINYI TTLINIRPPAITQYQTPLEFV*SVLITAV LHLLSLPGLTAGVTILLADQNLNTTFD PAGGGDPILYQHLF*FFGHPEVYILILP GFGIISHIVTYCYGKEPPFGYIGMC*AM ISIGFLGIIV*AHHIF
2997	16898	A	3018	98	402	LRSQHSKSFQISGKPSQEEWPQISPDST DYIINT*HFAQMLKNY*HQPHGLHDF FPKKKKKKKKKKKKKKKKKKKKKKKK KKASSSSKKDPPGGGPT
2998	16899	A	3019	399	229	PPPPGGGGPQGGPPPPRGGFLPKSPGGVF YPPRGGKIFSPPPGFFGPPRGFF*GAP P
2999	16900	A	3020	2	401	SDAVL*ALGFIVLVLEGGLTGIVLADSF LDLELHDTYVGAHFHYVLSIGAVFAII GGFVD*FPLFSGYTLDTYAENHFTIIL IGANVTFLPQHFLGLSGMPRRYSDDYDA YTT*NILSSVGSFITLAAALL
3000	16901	A	3021	413	67	PPPPGKIFKKTPKKKIFPPPPQF*IFFP

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						PLPPKFFFSNP*FFLGGFSPFFPPQK KIFFPKIPPNNFFSPPLKKKIFFFPPP* IFPPPRFFLKPPPPFFFTTTTTTTTTT FFF
3001	16902	A	3022	2	332	LTLSTLSIIAGS*GGLNQTQLRKILAYS SITHIG*IIAVLPYNPNITILNLTIIYII LTTTAFLLNLSSTTTLLSRT*NKLT *LTPLIPSTLLSLGGLPPLTGFLPKW
3002	16903	A	3023	1	412	RGPFFFFFCVFFFTTTTTTTTTFNKGR HSKRFFFKKKKSSRPTDRV*FYPK GWRSPFLFFSPGGRGFFPLSHQVGFSN EVLVVFKNLELFRGSPARKKKKKKHL E
3003	16904	A	3024	279	1	LGRNTELWKSCKGMDILKTCNGKLANEP FRQPRVLGIGGEAPRAGSGPPSRAPPA* TPGPSSAGSWP*PPGTGRAPRGAPAPSAP GARSPPGRPG
3004	16905	A	3025	151	401	KKPLGGPNLTGEGKKKFFSLKGGKKKPP GKFLKKTFFLGGGKMGKTPPKLKP*GK KKIFGKRGKKNPKTLAVKKFSKKKKK
3005	16906	A	3026	416	140	YLSPLKFFFTPPPLRMFLPPNPLKNIFF PPQLKIFWGGWAQNSPPPKKGFFSKNPK RVFLPPPPIRKRYNFPFHGKILAPPKNL* SAPPPIFF
3006	16907	A	3027	379	31	PPPRAGVFFFKNPKPKPPPPREGGRF* PPFPLKF*FFPKQNFLGGGGAIPTPPP KRGLGQIPTERFNLSPTQKRINFPPPG KGGPPPPPLKPPPPPPPPPPPPPSL NSFI
3007	16908	A	3028	28	420	MQQTMAHIFLCNKFANCAHVPR*SET KPMSTPLQFD*TYKGEKSKYAEHRTW KQ*CVFSLYQIIP*EKTWKNQCGTNF NQFFQQTTHL*NHTRDNQICFSKIGLEY YYRITTRQHLLKLRVCI
3008	16909	A	3029	1	401	LGNNGEAVSEKRKEKSQKEKSHNVVVG FFFFWGKPPFVPPQAEQGGRNFC*PKPWP PGWGEFPGPADRGNGRQKQPGRGNGF V*REKGGSMGGPRGA*NPGPKNPHWPP QGPEITGGTTRPHPSGIFKKT
3009	16910	A	3030	285	397	MFIKGDGLNKLRLPGAAAYACNPSTLGG* AGRI TRSGD
3010	16911	A	3031	265	2	KKESSCIKATNSNSLFFLF*SVFFFFVF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFF*HFKSALLWVTDLGFLNSD PRV
3011	16912	A	3032	410	49	GFSPPPP*KFFFSKPLNFWGGGPNFP PPKKRFFPKNPPGVFYSPPKKKKKFFSP PP*NLAPPKIFLKSPPPPPPPPPPPP FFLSNVSNGLTNMYILPCKDPSCTTFF ILGSLISL
3012	16913	A	3033	177	2	VTPPPFFFPETRSHSVARTGV**SDRCS LQPHPPSIK*SSHFSLPSSWDYRSMPPH AS
3013	16914	A	3034	75	395	MSYKHXXXXXKKKKKKKKGGAP*KKPWGG PKLTRDGKKKFFSLKGAKKPTWKFWK TLILGGRKMGTTTPPKLKLPRKKKIFKG *RGKHKPKSLPVEKFASRGRIKK
3014	16915	A	3035	400	83	KKEGPARVVSFVTPPLLEGPVGRSPQTR

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						NF*PTPPTHRKSLPS*KSKIDWRGIPLY PPPRVKPKKSFNPGNRRFC*TKIPPCP SPWAPKTHPPFQKKKKRVIK
3015	16916	A	3036	3	196	DSMPQT*NKSFARAKKKKKKKKKKK KKKKKKKRGGPPKKTLLGGPKLPGGKKK NFFFRGG
3016	16917	A	3037	1	411	FCYDVCVESGCADYSIVIIMKKKKK*K KKKKKKGGGPKKPNPGGAQNYPGVEKKI FSLKGGKKKTTPRGNFEEKPYFGGKNGA PPQKNKPLGEKKKFKREKGGKKLQFPW GKKISLPGFYLLKIYPPGRGFFNFS
3017	16918	A	3038	3	429	NFFFKKPRGGNFFPPPKGGFFSPSPK FFFFPPPPFFGGGGPHPPPPKRRFFQ KPPRGFFFPPL*EKNFFPPPPVFFAPP VFFLTTPPP
3018	16919	A	3040	1	111	IGLSGMPRRFSDYDAYAT*NILSSVGS FMYLQDQNK
3019	16920	A	3041	76	967	QLLKGGVSGVCPLLMFRCSRFLLVGS WSSLASGVKQPQFAVSVTLKAARLELF IPPRGLVVSLSASGVKLQTFVSVTAHKS SVDPKNSGAQLASPSGSRTRAAGGAACQ SRCRVALLSPWVDGTGRRGAGGGARR GGSGRTGAHGVGRLRHGGHLVPSAPW KGS*GLARNRAQRWAGTAGGPSTPSAA AGPGAASLTALCEQGNPAAPSAGPTKPT PTRNSSWPASVARSPPGSRSCSLHTSLQ AEGVGSSLGQPSKGLPQCSGGAEGLKLC RQSGSPGRGGTESERGL*GLPQCSGGAE GLLKCRQSGSPGRGGTESERGL
3020	16921	A	3042	39	141	LSIRGLNIIKKRQL*DWIKQDSTLCC P*EIH
3021	16922	A	3043	2	405	LFSTNHIYIGTLYLLFSTRAGVLGTALS LLIPAEGLQPGNLLGNDHIYNAIVTAHA FVLIFFIERPIIIGGYGN*LGPLIIGAP DMAVPRINNITF*LLPPSLLLLASATB EAGAGTG*TVYPPLAGNYSHPG
3022	16923	A	3044	3	134	HLNFGGRGCSEPRLHCTPSWATE*DSV SKKKSRKGTGLFI
3023	16924	A	3045	44	187	DPRVRQYQTPLFV*SGLIFAGLLLLSLP TLGAGITILLTDRLHTAVFDPGGGDP ILYQHLF*FFGHPEVYILLPFGIICH IVTYSGKKEPFYIGMV*AMISIGFLG FIAGAHIFTGGIDVDTRAYFTSATIII AIPGTVKVS*LRILRPNLCRLTSPISP NPRGRHHYTTNRQPPIHRRV
3024	16925	A	3046	434	40	GAPPPPPGRFFFFLNPREDTFPPPPQKG GPSPPPPPKFFFSPPALFFFGGWPNSP PPQKNFFF*KPEFFFFPPFLKKKIFFP PPLFFPPPIFF*TPPLFFFFFFFFFFF FFFFFPRGCKINFIVRGF
3025	16926	A	3047	1	399	LFTGGGLTGIVLTNSSLDIVLHDTY*VV PHEHYGLSIGAGFAIIGGSIH*FPLFSG YTLDDQTYAKIHPTIIFIGVKLTFPPQHF LGLSGMPRRYSYDAYTT*NILSSVGS LISLTAAILIIFMS*EAFASK
3026	16927	A	3048	116	367	GASMLSSMIFLECTVGGFFVFSVYLFK LQILRQSSMCFVLCFFEIRSCSVTQA GV*RRGHGSL*QPPLSHPSRDHGHV

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3027	16928	A	3049	6	345	SQLLRRLRKENCNLGGGGYSHQR*HQC PLAWATE*DYLKKKKKNSFLPKTGGFY PFLKKAPLGTTLSPKNNLPLSPLYKKRT GPWNWERKNFGKKKGGVIGLQGGKTIPK
3028	16929	A	3050	261	2	NKKSPPVNLWWKMGFFKFAKRVLSWK GGGGFFFSWRRSFTFVAQAGMQWRNLS SLQPRLPDLR*SACLGPDC*DYRREPQ YP
3029	16930	A	3051	160	2	ICVDEQAGVQWRYLGSLOAPPFLATLS CLSLMSSWECRQPPPLG*FFVCPR
3030	16931	A	3052	89	3	PLTSGLLLLT*OKLAPISIIYQISPSLN
3031	16932	A	3053	344	2	HVEAPIAGSIVLAAVLLKGGYGIIRLT LILNPLTKHIAYPFLVLSL*GIIITSSI CLRQTDLKSIAYSISHIALVVTAILI QTP*SFTGAVILI IAHGLTSSLLFCLAN SN
3032	16933	A	3054	266	2	FQPPISAYTKISPSLNVSLTLTSLI IAGS*GGLNQTQLRKILAYSSITHVG*I IAVL PYNPNITILNLTIIYIILTTTAFLL LNLN
3033	16934	A	3055	3	32	KYNSLIMPTMIATITILNLYFYLSPLLY **SSCPP
3034	16935	A	3056	3	33	KNNSLIPTTIATITILNLYFYLSPLLY **SSSPPS
3035	16936	A	3057	57	445	ANVWAPHGPAKLTNKDNYHIWKSRLKI ANMTIKKLNEVIGLTLDPFKTYVELVQ* RONAID*RKHQPVQKSPEA*PHYSOL IFHWGAKANHGRKDSL FYK*CW*NWTIS SQKLNLTDLTNTFTKIN
3036	16937	A	3058	311	1	RVGLLLKLNKISWPPPPFYGPS*EKEPL CFSQIGLFLTRTMVLNNLHSPVKTFRP NKIAPFRELFPPFKDRVSI CLPGWSAVV *SQTATSTSQASSDPGRV
3037	16938	A	3059	138	411	WERPWKAQEA VFWI*VSAFWAPPPLMEK QIPPDLEQHYRNVPGVNRNQPFVSFFLR WSLTVAQAGVWWRDLGSL*PLLPGFKRF LCLSLLS
3038	16939	A	3060	1	189	FCRVGQAGLKLTTSSDPPASAS*SAEIT GVSQRAWKITILKSSFSYFPNSCKMC FWLICLN
3039	16940	A	3061	3	406	DAWADAWLILPRFGRTSHIVTYYSKK EPFAYIGMV*AMISMGLGFIV*AHHIF TVGIDVNTRAYFTSATIIIAIPTGVKGF S*LATLHGSNMK*SAAVL*ALRFIFLLK KKKKRGAVLKVPWGGPSLPGCC
3040	16941	A	3062	451	82	PPPTNYFSPPPAFLPGGGPPRPPPPKK WSPTTPPPVIMPPPKKKKFFPPPRGW GPPPKIF*KPPPPFFF*KKNPPFSPPGE NRGVFFSTKPPPPWGKKNFAAPGAPPPP PPPPPPRGGG
3041	16942	A	3063	430	1	FFPPKQLIFWGGGGPKSPPPKKKFFPKK PPGVFFSPPKKKKKFFPPPLNLAPPKI FFKSPPPLSFLFFPPPPPPPPPPPPPP FFFFPLSVQTLKRTRAPPQPPPLD*EK APAPRVP*TGEGMPAVNVAFAPPPFYKE RPS
3042	16943	A	3064	1	409	PTRPRESTYQGHHTPPVQKGLRYGIILF ITSEVFFFAGFF*AFYHSSLAPTQQLGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M. eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						HWPPTGITPLNPLEVPLTT
3043	16944	A	3065	1	137	HTFNFSIYQKATVIKTVWYNNRHTVE SPEINPYIYS*LIFFLF
3044	16945	A	3066	4	426	KLEN*KNVLKEIKEDLNKQTDILFS*LQ RLITVRMSILPKLIYKPSAIPQIPA*P L*IKIIKCMRKGK*TRIAETIFFFFFL SQSFILSPKLDHRGGITANCTPPWAIKG KLLKKKKKKPPKTKPEKFFIQKATGAEG GVH
3045	16946	A	3067	411	187	RNLPNVPPRPTHFVLLVKTVGSQVGGG GKLLASKNPPSPAPPKSWDYRGEPPRPA PRKFFP*LNKFKIYGGPKN
3046	16947	A	3068	193	471	QCTCIKVHSGQKTGSTPLVIGELQIKIT LGCYYTPTLMAQIKKTDRTKCK*GYGAI GMLILCWRECKIVQSL*KRVWQFII*LN IYLAIKLNI
3047	16948	A	3069	323	478	FFXFXFLFFFILXYFYYP*KLFYLYLFX YIFKIYFIYNFIYIILFYIIFIIF
3048	16949	A	3070	1	378	GTRRFFHHSITLLILGLLSNTLTIIYQ*W RDVTRESTYQGHHTPPCQKGLLNGIILF ITSEVFFAGFF*AFYHSSLAPTQQLGG HWPPTGITPLNPLEIPLNLCVLLASGV SIT*AHHSLENNR
3049	16950	A	3071	201	2	TPPIQLFLKHYHT*NFNYNFFFEIGSCS IAQAKVQWCDLCLLPQTLGLKHSHLS LQSSWDYRHA
3050	16951	A	3072	261	1	EKAMGGGPFVKKSPGEGPTTKGWPLKG PLEGGQRLTGPFKSNRGLFFFFGSNE VSLCCPG*SRTPDFK*SACLSLPKCWDY RHG
3051	16952	A	3073	333	52	EIFKKKKKGGGRFFNKRVPFRPRVSNR PRAQFFLETFFFFPERGFFFFFETES YSVTQAEV*WNYLGSQQPFRKRFSHLS LPSSWNYRCK
3052	16953	A	3074	7	214	SQLQENRLNPGGGGCGEPRSCHCTPWA TE*DSVSKKKKKKKRGGWVPSLGGGP KKKNPFFNQEGGL
3053	16954	A	3075	180	419	QKHLSELHYLFKRDVFFFLKGSFVVSQ VGGQGHNLG*LKAPPPRLTHFSCLTLRE TWKNRPRYFFCFFIKTGFHVTRE
3054	16955	A	3076	371	208	QKLSGHGGSRL*S*PF*EAKAG*QLVSG GRGCSQL*SHQCTPAWVTE*RLVCKR
3055	16956	A	3077	349	3	TFCWQKYTMCRSLCHPPTTWSTKKKR PEFQKGQGDAPPYKKVQRGNPPPLKGR PSRGPPKKCKVFKAPVFLPFRFSPPPFF PPPLFFFFFF*DRVLPCCPGWSAVAQLT ATS
3056	16957	A	3078	124	1	ISSETPAVKSSFVPGVHVHACNPSTLGR *GKEITRSRDRDH
3057	16958	A	3079	205	1	CLVQNIWACVSHRWYIMSCKGC*RLGLM CVCVCVCVCVCVCVFCCCCCCCCYC*DE LSLCHSDCSAVA
3058	16959	A	3080	3	413	GHHTQPVQKGLLYGIIILFIT*EGFFFSG FF*AFYHSSLAPTQLGGHWPPTGITPL NPL*VPLLNTSVLLASGVST*AHRLI *NNRNQIIQALLITILLGLYFTLLQASE YFETPFTISDGIYGSTFFVATGFHR
3059	16960	A	3081	1	321	NSLNPGDGGCS*PRLHYCTPAWGTELDS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ISKEKKYPYHYVHPMSKMTIYNRQQNV NHIYIMLVEHSQTQENTCFMISGNFFFN LPIVLGEGEKNQHSISFKLFFNF
3060	16961	A	3082	117	484	VLKYFIDSEVNAVLFSISCSFVTFDVFPL FFFGKGVSFPCPPAGIKGGGFGFLEPLA SGFKRIFFPNPLEKWE*RARPPRGKFW NFFFFFLKRELFAPRWEGRGKILVYL KGPPWGYPHF
3061	16962	A	3083	381	227	CISRDDGFYHLGQAGLELLTSSDPPALDS *SVGITGVSHRTRPLLLLRLNVQF
3062	16963	A	3084	2	391	SHAYHIG*PSR*PVTGALSDLMTSGLA M*IDFHSITLLILCLLNTLSIYQ*WRD VTRESTDYHGHHTPPVPKGLRYGILFIT SEVFFFAFF*AFYHSSLAPTQQLRGHW PPTCITPRNTLDVPLLNT
3063	16964	A	3085	2	248	IMRSGDRDHPG*HGETPSLLKYKRLAGH GGMRLWSQLLGKGGTADSHHHVLLILET FYSLRERRHLTSVPTLGMNYWAQDIR
3064	16965	A	3086	276	243	EKWPD*SRAACPVLCRGNGQYSKGRCLC FSGWKGTEDVPTTQCIDPQCGGRGICI MGSCACNSGYKGESCEEAFRIPEKE
3065	16966	A	3087	3	130	GFYHVGQAGLELLTL*SACLSLPKCWDY RREPPRPAHTPPHS
3066	16967	A	3088	277	2	SSSVFCLLVWTSSSSSSSAARLPPLTG FLPKWALIEEFTKNSLIPTIATITL LNLFFYLRLIYSTSITLLPISNNVKIK* QFEHTKP
3067	16968	A	3089	404	60	FSHGKMRFFSPSPKIFFSPQSFYFLG GGGAKMPPPKRFFFKKTPRGFYFPP*K KKNFFPPPPVKFGPPRGFLKSPPPFFFF FFFFFFFFFFFFSPTFTFVFLMLKSD ND
3068	16969	A	3090	405	186	INKKPEAFTNTVDQMLTNSHRTFYPTA TACSLSGAHRFTSRMDHV*DHKTSLNKF KTEITLSTLSNHKLEP
3069	16970	A	3091	371	1	SPPLVQKGLRYGILFITSEVFFAGPF *AFYHSSLAPTQQLGHWPTGITPINP LEVPLLNTSVLLASGVST*AHHS LIEN
3070	16971	A	3092	263	3	NKRSPPVNLWWMKGSFFKFAKRVKISWK GGGFFFFFSWRRSFTFVAQAGMQWRNLS SLQPRLPDLR*SACLGPPDC*DYRREPQ YP
3071	16972	A	3093	1	392	FFFADFKKMFILINHFMELTTYFELKR NEATASENC*DAVKAVLGKFIIVLSTYI RKBERPRINNISFQIKHWTKKN*T*GKQ KKKKKKKVTGPEIPKFLIVKSGKPPKV ILTGAWGPIKFLSFITRL
3072	16973	A	3094	3	367	EM*ITITMYHYNTARRLKP*KTDNIKC **GHGTSGLTIYHWQE*RMVQPLWKIV* QLL
3073	16974	A	3095	3	257	HEVSQDGLNLLTS*SARLGLPKCWDYRR EPPCLAWLILPDDCVIFQKLKLLHNL NLSCIDVLMGIYSLSNFSQSNPFFFFF
3074	16975	A	3096	189	414	KGLVMVTS*CKMFFCLSIFFFFERGFC FFAQAGVQGHNLSSLEPLPQLKQFFCL TLPRS*KYRPAPPCCANFY
3075	16976	A	3097	1	299	ENYRPIFSMNTDAKILNKILANQIQCS KRITHRDQVGFLPGMQGFYI*KSISKI

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						NATHHISRLKKRNHMIPSIKAKAFNTHS*PMKKKKLAFQET
3076	16977	A	3098	362	126	FHTHTTTHTTHTTHTYIIYIIYIASFQWNAIRGRMKCINKP*KDMBBLKCILPSERSQSAAKYLLVDSNYITTEKAKL
3077	16978	A	3099	3	423	RHEHAYHIVRPTFP*PLTGALGALIMTSGLAM*FHFSITLLILGLLTNTLTITYQ*WRDVTRESTYQGRTTPPVOKGLRYGIILFITSKVFFAGFF*DFYHSSLAFTPLQLRGHWAPTGITPLNPLEVLLYTCLVLASGV
3078	16979	A	3100	392	83	LRTNCGHGAPFKNSPPFPQFLVKNSPAYONKEKDVGKPPFFFRAPDGAPFFKKKK*GLALSSRLYGGMISLELLGSSDTFASASRVARTTGQCHAGPT
3079	16980	A	3101	81	247	GGWGPPPLKPPLF*KKTGKNFWPPPFKGKPKPPNPRGGGKKGPKPPPIFFFF
3080	16981	A	3102	3	388	HEKKEPF*YIGMG*AMISIGFLGFIV*AHHIPTVGIYVDTRAYFTSASIILAIPFGKVFS*LATLHGNNMK*SAAVL*ALGFIIFTESGLTGIVLSNSSLDIVLHDTCYLVAHLHYVLSIGAVFAI
3081	16982	A	3103	3	387	HERHEELSNS*ANNLI*LAYTIAPFVKIPLYGLHL*LPKAHVAPIAGSIVLAAVLKLGGYGIIRLTILNLPLTKHIAYPFLVLSL*GIIITSSI CLRQTDLKS LIAYSSI SHIALVVTAIIQTPT
3082	16983	A	3104	3	381	HQQSHAYHIVKESP*PLTGALLALMTSGLAMGFYHFHTITLLILGLLTYYTLITYQ*WRDVSRESTYQGORTTPPVOKGLRYGIILFIT*EAFFFYF*AFYDFRLGPPTQLRGHWPPGTGITPLNSL
3083	16984	A	3105	412	111	FLGHPLFKKKMGKKRGLPKMGV*HPPAPKGKPPPLKKKKKKPGGGGAPLYSFSGGEGKKNPLTPGEGGPKNPNSPPPPFGGKKKNPPPLSPKKKKK
3084	16985	A	3106	298	98	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF F*L*I*Y*AICAINNRGAGAELYRSRD FVCY
3085	16986	A	3107	2	417	ATHVGLQDVTFPMIEQLITPHDHMLNI LIICFLDLGALFLTATKLTKTN*YAQ EI*TD*TILPAI ILNLMLPSLRMLYIT DEGDDPSLTIKSIGHQWY*TYEYTDYGG LIFNSYIRPPLPLEPGELRLDVDNR
3086	16987	A	3108	8	430	VGLVLFSELPLNGGILTFHQGIYSPP PGGRTWALMVGSWGLVMASDTLLGPLCH AFTPATQLLLNLAVASPL*PAALRIGCH SKITNALTHFLPRGTPTPPRPILVTIET MSLLIPPIADQRLAAGFTARHLLHL SV
3087	16988	A	3109	3	453	PRAIKFYRDWPGERHKRIAWKGDPCMHV LIKDEKGLMCQKKKKTPFFWAPKIPLV PPPAQNQGS*PNPPGGGNPLRPGP* RKPPPALMGPPSPSGGINPKSFFYLN P GAH*PRGEN*LGPVFENFLPLKKIF LWGELRCSQT
3088	16989	A	3110	398	2	SLFOKNPNPLVG*KKKGKALPQGPPLP PPLGGAGPGGSGRWGPPRPWGNPFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino-acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						F*NPKIWPAGGAPFSPPEK*AGGFF LPRGGGFPLTQIPPPPHLGGKSKPPFQ KKKKKNRQGTSMWMMQGWGPO
3089	16990	A	3111	3	371	SSDPPTSAFQSGSTTDMCHHHHAQLIFN FFVETGSCYVAQAGVQWHDHGSLLSQTP GLR*SSGATVLNAPALGPRRDPPTIME SLVLMKPRGSLIRSACPDCLVFWFSFF HEAEGCASEC
3090	16991	A	3112	233	449	FALFS*LATLHGSNMK*SAAGL*ALGFI FLTAGGLTGIVLANSSLDIGLHDTYYV EAHFHYGLSIGAEFAIIGGFIH*FALFS GYTLDQTYPKIHFTIIFIGGNITFLPQH FLGLSGMPRRYSYDPDAYTT*NILSSGG SFNALNAGSIT
3091	16992	A	3113	458	2	RGPPPPPPPKFFFF*TPGKNSPPPPPEG VFFPPSPPPNFFFSPPPLFFGGVPPIS PPPKSFSPTPPRFFPPPPPLKKNFFS PPPLELPPPPFFFPFFPPFFFFFF FFFFFFFFFFCGDLEGELEPGTGLACVI LLRANRKARTRG
3092	16993	A	3114	1	418	LNTTFYFPDGGGDPNLYQHLY*F*GHPD PDIHILPRPGIRSHIDTDYSGKKEPYAY VGMGWAMTSIGFLWLMVRARPLFTVGVG VDAQAYSSFASITIAIPTGAEVFS*LCP LPLSGMK*TGAAVWALGLRFIFTCGR
3093	16994	A	3115	1	425	PRINNISF*LLPPSLLLLAYAVEAGA GTG*TAYPLAGNYSHPGASGNLTIFS HLAGGSSILGAINFITTINIKPPAITQ DQTPLFV*SVLITEDLLFLSLPGLAAGI TILLTDLNLSTTFDPAGGGDPILYQHL F*FFDPAGGGDPILYQHLE
3094	16995	A	3116	2	383	GLSCTNHKDMGALYLLLGARAGVLSTAL SLLIRAELEGQPGYLLGNHDIYNDIVTAH AFVLIFFIVIPTVLGGFGN*LGPLIIGA PDTAVPRINNISI*LLPPCLLLRLACAI EEAGAGTG*TVYPPL
3095	16996	A	3117	1	259	PTRPALVVTAILIQT*STGAVILIIA HGLTSSLLFCLANSNYERTHSRIIILSQ GLQTLPLIAP**LLASLANLPAPTPTP HQ
3096	16997	A	3118	3	174	LIRGGRGCHELRSRHCTPAWATRARTLS QKK*KTTNPKKKLCLIFFGGKKKKLKKG
3097	16998	A	3119	155	1	PDFFNKSMDDKKKTARGWEDSSSFCFFK RDRVLLCCPGWSAVAQS*LTAAS
3098	16999	A	3120	420	2	PPPKFFFPPTPPPLGEGGAKTPPKKIF FLKKPPGVFFFPPLKKKKFFFSPP*FLA PKIFFKRPPPPPPPPPPPPPPPPPP FFFFFFFFFLVFLVFLVQVKVFLKKCN IQFPLASDNS*PSMIHEKFYCESNIEF
3099	17000	A	3121	48	387	RDVPLQKKEKKKKKKPKXQKKKKKGGP F*KIP*GAKIKPGKEKNFSPKRGAKKK NPGNFEEKTNFGGKKKKKKPKPN*REF GKKKFLKGGGKKTQIPWGLKIFFNGFD
3100	17001	A	3122	237	2	PFPVVLPPFPLKASSP*SL*PLIGGW NLPSSPNKGSFPKPPSNFLFRPP*GKNF YLALPR*PWPPQGF*LAPP
3101	17002	A	3123	448	130	PPRFFFEFFYSGFPPKPPFKTPVFLGVK PGVFFFSFYQKKPTNFGPKMGAL*RIPL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FETPIWVFFPIKGFHKKKPPVLN*PPTRK PPPDKILKKKKKDDCISRLARN
3102	17003	A	3124	453	3	SSAREGGGVPPFPKIIFFPPPIFSWG GGGTSPPPEREVFPKNHGGCFFSP* KRGKYFSPPPRMGPDPGVFFKGPDPNFFF FFFFFFFFFIFFFFFFFFFFTKKKNWF FFKAFRMSPKPVPPEFFFCNYRVVFRPR VRPRVRPRV
3103	17004	A	3125	443	2	YFPFGRVIVGDSLGLAGVLNPPRPHKGT PFFPKKIFSIIRPGWGGGPPLPQQRQMW GGPPPLEGLFRPQGIPIFPFKKIKPP GGVCVGVGVCV*KKKKNPFPFLWAGLK EPCFFFFFFFFFEMEFCSCCPGWSAMARSQ LNCNLHL
3104	17005	A	3126	3	186	PVIYSTIFAGTLITALSSH*FFT*VGLE INMLKKKKKKKKKKKKKKKKKKKKR GGGL
3105	17006	A	3127	171	38	KKKKLFFPPPREKNGPPKNFLKRAPPFFF FFFFFFFFFFFFWSERS*VA
3106	17007	A	3128	16	189	ILGEVIWV**FF*FIKKKKKKKKKKKK KKKKKRGAPFKKTPGGPQITPGEKKKIF SL
3107	17008	A	3129	401	85	LVNFFSPQEKRGFFPPPPKNFFFSPRG FFFLGGGGPIFPKKKSFSSKNPPGVFF SPP*KKKIFFPPLFWAPPRFFFKGPP FFFFFFFFFFFFFFFFFSQF
3108	17009	A	3130	2	312	ANNLI*LAYTIAFIVKIPLYGLHL*LPK AHVEAPIAGSIVLAAVLLKLGGYGIRL TLILNPLTKHIAYPFLVLSL*GGGVF
3109	17010	A	3131	449	3	FFFFFFFFLGGPPEIFFFFCDDPKPKPP LGGGKKKPPFF*NFQKPLGVLGAPPPP LCFPIKKKKGGGKKFFSPPLP*KGGPFK KFFFPKPPKGPFPFLKNLRGWVFFKPP PKKKALSFPKKKKKKKKKKKKRAAAR DLELADAW
3110	17011	A	3132	95	448	VINRE*KVCV*MKKKKKKKKKKKKKKK KKKERAGKGGG
3111	17012	A	3133	60	442	LGGFFFFGKKGFCLWCPRWAKAGIPV NGTPPRGV*RNFLAQPP*EGGITGPPPL PQ*FGFLRENGVPLRGPFGFEPPILGEP PPLFPQKGGKNGRNPPPLKGFVLVFKK EFSSLVPSWKARGDP
3112	17013	A	3134	236	45	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFGAAD*VILERYFQ FEATIMGV
3113	17014	A	3135	441	88	KQQTTPGLIFF*KAPRRRIFLPPPIMV FSPPSPFKFFFLSPFIFFGGVLPFFPP PKKGGFFKNRRRVFFCPLKKKNFFFLP PFFPGPRVFFYPPIPIFFFFFFFFF FFFFF
3114	17015	A	3136	2	328	TMLSPKPOQLNQONCSPEHYEPQLKTOR TWR*KKKKKKKKKKKKKKKKKKKKK KKKKRGGGQKKKMVGGEKKKPG*KIFF FFIKKVKKTALGDKKKTQFWGGS
3115	17016	A	3137	281	2	KATKSGTPIPSQQQSLAWSWAGIGSAQ PPALLHS*PIGKIFKNCMPVGRKSPQLP RNTSWQLGAVAHPSNSSTLGGRGGRITR

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						SGVRDRTRG
3116	17017	A	3138	448	3	FFFLPPSPFFPY*KRGSLEGRVVFNFPPVFPWPWSQIFGQALIFLPPPPPLF FSFPVGFQTALFPFNGFFPGFFHGLFP LLRFCPRK*VFWGGFFFFFLLRDKVS LCHPGWNAVQSEFTALTSKAQAPTRP PTRPPTRP
3117	17018	A	3139	2	436	DR*LFTSNHKEIGTLYLLFGA*AGVLST ALSLLTILAE LGQPGNLLGNDHIYNVIVT AHALGKIFFIAPIIIIGGFGN*LAPLII GAPEMAIPRINNIS*GLLPPSILLLLAS AIEBAGAGTG*TDYPPLAGNYCHPGASG DLIIF
3118	17019	A	3140	362	2	KPRRGKFFPPREGGGGFP PPPPKNFFFP KGGKFLGGGGKNSPPQKGFQKNPGG VFFPPPKKKNIFFPPGKMGAFF* GPPPPFFFFFFFFFFFGSQGVK LKSPKCKL
3119	17020	A	3141	440	102	PTPPPCCKFSFKRPPKTLFFPTNLV FSPIPP*NFFFSQALIFVGLAFIFPP QKKFFSKFPPLFFITPPLIKKFFVPPP PFILSPLKIFYKPPPIFFFFFFFFFFF
3120	17021	A	3142	1	79	EKLDYFSIIFIPVLEFVTSIIEFSL*Y INSDPNINQF*KLDYFSIIFIPVLEFV TSIIEFSL
3121	17022	A	3143	3	441	FFFFPPLKKKFFPPPPNIGPPPKSL*K PPPPFFFFFF
3122	17023	A	3144	223	3	LPYWKLPYLKH***LQDTNQESRG*HPL RPRPFKNQMKSGTVAHACNPSTLGGRG RITRSGV*DHPGQHGEI
3123	17024	A	3145	65	414	KKKKKKKKKKKKKKKKKKKKRGGP PKKKTRGGPQNP PKKKKFPQKGGKK PPLGF*KKTPLGGEKIPPPPKNTTP KKKKKF*GGGGQTPPPPPGKKFSPRN KKKK
3124	17025	A	3146	410	31	RANQKAFRGKPLCDLAVGNLSSRTQIA LTI*KWINWTILKLRTSGH*KTPIKTIK RYPIDGKISDEBLYLY*QVL*IGKKK PDNPVEKWANDLKRSFMGNILTVFKGM QR*LGSMAHICSL
3125	17026	A	3147	182	241	SHPSHHSTINITNKGLL*TPLPINPLV NLNLGLLFIATSSLAVYSIL*SGGASN SNYALIGALRAVAQTISYEVTLAIIILS TLIRGSPNL
3126	17027	A	3148	254	1	KTKKGLKIKDPLTRF*ISVC*ITKSI*F FKLLPFFPLKEHIPKLYLFFFLFET EFRSCCPGWSTMV*SLLTATSTSQIOAI
3127	17028	A	3149	499	2	NTPPAAGGCGFFFFFGKFNPPPHPTP RFFFPPLKNFFFSRVFFFWGGAQKA PPPKVFF*KIPRGFFPPPKKKIFFF SPGFFGAPPGFFLGGPPSFFFFFFF FFFFFFFFFFFFFFFFLINFLLSLQGF LVSKELFLGLTVKFTTRGFRGFCGQ
3128	17029	A	3150	256	146	KNAKVTQVCPEFNKGPG*HTHTHTSHT HTHTHTLQ
3129	17030	A	3151	333	1	TISCLTRGEHPLSPRRAGPYTGSPLHC CVDVVDKVFSSWKDLTDWPLGLDIEYF TDGSSFILRGVCRAGYAAVTLDSAVEVL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3130	17031	A	3152	43	379	SVSAETSA*KAE L TALTRALWLKKEQK NKTSLFGWDYIWEWGAPEPETPPKRAAG ALHSLAQPFVSVALPCCFFDPCAPSLSPG *HALRPLPLPLGLASEIQTAPSWHVPKKS LSPAPQPCPIPTLVFVGKTPP
3131	17032	A	3153	398	12	NTTPGGGKFFLKKTREEKFFPPKKRGF FPPPPPKNFFFPQGGNFFGGGGQISPP QKKGFFQKNPRGVFFTPPKKKKIFFSPP GKMGAAPPGF*RGPPPPPPPPPPPPPP FFFFFLLKKSRLAI
3132	17033	A	3154	371	105	SPSPQVNFIKGPKPPPPK*IL*RAPNPP LPKKKFSNPFTWGPQPQPPSKFSKFAR FPFLPPPPFPKKEPPKKKIFFPTKEGTV I*KNPPFSGFQSPDSIK
3133	17034	A	3155	3	371	DVGADPILHTSTGL*LAMQY*PEA*TAF SSIAHIT*DVYVG*VIRYLHANGA*IFF ICLLHIGRGLYRPFYLSKT*KIGLIL LLATITTAFIGYVLP*GPI*F*GATVMT NLLSAIPYIGT
3134	17035	A	3156	1	398	IAIPGVKVF*LATLHGSNMK*SAAVL *ALRYIFLFTTEGLTGIVLPNSSLNVL HDPYVVAHFHYVLSIGAGFAIIGGFH *FPLFSGYTLDTYAIHFTIFIGVNL FFPQHFLGLSGMPRRYSYDYP
3135	17036	A	3157	401	46	PPGGRNFFPKKTPGKKIFSTKKKGGFPP LPPKNFFSPGGFFFGGGGPNFPKKK GFFSKNPRGVFFSPP*KKKIFFPPPG*I WAPPRVFLKGPPPPPPPPPPPPPPPP KKSURA
3136	17037	A	3158	404	18	FFSPPPPPPGGVFPNPNKNPPPPPP PFLLGGGPPPPPPPP*PPPPPTPNVF FFSPPKKNFFPPPPGPPPPPKPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP MEKGRPRGDIGSNPPS
3137	17038	A	3159	3	192	SLVIAGCPR*NLSSTLNLPTEPSKSPCK FNC*KKKKKKKKKKKKKKRGGALKKN PWGGKK
3138	17039	A	3160	205	80	VQRDNFGFLQPSPSGVKLFCLSLPNKW DFRCGPPNPG*FFS
3139	17040	A	3161	3	384	LIVPTIILLPLT*LSKKHII*INTTTTHS LIISIPLLFFNQINNLFSCSPTFSSD HLSHPILKKKKKKKKKKKKKKGGGA FKRTPGGAHWWGGGRETFFPKGGKKKN RPGVFWKQTFWGGK
3140	17041	A	3162	348	70	GPPPKKRVFSKTPKVVLNKPPQKKKKFI FPPPVNLGPKNFLKGPPPPPPPPPPPP FFFFFYFFWMGCDR*CSWRHSSPPRLSG TPKCSPSVT
3141	17042	A	3163	2	353	LKTIPLTSTCLTIGSLALAGIFLTGPFY SEHII*TANVLYTNA*ALSIITLIATSL TSAYSTRIILLTLTGQPRFTLTNIETK KKKGPPFNRYPLGAQVYGGQNEKFFLI GREII
3142	17043	A	3164	1	221	PTRPDCSELRSCHCTPAWATEGDSISR KKKKLSTRTAF*YTRAINS LIYSLNIGT FKTYFPKIKTYDRHDF
3143	17044	A	3165	26	383	IPFYQ*SLI*YTRKKKKKKKKKKKKKK KKKKRG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3144	17045	A	3166	251	381	GNLCAGWARWLTTPVVPALWEAED*SRG QEIGAILANTVKPHL
3145	17046	A	3167	391	115	LFKKISPHAGIWGFSPPLTP*NFFFSLE PFIFGRGLAPIFPPPK*RFLSKNPPVVF IPPPLMGKPPPPPPVRLGPPIYSFKGA PPPPFFFF
3146	17047	A	3168	94	389	SPGILGQKQIGPIGNHVPGLAAPVTP *FRFKPRLP*GFGPKASPLALKPERAQ VGGTTPPPGPRGPNQPPPFKENQPGLG RFRGKLAEKRGFHL
3147	17048	A	3169	3	363	WATALQPGQQSETQSQKKKKKKKKKRG GPPPPFFFFKKKIFFSPPGAKNKGKFF* KPPKKKKKIFFPPPPPLKKKKKKKKKKK KKKKKMGGAFLKKPRGAPPPPGKRKLI FFFLKGV
3148	17049	A	3170	2	171	KEPLGYIRMV*AMISIGFLGGIV*AHHI FTVGIDVDTRAYFTSATIIIVPTGVKV FS*LATLHGSMNK*SAAVL*ALGFIFLF TVGGLTGIVLTNSSLDIVLHDTYYVVAH FHYVLLIGG*FYLRYNHCYPHRRQSI
3149	17050	A	3171	390	27	QSLTVKSPYPVVLIKTKGHH*VMNAGL TRYQSLLCENPHIRSEVCITLNPPELLP VSESPVKHSCVQVLDVSYSSGPNL*DHP *TSVDWELVVDGISFANPCVKVSLKMTS PAPVTPRS
3150	17051	A	3172	127	310	KNPGGAKILRGGGERKNFFLKRGGKKKHL GIFGKKTFFWGGKKWAKPK*WRFFSPF SP*KFFFSLKALIFFGGFCPPFSPPKKS FFSKNSQVFFFSPPFKEKIFPPPPP*NF GPPRVFLKGPPPPFFFLGVFFFFFF
3151	17052	A	3173	376	3	FFFFFLRRQSLAVTLAGV*RCNLSSLQS PPPGIK
3152	17053	A	3174	365	14	RENFFSPEGGAPKNKPPPPPPPGGKKK IFFQKKKKKIFYPWKNFPPPPKKKKKN P*KPGPLKSQGFFFFKKNONLWGPPI SFPKKKKKKAKTVQERKYNSTQLVSA ETQLL
3153	17054	A	3175	1	377	VPLHSSLGGKARLHLRKKKKKNPGFLKN FGPLALLGMGVGNIKGLKQKGKNPAPG AHTGGGCFSLRGRNTPFKRAEGIIICYN SPH*KET*KALEPRGYKGL*QALALPNL KSGKMEHILRGAP
3154	17055	A	3176	352	125	GHEVLDSSDLPASASQSAGITGVSHHAL *EILLSMFETTWACDLPONISFIKSSI PCFIGLDFIMPHRYCRFFF
3155	17056	A	3177	139	366	TAHTS*GY*VKNYINLSFCFFFFFLERN HSALQPGGQGHNRSSLQWFPGLKQFSC LSLPRSWDNLVLPQHLVNF
3156	17057	A	3178	206	1	KGTLPKKDFFKNFPKKVFLGVPKNSLF *KILTLPVLNPNYPFFFFFETVSLCH PGWNAVVRLEP
3157	17058	A	3179	330	1	IVSTLETCTYIAYNEEKDTFITLRIYVI GGNGKFLGI*IKQHIKKIIHHDQVGFIP GMQGWFNICRSINVIHHISRIKKSRAQ WLTVPVLPALWEGDAGGSPEVRSSRA
3158	17059	A	3180	3	399	HASAPLQSSSLGYRARPCFKKKKKKKGG GGGGFFFPKGGGFLPKKGGFSGKGGLG KWGLGGAGKTPGIKKPLKGPPKKRGGK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KGQKGPHF*KKKKKKGGKKLKKGGP*KP FKKPLLGRGVQP*NPHLLGG
3159	17060	A	3181	2	204	CPTACFFW*NKELLMPKKKKKKKKKKKK KKKKKKKKKKRGGAPFKNSLGGPHPPGAG KKNFFFFWGGY
3160	17061	A	3182	71	377	PKRGGQPKQKKIWWPPPPGAPPQKGMGF FNPRGFKKQITFFPPPPPPPEKKPPFF* KKKKKKKSNCS
3161	17062	A	3183	151	2	FFFLEELVPLLLKLFQKTEEEGCSNPF NEAFIILIPKPF*TTKKENF
3162	17063	A	3184	152	387	YFQGFYVACICTSFLFFFLKREPC FVTQVEVQGNFT*LNPLFLGLKKFFCL TLQIGWNNRPLPPQVIFCFK
3163	17064	A	3185	22	336	YEKCTALLQMVSSFIMMEREGTHQYSFY RKDFSLASKVNIVSYLSPIVE*FFFFL RGSPPAPQAGGQGNLGSWKPLPPGLMP FSCLTLPGGWNCRPPPPGPVN
3164	17065	A	3186	344	1	WVLKKIFFYPGRGGPPFIPPLGGQGGP IPWARGF*PRGPPPKNGF*KKKKRGG GGPPPGFPPPGPRGGVPFFLGGGGPRK PKKITKKNPGEKKKTSFKNQKRKTIK TT
3165	17066	A	3187	296	1	NPKKILTLPKTKVYKCEGENQVPIIFQ GIKNIFWKGF*PKKEREVCV*SMRHVI PVFPKKRGSKRNSKCCYKDTCTRMFIV ALFTIGKTWKQPKY
3166	17067	A	3188	2134	1	GVAHACNASILGGQGRII*GWSEFTS LANMVKPC
3167	17068	A	3189	1	159	LQDHPG*HGEPPSIVKIQKLARHGSRL *S*LLGRLRQMRQETCLNPGAR
3168	17069	A	3190	119	340	QIKKNRLVSGRGKNNKRK*IKP*VDIF FKEDIQAGKQMKRDLISLIIEIQIKT TITCYLIHARMGTITRD
3169	17070	A	3191	75	1	LSVNNFWPGTVAHACNPSTLGG*GG
3170	17071	A	3192	343	1	IFILGGGPPCCSPVFFQFFGGGGGFFLP QNFFPPRGKIFRFFFF*KKKLKRNWGF F*NFFNPPLGFFNLFFFPKKKPNFFP LGGFFFFFFFFFFLAGGDSLALSPRL EC
3171	17072	A	3193	105	368	KFKDPPPPPPFFWPPKQLPPPPGKIGA PHF*TPKGGPPPKKKKC*KKKILKGGRG KKKKKTTPKRPQKIWGPSKKKNPWGGGK TPPL
3172	17073	A	3194	1	365	FCRDEVLLFCPDWSPTGLKQFSLCLP KCWSYRC*PPYPAQGVFLK*HLTKSLSC LKLPMASLCIQDKVPAPQPCVKGLSKFF LCHLLSTLIPFTHSLFFFLGWFLRQHR SVTQAGVQWR
3173	17074	A	3195	1	362	GNQPKRLNAGTYLLFYTLLEGSVPLLI MYTHKTLWSNLNILLTLTGQELSNC*AN NLI*LAYTRALIVMIPLYGLHL*LPKAH VEAPIAGSI*LAIVLLKGGYGIIRLTL ILNPLTNT
3174	17075	A	3196	137	3	KGQPRFPPISLKKGSQGGKGGFFFFFY RIPLCHPGWCPVVQSW
3175	17076	A	3197	1	266	EGRGCSEL*SCHCTPA*VTVRYPVSKKK KKKKKGGGKGGKGGKNTLFGPKRKG LRGPQKRGKKIGPEKKVGNLKKGIFFR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EKTF
3176	17077	A	3198	217	446	YWSEHYAMTQVLEGFSYSLQDHFYFCFR SIRRIIFYSLIKPSIND*GERELEPITT SQALQIAGRAGRFSSRFKEG
3177	17078	A	3199	345	314	QPGPEGKIRFPLKIPNLTPSGGKSLKFP LFKRVPENCLSLRG*GCN*PI
3178	17079	A	3200	2	330	SRHYTPAW*QSKTLPKPKKKKKKKKKK PFFPKNTQKKPKKKKRGGLNWGVKTPPP LKTQKMGISPGKKLKKNLPLKPKKKEG NPLF*FRGF*KKKAPFKKKKNPPK
3179	17080	A	3201	2	385	PFPFLGGPQIPKFLKFFLRAN*NLGGLF FLGGVLKKIPLRKPFSLWIKFPPTPPFG KKIFFKTFQKPLFFF*KKFFFCFPFP FFLSRGFFVFFSPKKPFFFFFFF
3180	17081	A	3202	355	2	FFFFFFSETESCSVAQAGVQWHYLGSG*A LEPRFTP
3181	17082	A	3203	156	1	LKSLLEAKVGGLLLEVRSSRPA*ATWRD FISTKN*KISQVWWYILVVVTWE
3182	17083	A	3204	352	175	QPRGRPAPAHPP*CPLRLALPC*CPCPA CCPPWAEASPSGVQASPARAPACPARAL LNE
3183	17084	A	3205	280	373	QRGTRIFSDLQT*KKNKSPFKILLID NALGHSRVLTERRYKDIRPANTTSFLRP MVQELIPTFQS
3184	17085	A	3206	1	367	EIESIQIDGHTKKNKFLGIHLTYLTKEVK DLCKKNYKTLLEKIIDDTEKYDMLMD*N NIVKMAILPKAIYRFDTISTKLLMSFFM ELEKIF*NLV*KA*MAETTISKKNKAGG ITLLDFKLYY
3185	17086	A	3207	368	12	FAQKKKKKKKKKKKKKKKKRAPQN* RAPQKPLKPPPRVFLIPPLGSPPPPAF FWRGGPPPGFFSKKKKMLRTGGGRLF LLA
3186	17087	A	3208	2	356	KYLFSSIEGKEKMKGIANLNFETISEN CPSLARDLDIQKTRHANPNLKKSPQH IIVKLSKVVDKERILKTARKECFITYKR TPIRPGMVAYACNPSTLGG*GGWIMRSG DQDHPG
3187	17088	A	3209	359	170	INIKQLPRCGGTCLWSQLSRRLRRDCY SLGGQCSEL*SSQCSPAATERDSVSK YKINNFL
3188	17089	A	3210	295	122	VIKTV*NNKDRHIDQCSRIESPKIHLH IDDQLIFDKDVKTPE*RNNGLFNKWCWE N
3189	17090	A	3211	218	466	ATFDTTLPSCYQAPNNRFDLSD*EQE IDMTVNIILPLRSLNIVITNPYNI*HH QHDLDTYPTDTGQLVNCAIFINLLQP
3190	17091	A	3212	340	355	LGLQG*REGNFGSLQTSPPGFKRFSGLS LLSSWDYRV
3191	17092	A	3213	254	40	WPGTMAHACNLSTLGG*GGCITRPGDRD HPG*HNNNN
3192	17093	A	3214	198	25	YNEKEKPVKMLKIANSLGAVAHAYNPS TLGGQGGRIMKSGDRDHPG*HADAWVET VL
3193	17094	A	3215	376	3	PPGVF*RGPPGFRTLPKSSSSSSPPPKI LGGPPFLAFFGGAPPQKKPPSSSSSASS PPSSSSRAPLKKGGPFNPAGGFPLFGGP PRGGPPFSSSSSSSSSSSSSSSSSSRRSR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SRTSRTGRTRG
3194	17095	A	3216	393	260	VSQDGLDLLTS*STRIGLPCWDYRREP PRPACTLCISSTYNDP
3195	17096	A	3217	3	387	HASASSGSRAPPPPPFFFNKKTGSKELET TRGTVLKTCLEFFKKKKKVLGGPKPPLGN PKGVGKPLKGFPGPNPWP*KGPGCHF *KNGF*DPGPKKSHIPSWVGGKSSLLP GPLGGPSEVYFSPPLRA
3196	17097	A	3218	77	406	RMARPELGLPGNLLSNDHIYNGIVTAHA FVLIIFLIVIPILINGGFGN*LIPLIIGAP DMAFPRINNISF*LLPPSLLLLASAI EAGAGTG*TVYPLAGNYSHPGASVK
3197	17098	A	3219	394	2	KRRYFPDGLNFFWGPGLKIFVKKKVSS LKKKKKKNFFPVFLQGWGKNKFKGGGL KFSKPNLI*FFFPQKEAR*KVFFFFFRS PQKDPLREFFFFLRQVSLCHPDWSAVA RSQTSASISRAQAGRV
3198	17099	A	3220	376	157	KFFFS*P*KKFFSPKPLKFGGGVGIIPP PKKRFFFKNPQGVFKKPPQKKKIPFQP PVNFGPPRDLKGGPPPPPPPPPP
3199	17100	A	3221	394	1	VPPQKFKTPGPPPPPPPPPPPPPPPP PPLGGFLNPAPKNPPGPPKVGFPGGP PPPPGGFFFSPLSF*NGERVFFGPKI PKRKFLLKWKGGKFFPKKPIFPPPPKK KKKKKRAAARDLELADAW
3200	17101	A	3222	207	402	SILM*LCCLFPLPGVTPIDGAPHSYRE CYPVLLDGVVMVGWVDKDLAPGIADSLRH FKVMREKRI
3201	17102	A	3223	309	3	YPPFHLIDLAIHPCVCFKFKYKATVTQT AWSWYQIRYIDQ*NGTEISEIPPHIYNH VICDKHDKNKQWKGKDSLFNKWCWEN*LA ICRKLKLDPPFTPYAKI
3202	17103	A	3224	3	382	LDREPPPPFFWGAHMDIPQVNLNLSINK GHWANFNFLGYKKKGWEKKKKKKKKK RGGFP*KKPPGGPK*PPGGR*IFPYMG GKKKPPGGFLEKPPPLGGAHLGNPPQK YTPPGKKKNLKRET
3203	17104	A	3225	133	2	FFFETESHVTRLECSGTISAYCNLCLE GSSDSPASAS*AAGI
3204	17105	A	3226	349	2	AGVPPGNPPLWGGEGGGSPRGGGLKPGF PQRGNPFFFKKSQTPPGGGPPLIPPPW GGGAGGSPLPQGGRFQ*TKIGPPSPRG KKKKPPFPKKKKKKKKRKEKSEMPGFMV LNA
3205	17106	A	3227	3	239	LNKVGRCSEPRSRHCTPAWATE*DSIS EKKKKKPESRGILKVKGLTQALFYLA LYLHPTAKQIQWFFIYFSK
3206	17107	A	3228	205	1	IGLKIQNSCPLKDSLKKIKRQATDWRKY LQNTSDKASVFIYKEHLQLSNYKAVDP IK*WAKEMNKLH
3207	17108	A	3229	174	1	VQMLEDKSFEETP*FSSETLVLKIPHVQ PGAVAHTCNPSTLGGRGGRITRSGDRDH PG
3208	17109	A	3230	2	340	KNHSVYLLCVFSIPPPPTFCFF*F*VFNT F*FKLN*IN*FTYIDRVLLCHPGWSAVA *S*LTAALNSWAQAVPCLSLLAHHHAN LIIFKKTAYIIHIWVWYDTTYPFKVYN S

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3209	17110	A	3231	1	313	KKSTPYQRGFDPISPARVPFSIKFFLEA ITFLLEDLEALLPLP*ALRFIFLFTV GGLTGVVLANSLLDIVLHDTYYVAPHFH YVLSIGAVLAIIGGFH*FP
3210	17111	A	3232	207	355	ELSPRLKKTLY*LGMAHACNPSTLGA RGGQIA*AQEFKTSLGNMAKP
3211	17112	A	3233	3	355	TTQQ*LIKLTCKQTIAHNTKGR*ALI LISLIIFIATINLLGLLPYSLTPTTQLC INLAMAIP*ADAEVIGFRSKIKNALAH LLPQGTPTPLIPLVIMETINLLIEPIA LARRL
3212	17113	A	3234	2	355	KYLINNRLITNQ*LIKLTSKOMITIHN TKGR*SLILISLIIFIATINHLGLLPY SFTPTTQLSINLAMDIP*SGAMVIGFR SKIKNALAHFLPQGTPTPLIPLAIET ISLLI
3213	17114	A	3235	43	370	QGCVKGVLEEQVRRGWILDSSEKTDL KORGPSGSWEHVGWVGVMG*SEAWTG QARWLTPITALEAEVGGSLRPGVQWH NLGSLQPLPRFKRFSYFSLPSSWD
3214	17115	A	3236	15	356	LIQPSLKLMSIHNTKGR*SVILLSLI IFIATINLLGLRPYLFPTTQLSINLSM VIHL*AGAMVIGFRSNIKNALAHLLPQ TPTPLMPILVIEIETIRPLIPLIALAVRL TA
3215	17116	A	3237	1	376	GTRNTLTITIQ*WGDGTRETYQGHHTP PVQGLRYGIIILFITSEVFFAGFF*AF YHSSLAPTQL*GHWPTGITPLNPLEV PLLNTCVLLASGVSI*AHHSLENNRD QIIQALLITIVLG
3216	17117	A	3238	1	358	GTRNG*YTNA*ALSTIVIGASLTSAGGS RIILLTLTGQPRFPTLTINENNPTLLN PIKRLAAGSRFAGFLITNNISPGCFPQT TIPLYLKITDLGVTFGLLTGLDLNLYT NKLIIKA
3217	17118	A	3239	258	390	RQGLMLAGLVLSNWPQLQSSHLPKCV DYGREPPCLGN*LIL
3218	17119	A	3240	2	372	ARARFHHVSRDGLDLT*NTHLRLPKC WDYRREPLRPGKTFLLKKKKNSIFLFF REGFKESILGIKFFRPTGGVLITGNH GWGCKTGTLLVPSRFPGLAFKICGLWA HDTFHRVRNWL
3219	17120	A	3241	3	283	HERLWGGWKTGAAGLGRSSRPTASLTQ T*TMTH*SRITGCGSTGSGRTWTRSHS CAWGMAGLYRVAVASRGPRGMM*PTPPH WLCWAWKVP
3220	17121	A	3242	170	3	IKSQAGLVGFLGPPSFQDSLNLVVFVGF FCF*DRVSFCSPGWSAVVQSEPTAALV
3221	17122	A	3243	2	385	ARADVTPSYLSDTIMRDIPTGGQVFS *LSTLHGSNMK*TAAPLLTLGFIPLFTA GGLTGLELTNSWLDIVLHDTYYVGPDFH YVLSIGAVFAIIGLLH*YPLFSGYTLY RTYAQIHFAIIFIGEN
3222	17123	A	3244	1	106	GTRYVGQAHKLCLTSSDSPASTSQSAGI TGVSHSA*PASTSQSAGITGVSHSA
3223	17124	A	3245	2	360	ARANTLTITIQ*WSDVSLNTYQGHHTP VQGLRYRIILFITSEYFFSGL*AF* HSSLSPPTQL*GHWPTGITPLNPLKMP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LLNTSVLLASGVST*AHSLIENNRNQ IIQALLI
3224	17125	A	3246	17	160	GG*GCSCSEL*SCHCSPAWVTEQDFDSK KKPAILASCLKHLNPLSSH
3225	17126	A	3247	236	2	WAHIYMTPLSPSPFLKPVQ*KNFYIYST YSLDN*NPSSPKAKRAPKSYTLPLYLHL CVCVCECV*VCVCVCVCVCVWV
3226	17127	A	3248	2	2220	FFGGRRPSPPGYFLNNHSSPSPVVKL NPGPA*FYPTTKGKNFPPQR*PSPPKN IKTPPPSFFSS
3227	17128	A	3249	2	372	AYTISFIGKISFYGLH**LPKAHVEAPI VGSIVLAAELLKGGFGIHLTLIFNPL TKHIAYPFLGLSL*GISITSSMWLRQTD LKSLIAYSSISHIALVVTAILIQT*SF TGAFLLIIDHG
3228	17129	A	3250	293	56	EGSPKVI FNKSPPHLFLFLFFFFI PFF *FFFFFFF FFF FFF FFF FFF FFF LYL LAMEFYSFFFKQDNQRYRQYSIK
3229	17130	A	3251	169	370	LKMTELRGAPASKPRGQEPHPHYPCHHH HHHHHFL*VTKGQGP HHWPSPTRDPGW L*SPS*EDQRR
3230	17131	A	3252	22	156	GERIGLGLGGQGCSEP*LCHCTLAWVGD TVRPECLKKKKKKKGPPF
3231	17132	A	3253	3	400	QNQTPLLD*GGLITAVLLLLYLAVLTGG ITILLADRS LDSTLFYPAGGDPILYQH LF*FFGHPEVYILILPGFGIVSHIETNY WGGKEPPGFVGMV*AMIAMFLGFIG*A HHIFTVGV DVHTRA*FTSAT
3232	17133	A	3254	373	31	REVGPPPT*KIFFPKGLNFWGGGPKF PPPKKGGFFKSPVGVFPFPPG*KSFGP PGFKKPPQKGKNISFPAGGKIGPPRGTL KRAPPFFFFFFFLLWVVQVERP TL
3233	17134	A	3255	1	379	LNLIQRQ*R*V*KFL*LPPQT*KKKKKK KKKKKGGGAFKKNLGGAKFNGGRKKKI FLKGGVKKKAGGGFKKRGKGGKCYLGI FEKKPFFGGGKNWENPPKKIKGLREKKK F*GEKGEKKPEKAG
3234	17135	A	3256	42	376	FCYISLVHHCIVNDLSFERKKNI FVPGQ INSISSIA*EAHCNKSLHVKKKKKK KKKKKKKKKKKKKKKKRGEKKKKKK KEGRSSLKKEK
3235	17136	A	3257	353	67	CYPLSPLKFFFSRSLKFWKGVGPIISP PKKKVPSONSQEAGFPSPNVLKRPPGN FKTTP*KEKKNPFPVPVKGPPEKSLKR PPLFFFFCGLQ
3236	17137	A	3258	2	129	PHRISQDGLDLLSS*SARLGLPKCWDYR CEPFRPAKNKILLS
3237	17138	A	3259	205	415	QOKNRRLLHFKGARTHNSYNRGQPTTFS ITAHMYPRLRQSHITIVLRVHHP*VP IEGPVSV*ALLHSSSTIVVAGNLLIRFH PLAKSPLIQTVTLCLGANTTLVAGGWA LTQNDSKRIAAFSTSRGLIIVTIGVN QPHLALLHICTHAFVKALFMCSSGSIH NLSKEQDIRKIGGLLITIP
3238	17139	A	3260	3	393	SFNLSTLITTOEHL*LLPS*PLAII*F ISTLAETNRTPFDLAEAEVSGFNIE YAAGPFALFLIARYTNIIINTLTITIL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LGTTYDALSPELYTTYFVTKTLLTSLLL*IRTAYPRFRYDQLIHL
3239	17140	A	3261	2	400	ISDLSEK*FKRLVVKLIMEAPERGKAQC KEIQKMTQEVKGEIFKE*IA*RKKSKE QETLDTLIEMQSALESFNRIRKQVEERN SELKDKIFELTQSNKDKGKRIRKYEQSL *VAWDYIQ*PNLGIIGIPEBE
3240	17141	A	3262	450	129	NNLAFN*V*EFCVLAIKLLKVKRYPIEW EKMFANHISDKGLVSGIYKELFRLSNKQ AIDLTF*KWAAGHGGSPL
3241	17142	A	3263	238	3	KEKKIGLKKCLQSSHFSIHTAWSIIYIM FSPLTIIISRRKMQPGIYAHTCNPST*G G*GRWITRSGVRDQTGQHGKTP
3242	17143	A	3264	350	3	SPTLLGSKDPNLLGFRFPLWKKGKIIRA PLSLGLN*RFFSEVVLIP*KPPKNWPGG TFLVVCFLKRGFPFLSQKKKKKNPGAVA HACNPSTLGGRGGRSQQLETSANTV KTR
3243	17144	A	3265	69	200	RLECSGVISAHCNLLNLPSSGDSFASAS* LAGITVMVKLPVIAK
3244	17145	A	3266	223	408	GGFFFPFPGGEGCNFGELEPLPPGLRK FFCLGPPRRGD*GPRSSSPGSFWVFKKN GVSP
3245	17146	A	3267	185	420	DQGLWGFIIYFYRQSLA*VHWNPPSSL* PRTFGLKHTPVPSLLISWDYGRTPPHLT NFCIFFDRGSFFF*DRVSATHA
3246	17147	A	3268	3	392	TGCHSIPQAGVQWHNHGLLQPPGLR* SSCLSLPSSWHY
3247	17148	A	3269	1	398	KFSCISSKHQKLKLTTPKPPKPPKKSPL VLPIGKKIRETFWGAFKSPPPNQPKGAQ TLPLKIWDKMGGGGLALVV*KAPPGNF KGPPGKPMEQP*LGPGPPLKWKGGLPH QKGGFSKAPGEKKKGEGRL
3248	17149	A	3270	422	183	ETEVSLSFKVITTEKSPNLEKDTNIQVQ ESYRTPSRFILMKTTSRHLIIILPKVNN TERIL*MQQDRGNNIQWSSGCSA
3249	17150	A	3271	3	35	KNNSLIPTIIATITLNLNYFYLSPLLY **SSSPPS
3250	17151	A	3272	155	1	KDFFFFFLRQSFTLVAQAAEWCDLCSL QPKPPGFK*FSYNSLSSSWDYIG
3251	17152	A	3273	413	71	PPSTGLFLTEEYEVSPFPFPL*KFFFPF SGLFFGGGVPPFPFPKKGFFPKYPRLV FKGPLLGGGGLPPPPP*ILPPLGSFLPA PPLFFFLFLL
3252	17153	A	3274	336	45	DRVLSCSPAWRAMARSHDFG*LQLPPPR VKVFSCLSNPSSWDPRHVPPRKGNFVFL VKTGNPNWLGQGGCRERRLCPCIPAWGT DKDSVSKKKKKS
3253	17154	A	3275	206	366	SVFFFLVLFGLFYGALLCFPNPWLECSGT ILVHCNLFPGSKDSSASPS*VAGT
3254	17155	A	3276	334	75	ENTRRVERRRRTHIIYNNFF*EFMNRFF FFIFFDGRFSCVFFFLFYFFFFFFFFFF FFFFFFFFFFFFFWFSARSFIYFLFPRH VT
3255	17156	A	3277	144	17	KAPPLFFFFFFFFFFFFFW*FRG*T HWNGDACMCNLTKS
3256	17157	A	3278	2	109	YHIVKPS*PLTGALSALLMTSGLAM*F HFHSITL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3257	17158	A	3279	404	65	NLVSSPKRSVFFISPSQKIFFFFFNWKE SKISLPKEGGPLLLLIRQRTPIFFFFF FYFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFL*TA CLP*TFKFTKTK R
3258	17159	A	3280	226	383	GI*KNSMDGCCLGPFVVFETGSHSHPGW SIVWRNLGSLQLLPPKFKRFSCLS
3259	17160	A	3281	91	26	LFFFFFFFFFFFFFFFFFWSERS
3260	17161	A	3282	3	321	HTVIYYFGKNEPPGYIGVA*AMISVGS LGFMA*AHHIFTGGIDVYSPAYLTCATII VAIPTGVKVPF*LATLLGSGMKRSAAVL *TLGFIPLFTARGLTGIVLSNS
3261	17162	A	3283	393	112	PPLRVFFPPPLKNFFSSRRFFFWGGV APFFPPPKKGFSSKIPPGFFPPPLKKK IFFSSPP*FWAPPGFELKGPPIFFFFFF FFFFFFFF
3262	17163	A	3284	360	47	PPLHRWVPPPPP*KFFFSPTKFGKV SQNPFPKKSFFPKNPPGVYSPPKKKK KFFLPPPIFFPPPRFFFTTPPPFFFFFF FFFFFFFFFLFFWSVSF
3263	17164	A	3285	386	157	FFSPNPLIFWGGGGKFPFPKKRFFSKN PPGVFFSPPLKKKFFFP*NLAPRD FLKGPPIFFFFFFF
3264	17165	A	3286	3	385	DAWVPCPLYLVFFPCRFBKISAILILKI LIFNIENKSI*YLLKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKPTPKKKKK KDSR
3265	17166	A	3288	81	270	IIKLEKKKKKKKKKKKKKKKKKKS*KGNE KTRGPKKKVHRDVTKKILCYKICPFNKG ISLIGT
3266	17167	A	3289	3	145	LGRLRQENHLNLGG*GCREPKSHRILA WATEQDSISKKKRIGGPV
3267	17168	A	3290	404	47	GPGGKIFFKKNPBEKIFSTQKKKGFFFP FPPKNFFPPPGGFFFWGGGPIFPFPKK GFFPKIPRGVFTTPPKKKIYFFPPREI WAPPGIF*KGPPLFFFFFFFFFFFFFLV LNDILA
3268	17169	A	3291	106	362	KKKKKKKKKKKKKKKKKKKKKKRMRNK KKKKKGRGGKKKPRGAQIIIRGKKKII FFKKVK*KGGDL*KKKSFCGNNLE NTHKE
3269	17170	A	3292	3	226	NPLVNLNLGLLFILATSSSLAVYSIL*SG GASNSNYALIGALRAVAQKKKKKKKKK KKKKKKKKKKKKGGVL
3270	17171	A	3293	337	2	FFNRELLKSKNKETEKNDYHKERIWHF DRPYKFMFLFCFGLIFFLYLPFFIYF FFFFFFFFFFFFFFFFFFFFLNSLNI*F FSINTHKCGNRGQGGGAIGRLSNGRV
3271	17172	A	3294	327	21	KFFFSPPNKYFFVFPHKFTPTKMLF* KIPPPPLISPPKENHQCPPPPIFAPP SHPPFGPPHFFFFFFFLFFELWRTGSRY IAQAGLELLGSSYPAS
3272	17173	A	3295	367	101	FFFSFF*KKNFFPPPLWPPPPNPL*N PPPPFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFLVNSLCRRYR*SLLY YAWL
3273	17174	A	3296	178	2	KGPPFFFFFFFFFPDSDITLFIITKNEK KTRCTSIGE*ITWYHTTGEYYSVMKRN

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3274	17175	A	3297	147	1	RGPPPPPPPPPPPPPPPPPPPPPPPP FFFFFFFFFFFTW*FALIFLV*NPF ⁻ AITF
3275	17176	A	3298	3	347	PFGEGETNGRFDLDTKKALVSKKKK KKKKKKKKKKKKKKKKKKRGGALKKN RGQGKTGTGEKKKKFFFKGEKKKTPGNF *KKKKFLGGDNLAQTTPKKKNLWGKKKNFWG
3276	17177	A	3299	405	2	WRPKPENSPSPGGPNPQQNK*TPFPKP TPKLGRGCCGAQPFPLPVARGENPPNP RFLGFN*PKFPFPFPFAL*GGNNETFFQ KKKKGPFPWAGVLPTGGAEGESIPHLSP ASGSRRHPWCFMLCRPSRLCLL
3277	17178	A	3300	125	376	DQPVNSETSSLLQKKKKKKLPFGGGG PLFPFHLCGGGGGTRPPG*RKRKSGV PQPPPPGGRVPPPPPHPPKKWGNKGPP PGKSFFFFFFFFRWDEVSILFCTGWSQTOT POLQSIIHLSLPRWLIDYGREPPLLAIHF FPTRPRTRG
3278	17179	A	3301	348	1	PORLKILGGGGPPNSPPPKGFFPKTFR GF*NPPPKGKKKNFPPPRKIIPPQGGF* RADPLFFFFFFFFGWFFFFFFFFFLLENG VSLYCPGRSRTGLKLSSLRASLRAGITGV
3279	17180	A	3302	2	354	GRVGGRVGSPTTLTT*NPHSEKHTPSCS YPKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKRKKKKKKT*GGGAYIKKKG GGSPRTEENQYCFLGGKKNILRGSCCLKTTH
3280	17181	A	3303	362	26	SSQAAPTKKKKKKKKKKKKKKKKKKK KKNFGGGKNGKGGKKKIFFFGGGKKNP GGNFKKKNFFGGGKIGENPPKKK*FRFK KKKFRLRGKKKKS
3281	17182	A	3304	371	3	NQKKPPPVVVFFFVKKKKNPPATPPP GRP*FFPPQKKFPPEGGPPPFKKGAFF PPPKKNPFEPFFPGGVFFF*KKNIKVF PPPKKKKKKKKKKKKKKKPKKQKKGR PARDLEPHAS
3282	17183	A	3305	2	196	DR*LFSSTNHKDIGHTLYLLFGA*AGVLGT ALSLLIRAELEGQPNGNLGNNDHIYNIVT AHAFVIIIF
3283	17184	A	3306	4	339	LFSSTNHKDIGHTLYLLFGA*AGVLSTALS LLIRAELEGQPNGNVGNNDHIYNVIATAHA FVIFIFFIVRPPIIGGGFN*LNPLIIGAP DRAFPRIINISF*LLPRSILLVRASAIA
3284	17185	A	3307	2	367	KPPAITQYTPLFV*SGLTGGLLLLLFL PDLAGITILLTDNRNLNTTFDPAGGGD PILYQHLF*CFGHPEGYILILPGFGIIS HGTYYSGKKEPLGIYIMV*AMRSIGFL GFIE*AHHIL
3285	17186	A	3308	243	370	KGHRPQMVTVCNPNSTLGQGGWIRRSG I*DQPGQGVDTPSL
3286	17187	A	3309	2	363	LVPLIIGADPMVFPRINNIGF*LEPPCL LLLIIAYAIMEAGAGTG*TAYPELAGNYS HPGASVDLTIISLHLAGVSSIILGAINFM TTINI*PPAITQYTPLFV*SVLITAG LLLLCLPG

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3287	17188	A	3310	1	364	LYITGPTLTALTIALLL*TLPTIPNPLVN LNLGLLFLATSSLAGYSIL*SGGASNS NYALIGALRAVPQTISYEVTLAILLST LLIRGSFNLSTLITTOEHL*LLLS*PL AII*FISTL
3288	17189	A	3311	215	2	GMAKLKARFLPKKGGKRSLSPLWNGSGF PTSGTGGETFFFF*DRVLLCQPGWSAVA QS*LTASTFWAQAI
3289	17190	A	3312	153	3	MNKCICMVCVCMVCVCRSHKHTVCAWVCV Y*V*TYTVCVCVCVCVCVCVCVCVCVC
3290	17191	A	3313	149	1	KTPPGFFPGFKGPF*FKGPPLFFFFF ETEDGVLLCRPGWSAVSRDRA
3291	17192	A	3314	282	69	KIGKTAPFFSWPRVPFLKKKKKK*GL TLSSRLVEYGMISLELLGSSDTLASASR VARIIGQCPHAWLT
3292	17193	A	3315	479	60	MMQHSIKHALVEITGWVRWLRVPVIALW EAEVGEFNSISKTNNRKRSNIVKMSILF NLIYRINAPFFKFLIALLNKNSKSIW NLKS*STQ*SSRNVGGITISDF*THQ QATELRQEFHHTGLVHRSTVSRFRFHA
3293	17194	A	3316	129	3	SFHQKVPDVAHAACSPSTLGG*GGRT GSGDQDHPQHQGE
3294	17195	A	3317	3	156	EFHRVSDQGLDRLTS*STLLGLPKCWDY RCEPPRPASFPSTLTVRISPF
3295	17196	A	3318	36	340	TGLVIAEHLFFFFFKGFWFCPPGGRAG PQGNLMEFPVSGGKGFICPGPPKSGE*R APPPSRGKFWFFKKKGLFPWPGGV*TS DPRGTPPPLGPKGGEYR
3296	17197	A	3319	326	2	KAPFLNFKPHPGFA*GLKFKPNSLLPI* SFIRKT*AFLICL*IQLNRADGKIPLKP GVIPFKKCFPNFTPLFFKNCSTPNL FFFFFFFFFGDGLSLCRPGWSAVA
3297	17198	A	3320	175	312	QAGVQWCDLSSPXPPPSGLT*FY*CSLP RTWEYRCPPSRPCNFSIF
3298	17199	A	3321	363	51	RWGPRLPVAWLPSVSRRAECSPPGRGAH GQGGGGGQAR*REGPDWTGGAPVGMG SPSLNRGAGRPPQPGPSSKSRGRVRC TPHSLIGCGLSFFICKMG
3299	17200	A	3322	344	187	LRQETCFNPGGKNFG*QKLPPCPPAWAT RGWVSKKKKKRKRKEKIRICVLT
3300	17201	A	3323	3	313	TRRERERERERERERERERERERERE REREFFFFFFFF*KNLSPPPGGKRGGGG FHSPPFWGEKDFLPPRPKGGGERGRPP PPVFFFFFFKKEGAPPGGGV
3301	17202	A	3324	365	1	SLGWVRVTPPPFPLGPRGSGPPRPDKRG SPGRVKFGGVKPPFKVKP*PPPKRLDPS GA*FFFSPPKICQGPPIPRKKKKKEAELS ILCTKFPPLQEEBVMQVPPFPCTCSSEPG INICKRHC
3302	17203	A	3325	1	269	ARALSLSLSLSLSLSLEFFFFFLAPT QILGGGLFYPPKGAHLSNRLGGGRVFF GPPGKKTAPLGGGRVIKKTPPGTPL*L SPPPGGPPFFQGGQKLSPPPAGLTGGP PPWGGKAPPPKFGSGPKKKKKTLENER ERERERERERELV
3303	17204	A	3326	1	316	ARGERERERERERERERERERERFFV SPPGPDTLQDRGGVSLFASDPTHEIYLP CPLRGPLSERDPBELHGVCFFSEPSHRW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M. eth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3304	17205	A	3327	2	369	FPEEGVGDICQC*HRGECGSP ARGDVTRESTYQGHHTPPVQKGLRYGII LFITSEVFFAGIF*AFYHSSLSPTPQL RGHWPTGITPLNTLEVPLNTSVLLAS GV*IT*AHHSLENNRNQIIRALLITII LGLYFTLLQA
3305	17206	A	3328	1	259	GTRKKHSTILIIREIDIKFMPRFHISPI RLVKI*ALANIRC*QCCGKVGNNLLHC*F SKLVQSTGRAIWHALVLSLARSRLSLS LH
3306	17207	A	3329	2	352	ARGTLLLLCLLFFALTIYFRWCDVTRKS TYQGHHTPPVQKEPLVLGGKLFITS*VI FFAGFF*AFYHSSLTPTPLGGHWPPTS ISLFPNPKPLNTSGLLASGVSI*AH HSLIQ
3307	17208	A	3330	3	361	HEEPLGYIRMA*AMISIGFLGLIVRAHH IFTGGIDVDSRTYLTSAII IAMPTGGK VFR*LATLHGSNMK*SGAGL*ALGFML FTVGGTLTGIVLTNS*LDIGLHDTYYVVA HFHYVLS
3308	17209	A	3331	1	340	GTSGDTRAYFTSATIIIAIPTGVQVFS* LATLHGSNMK*SAEAL*ALRFIFLFTVS GLTGIVLANSSLDIELHDTYYVVAHFHY VLSIGAEFAIIRGSIH*FPLL*GYTLDQ T
3309	17210	A	3332	2	352	ARGDVTTRAYFTSGTIIIAIPTGVKGFS *LATLHGSNMK*SAEAL*ALGFIFLFTV RGLTGIALANSSLDIVLHDTYYGGAHFH YVLSIGAVFAIIGGFIH*FPLFSGYTLD QTYAK
3310	17211	A	3333	85	370	QVSHRVRPCFERRRERDRYRHTQRECE AKEIYSGFFLSASEMESCSLAQAGGCKE LRMCHCTPAWVTQGDVCS*NKK*HWEKK GLWFLGVNIST
3311	17212	A	3334	362	3	QEVKVSMMNRDHTSLQGEQKRNVSVKK KKKSSQEKLRVHTQTH*IFI AVLPIV AKNGKQKFPSTCEWINNM*YIHTMEYY SATKNQLIHVTT*MNLNNIYTKFLKARQ KMITYSC
3312	17213	A	3335	3	351	HEGTTLHHLFLLTGSNNPLGITFHSDK KTFHPYTIKDALGLLLFLLSLMTLTLL *PDLLGDPDNYTLAHLNTPAHIKPE*Y FLPAYTILRSGPNKLGGPALLLSILIL AIIP
3313	17214	A	3336	17	350	FIFLTETNRTPPDLAEGESELFSGLKI KYAAGPLALLFITETNTIIIDTLSTTI VLGTTYDALSPELYATVPVTKLLVTS FL*IRTAYPRLRYEQLIHL*KNFLPL
3314	17215	A	3337	2	349	ARDSLISPIRLRHPNLRQNAFHYH RGKSNFLPTLSRPIRNAPTLGLPRCI HMKHPHIIICRLIH*FPLFSGYTLDQTYA KMHTIIIFIGVNLTFPPQHFLGLSGMPR RYSYDPDAYTT*NILSYVGSFISLTA LIIFMM*EAFASKRKVLIVEEPSINLE* LYGCPPPYHTFE
3315	17216	A	3338	2	386	ARAILNAMAFILTERKILGYIQLHRGP NVVGPYGLLQPFADAIKLTKEPLKPAT STITLYISGPTLALNIGLLL*TPLPIP

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						PLRNLNLGLLFIATSSSLADYSIL*SG*ASNSNYALIGALRAVV
3316	17217	A	3339	175	16	ILGDLFPPAWLHPFLFLLLFSSRPSLAVTEAAVQWRNLGLLQPLPGY*SSWC
3317	17218	A	3340	1	369	GTSNLSLLPIVATCGLAAN*ML*GGKIN*YTLRVALAAIHTILYBITLSIILL*TLISGSFNLSTLITTQEHL*LLPS*PLAII*FISTLAETNRTPFDLARGESEL*GLNIEYSAR
3318	17219	A	3341	1	363	GTRGGTILPAMVLMILIDVPSLRILYITNKVNEPSLTIKSNQHQQW*TYQYTDYGGILNSYILPPLFLQPGDLRLDVRNVLPFIETPIRIINT*QDGLHS*AGPTLGLKTDALAGRVNQ
3319	17220	A	3342	181	315	PKSPPTPPPTTXXXXXPGGNPPGPTL*GPFYWGGERGPPF*TGGP
3320	17221	A	3343	3	183	HEVSQSCRELLTSGDPPASASQSAGISGMHRAWPV*TFHIFNIYCGPGTVLKPYNL
3321	17222	A	3344	83	354	VLGARCPCAGVSRVSMPEWFLWQOACLLPWWRCCLSTLYANRADRDVP*TSRTGPVMVAHACSPSTLGGQGGWVTRSGV*DQPGQDGETP
3322	17223	A	3345	124	379	GQGICFMVVSGLSLHRLAHCRTYVGVNNLLCSSSLPFLPLPLPPPEGPGWDDINIIIFIIFRDKVLLCCLGWSAVT*SQLTTA
3323	17224	A	3346	3	368	YEPID*PLTGALSALLMTCGLAM*IHLSITLLILGLLSNLTIIYQ*WRDVTRESTYHGHRTPPVQKGLRNGIILLITSEAFFAGVF*AIYHSSLAPT*PQLGGHWPTGMTPLNPFVQGPLL
3324	17225	A	3347	1	352	GTSAGDVNYG*IIRYLHADGAKIFLRCLFLHSGRGLYGSVYVSKT*NIAINLLIATIAFAFIGYVLA*GQILF*GATVSTNLLSDIPYIGTDLISQRI*GGYSVDRLTLTRFTTFH
3325	17226	A	3348	2	360	ARAEISPLHSNLGNESETPSQKCKKKKPPGGGKKNWNPYPSPGTPPNPPKGG*REPPPLTKRVF*KKKVFFEGPRVKKNLGGKGGKRGPPAR*KNPVFKAKGGRNFGPQAFFFKK
3326	17227	A	3349	226	366	PQSFCVSVASWPAGDLMEI*AWQKFYKPGKVPMDPEGCLLPLAKKKEEEEEEEEEEVEEEEEEEEEEEEEEEEEEEELV
3327	17228	A	3350	2	374	ARGGGYSPHRATLRTVTFHSLPFFITAGLAAIHLLFLHETGAYTPL*ITSHSEKTTFHPYTMKDALGVLLFPLSLTTLTLCSPNLLGEPHDYTLTNPLNTRPHIKP*DCLFAYTNMRSGPN
3328	17229	A	3351	1	266	LGLVEHPLTLTTLTSSNISDAQEIQSV*NILTAIILNLMVLPRLMLYITNEVFDPSLTIKSIGHQWY*AYEYTDGGLIFNCYILP
3329	17230	A	3352	207	362	ILFLLKQKIYVLPQFSN*GSSIPELAHS DAYQTKEICSSGKVYKYLQCBKW
3330	17231	A	3353	178	365	NHGIDKGLRYRIYTVQEDNSVKR*LKD FNQHLSDKNIRSADKHKRCPTSLVINI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						MPIKPP
3331	17232	A	3354	359	3	LQVRSIMPLGQFHPP*NFFCSFFPKPKI PFFFLFFLKGVFVFFPGWRARGQFVWVG PPPPKFKKFFFTLLRNWGFDPFPPSRG KFFFFFWYF**RLRFTMLTRLVFN* PQVISC
3332	17233	A	3355	2	354	AREPSP*PLTGALSALLMTCSLSM*IHL HSITLLILGLLTNTLTITQ*WRDVTPE TFQGHHTPPVQKGLGYIILFITSEVPF FAGFL*AFYHSSLAPTPLGGDNFPTGV TPLNAL
3333	17234	A	3356	1	364	GTREMICCSALSPRIHLSFHRRWPDWEC ISKLTIRHRTTRHVLRWSSLPCLPINRS WICHRRRLHSLISPLRLHPKPNLRQNP FHYIHGRK*SAAVL*ALGFIFLFTVGG LTGIVLANSSLDIGLHDTYYVGAHFHYV LSIGAGFAIIGGFH*FPLFSGYTLNQT YAKIHFTIIFMGVNLTFPPQHFGLSGM PRRYSDYDAYTT
3334	17235	A	3357	2	376	ARGGQPEDYILILPSFGIIFHIVTYYS KKEPFYICMV*AMISIGFLGFIA*AFP IFSVGIDVNTRAYFTSATIIAIPITGVK VFSWLATLHGSNMK*SAAL*ALRFIFL FTVSGLTGIVLCN
3335	17236	A	3358	357	139	AQPWFFLETVFCHAAQAGLKSIGSSDL PTSASQSVGTTGMSHAWPERS*QNTF TYVQSIYSDDIRKSMF
3336	17237	A	3359	277	1	SCQKDISIGFLFVPGFRVKGVAQEHV VRMYVLVPTVGGDGKERER*RGIRHTPP PSERVQRERERGRDRDREKERASQRK EMDRETS
3337	17238	A	3360	261	2	TICKCAWLCFSKTLTNTCASRSDLAH GP*CPNLCSGIFSSAWTDISRLILFFCL FVLRQSLTVAQAGVQWNCNLCSPQPLPP SC
3338	17239	A	3361	199	354	HLPYWPMFMATFNFFFFFETEFHFFPQA GGQWDFG*LKPPPARLKQFSCLN
3339	17240	A	3362	3	364	HEDRDTPAYFTCANIIAIPITGVKVFN* LATLHGSNMK*SAAV*ALRYIFLFTVS GLTGIVLSYSSLDIVLHDTDYVVAHFHY VLSIRAVFAIIGGFH*FPLFSGCTLNQ TYAEIHFT
3340	17241	A	3363	3	360	HEETIIPKDKYSFLHDSQTSFCFSNSI PTPSNMEETQQSVSGCRLP*AGMGETC GQGSRAAQPLPSLPLQNLKLLRISLLLI EAWLEPERVLKSMFANNLGYDTSDDY HLLKOLE
3341	17242	A	3364	352	27	VYLSSQRNSAASVNRMTVVTDRLSPYT LGWHRPDLRFHFVFSLFVYTFVERGSQ IAQAGVQWCDHSSL*P*TPGLK*TCSC LP*VAGTTGTHHTGPLILLNLN
3342	17243	A	3365	347	99	GGPPLPRGFSPPPGARPLAPPWGPORS PPPPPKTAPQKKKAPSI PAGQWLVQ NPRPQPFKKPPGVGF*NPPPLNMGF
3343	17244	A	3366	3	319	HEECLAHTLCFFNLMS*RTTVILHRMFS IVTAI*YLLSSQYVIGYIYVCIHHTH MYIHTHRHRTFICVCVCYIYTSIC
3344	17245	A	3367	3	474	YELLLLNGEILNARAFLLITERKILGYI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QLHRGPNVSPYGLLQPPFADAIKLFKE PLKPATSTITLYITAPTLALTIDLLL* RLPIPNPLDNLNLGLLFIATSSLPVYS IL*SG*A*NSNYALIGALRAVAQTI**E VTPTIILLSHYKKWLRN
3345	17246	A	3368	2	348	ARGLQDATFPPIIEELITPHDHALIIIVL ICFLGLYALFLTLTKLTNTNISHAQEI ETV*TILPAIILVLIALPSLRMLYITDE VNDPSLTIKSIGHQWY*TYQYTDYGGLI FNS
3346	17247	A	3369	64	363	KKWGFVPQKKGGGRISVNGTPIFKGKG NFPF*PPGEGGTGPGPKPK*IWIFKKR GGLIFWPKQFPTPGPKGTHPPGPKGGK *RGPPSPGGFNFKRG
3347	17248	A	3370	34	355	AKGKEYIETVAEKKKKKKAPPI*KAP *NPGKKPLALKFPFSPKAPPALFCP *KGPFRVFPKKKKKFPFGRKGFFFTG GKPP
3348	17249	A	3371	1	374	FLHSLHLSLRLLYLP*KFSMFIIILLKAY YTLCVCVCVCVCVCVCV*PLNKIHINHF TCSTVRGRSNPIFFPELLN*RPFYTT
3349	17250	A	3372	429	3	FFFFLKKQKISRVPFRGPEFFGQRKPFW AKGPPRAPQKGGEKGNPSPPPLIFFK KGEKPQGGPLFKKGLGFFSPPKVFEEKG VFKSGPGGP*NFGFRGFSPPSPPKGGK KRKPQSPGFFFFFIFEILGCSGRSRSR T
3350	17251	A	3373	2	404	LGTDLSLIIRADLGQTGDLGNDHIYNA IVTAHAFETIFFIEIPRIIRGFN*LIP LIIGAPDMAFPRINNISP*LLPPSILL LASAIVEAGAGTSGTDYPLSGNYSHPG ACVDLTILSLHLAGVSSILGAI
3351	17252	A	3374	2	417	AFV*LAHITRDVYVG*IIRYLHAKGARI FFMCLFLHIGRGLYGTFLYSET*NIGI ILLLATIATAFIGYVLL*GQISP*GATE ITNLLSAIPYIGTDLIQ*I*GGYSVDSP TLTRFTTFHILPFIAGPNPLHIT
3352	17253	A	3375	85	1	FWPGAVAYACYPSTLGG*GGWIMRSGVR
3353	17254	A	3376	396	1	KEGYIKGPRGENFF*KNPERKIFSRQRK GGVPSPLPPKKFFFPKGLIFLGGGCP FPPPKRVFSKNPPGVFINPP*KKKKIF SPPPENWGPFRVFLKGPFFFFFTFFFF FFFFFTLFLGGCGYNTKLR
3354	17255	A	3377	3	118	LLPPSLLLLLAYAILVAGAGTG*TDYPP LTGNY*KTKA
3355	17256	A	3378	301	82	ERKGPQRGGKKGPKAQKPEKKPKKRP PPPQN*FFSNPPKKKKGKDPPSKKRG GKGVPPPRKKKKKKKE
3356	17257	A	3379	2	195	DR*LFSTNHRDGTLYLLFGA*AGVLST GLSLLIRAEQGPGNLLCNDHIYNVIVT AHAFVIF
3357	17258	A	3380	21	411	VFCTNH*DIGTLYLLFGA*AGVLSALS LLIRAEQGPGLLGNDHIYNVIVTGH FVMNLFIVIPPIVGGSGN*LGPLEIGAP DMAYPRINNIGF*LLPPSLLLLLAYAIV EAGAGTG*TVYPPLAGNY
3358	17259	A	3381	2	421	GRVGGRVGSTNHRDGTLYLLFGA*TG V LGTALSLLIRAEQGPGNLLGNDHMYNV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IVTAHALAKIFFILVPIIIGGFQNGLVP LIIGAPDMAFFRISNISL*LLPPSVLLL LESVIAEAEAGTGRTVYPPLAGTYSNPG
3359	17260	A	3382	3	185	VIYSTIFAGTLITALSSH*FFT*VGLEY NMLAFIPVLTKKINPRSTRAAIKYFLTQ ATASIILLIAILFNNILSQQ*TTTNTTN QYSSLIIIMAIKLGIAFFHF*VPEVT QGTPLTSGLLLLT*QKLPSISSRKQPH P
3360	17261	A	3383	5	398	FFGHPEVYILILPGFGIISHIGAYYSKG KEPFGYLGMA*AMISIGFLGFIA*AHHI FTVGIDVHTRAYFTSATIIIAIPTGVKV FN*LATLHGSNMK*SAAAL*ALGFIFLF TVGGLTGIVLANSSLDIVL
3361	17262	A	3384	1	250	LGNTGETLSLQKNV*KLARCGGTCLRSQ LLRLRK*EHCLTPGGRGCSEPRSCHSSP AWATGQDLSQQQQQKYPLRIFSAIIS
3362	17263	A	3385	456	0	IFFFSQVETGIHHIGQAGLQLLTSGDAP CVGLQKSWDYRPEPLHLAWLIHSLLSNF YYC*FGPKLSVFILINVCNKTCSNM FLFSYS*NPCAQ*KNEGPLLKNKPCRIT DAWADAWVAPVF
3363	17264	A	3386	1	225	PSRNFLVLVDKLLKFT*KYRGPERTAKT TLKKKKKVRLTLLIFKSYKTIIVITIG WYGFQDRQVD*WNRISLE
3364	17265	A	3387	3	400	LLILGLLTNTLFYYP*WGDATESTYQG HHTFPVQKGLRYGIILFTTSQVFFAGF F*AFYHSSLSPTPLGGHWPPTGITPLN PLEAPLLNTSVLASGSIT*AHPLIE NNPNPIFRALLITNIGLYF
3365	17266	A	3388	24	407	IASGRPFPPPPFPKGFISRGGGPFPS PPKI*KNWGKGSFPPPPQREPCKRGVP KNPSLSFYFPGGKPPPLGPPKLVPPSS* PGKKAFFFF*TPPPGFLTPLGGLSPLK GGYLLAPHFVPTGGL
3366	17267	A	3389	148	413	LNLNNNNNGKNHLLNTYSCT*LEEKKKK KKKKKKKKKKKKKKKKKKAPGGGF
3367	17268	A	3390	157	14	RVSACCQVWW*MPVVPATREAREARELE PGRHRLRSCHCDRDPVSKS
3368	17269	A	3391	2	398	LFSTNHKDGTLYLLFGARAGVGTALS LLIRAEELGQPGNLLGNDHIYNVITAH FVINFFIPIIIGGFN*LVPLIIGAP DMAFFRINNISF*LLPPSLLLLVAYIV EAGAGTG*TVYPPLAGNYSH
3369	17270	A	3392	2	395	DQKDIGTLYLLFGA*AGVLGTAVSLLIG AELGHPGYLIGNDHVYNVITAHAFVII FFIVIPIIIGGFN*LVPLIIGAPDMAF PRINNISW*LLPPSLLLLLACAIVEAGA RTG*TVYPPLAGNYSHPGA
3370	17271	A	3393	396	54	GYPNLTFTVSSLTSPSPSPSHPPSHVCS PTPAIPQTPRSPSESTPPTVSLTTP LSLGAISSLASAGPQGASPASPGFWGTS PP*PYS*NRPQTAACGVFSQLFFIRPEV P
3371	17272	A	3394	417	60	KGWVFQRIWPGPGGSPRYSRPFPGGPRG LIPLGSGV*TPPGPHWETPFFFMNQPI GQGGGGPLIPLGGVKPEKIFYPGNQSF H*PKIPPHPPPLGAKQNFPPKKKKPKQK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TKGFWV
3372	17273	A	3395	417	3	FFFFFQHHFGFEAAA*YWHFVDVV*L FLYVSIY**GSYSFSINS
3373	17274	A	3396	229	1	RSFWTKTMGFSCYKDFP*TGNKDTTYQ NLWDTAKAVLRGKPIALNVPINKLERSQ ISNLSQVKEGQAWLMPVI
3374	17275	A	3397	344	165	ELKSPQPRKNGCFFLAVDPEGF*NLN FCGNGQGLNAPGGYPCPIPMGFVFNAYG KTF
3375	17276	A	3398	1	409	HKDIGTLVLLFCARTGILGTALSLLIRA ELGQPGNLLGNDHIYNGIGTTQALVRIL FVIVPIITGGFGN*LIPLIIGAPNMAVP RINNISF*L*PPSLLLLVAYGIVEAGAR TG*TGYPPLAGNYSHPGACVDLTM
3376	17277	A	3399	3	396	KDIGTLYLSFLS*AGVLGAALRLLYRAK LGQPRNLLRNDHIYNVIVTAHAFVIF IVIPITIGGFGN*LLTLIIGAPDMALPR INNISF*LLPPSLLLLLAYGIVEAGART G*TAYPPLSGNYSHPGASV
3377	17278	A	3400	49	350	KNSHTEVQAGQEQKSPFRSKHKAGRAG SDPAPYVLGAGCLCRSISFLFFFSLFF FFFFKRDGV*QGYSSGNTPGVKQSSCL GLPKYWDYRREPLHPA
3378	17279	A	3401	1	398	KPPAITQVQTPLFV*SVLITAVLLVLSL PGLGAGITILLTDRSLNATFFDPAGGGD PILYQHLF*FFGHPEAYILILPGFGIIS HIETYYSGKKEPFYIGMG*AMISIGLL GFIA*AHHIFTG*IDVDTRS
3379	17280	A	3402	388	42	TPLENPPGAKCVNPPFPKLLKKKNPSRA MGGPPLPPLWGGKPKGFP*NRKSGAPV THFAPPAPPPGGKREPPPKKKKKKKRK EEKESNRAVQIKKRGKKGRPLVLDPAE ESQ
3380	17281	A	3403	413	2	SPHPLKNFFLPKPPNSGGGLAPFVPPQ K*GSLPKIPRGYKSPPFKEKTNALPPR GKPGPPRASSKRPLFFFFFRGRVPLCH PG*STVQCVAQCTLELLGSSNFLTSS PVTWGRQGPFRPINFFIFFRGRVP
3381	17282	A	3404	433	274	LGVVAHACNPSTLEG*GGRTAWSPGVQD QPGQHSETPISTNFFWYFRISYFHI
3382	17283	A	3405	131	427	GPPPPQFFFWGKRGGPNPPFFFSKRD VF*QFFLRRRGPQKFFKPPFFCLQKTSL FSEKKKKKGFGPPLFPQKKKCGGGPHY KKEGFTLNSFLPQGDGVSSVAQAEVQWR NISSLQALPPGFT
3383	17284	A	3406	413	137	SPPPPPGGGIFFFFKPR*ETFSPPPNLG FFSPPSPLKFFFPKGFIFLGGGPKFP PPKKRFFQNSPGGFFFPF*KKNFFFL PPVILGPPRVFF*GPPPPKK
3384	17285	A	3407	319	540	IVFKDQCEESFTTLNVDIRNHQNLDSL EQHGKGDLL*GANAYHCEKCNKKVRAVQ LCLILITFNGFRKNRFFW
3385	17286	A	3408	2	403	SLHLGGGSCIVGAIYFITTINIKPAGI TOYQTPLFV*SGLITGILLLLSLPLVLA GITILLTDRNLFTTLNPGGGDPILYQ HLL*LLSRPEVYIILPGFGIISHIGTY YSGKKEAFVYIGVV*AIISIGC
3386	17287	A	3409	2	142	KKENYRPVSLNRDAKSLNQIQLHI*KTI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						HCNQVGFIPGMQGWFNIL
3387	17288	A	3410	407	48	PPGGKIFFYKNPEKKIFPTQKKGVFPP FPLKNFFFFPRGKIFGGGGQNA PPPKK GFFPKIPQGVF*SPPKKKKKNFFPPGKI WAPQGVFLKGPPPPFFFFFFFFFFFFFFF FFFLGVR
3388	17289	A	3411	3	402	SYRLE*QLEDKAAPPQDFTQQLRWPEKQ HRMVWPKDEDMHKQLVEASETLKSQAKE L*DAHQQQKLALQEFLEFNELMAELYSH NHKVWDKEEBMEVAMHKADMMWQEI*RS KKLTKRMLFTQMRRTITPVIPS
3389	17290	A	3412	1	224	LLFQLRLRLRQENHLNLEGRSCSELKMH HWTFPWGT*DC* LKKKQSAYLENNITI KKLTGSRTIEDICTEYNK
3390	17291	A	3413	202	1	IVMSWPGVVTHA*IPSTLGGGGWITRS GVRDPLASAFQSAIGITSVSHCSQLIFVT VFYLSPLSHLY
3391	17292	A	3414	407	309	PSFKASKDRLTLLLGANAAGDLKFTPMF IYHSENPRALKNYTKSTLFPVLCIRNI KAWMIAHLFTAWLNEHFKPIVETHCSGK KISFKILLINKAPGHRRAQMERHKMN VFMLANTTPILKMDQGVF*TFILCLSI
3392	17293	A	3415	404	46	LKKPFFQKFLKILKKKKGGGGGPPPT PPFGGGRGGVPPRAGVSKNPVPQGETLF FFKNPKFFGVGGPAP*FLLRGVNNKNF FNLGGGGFKKRKFSPPPPPRGKKFFPK KKKKKKE
3393	17294	A	3416	23	404	SVLITGALLLLSMPVLGAGITILLTDNRN LKTTFDDPAGGGDPILYQHL*IFGHPE DNILILPGFGIGSHIVTYYSKGKEPPGY IGMA*AMKPIGFLGDIAGAHVFTG*ID VNTRSYFTSDTINMG
3394	17295	A	3417	38	469	SGTTHASALFDPAGG*DFILYQHL*IF GDPEVYILILPGFRIISHIVTDYSGKKE PPGYIGMA*AMRSIGFLGFIG*AHHIFT V*IDVDTRAYFTSATIIAIP TGKVFT *LATLHGSNMK*SAAVL*ALRFIFLFTV GGLT
3395	17296	A	3418	1	419	FSTNHKDIGTLYLLFGA*AGVLGTGLSL LIRAELOPQGNLGNHDIYNGIGTAHAF VIIFFIVIPIIIGGFGN*LDPLIIGAPD MAFFRINNISF*LLPPSLLLLLASAIGE AGAGTG*TVYPPLGNGYSHPGASVDLT
3396	17297	A	3419	397	107	KNSAPPPSPFLP*GPKFAFFPPGKKVQ KKIF*KFPAPGPQGVYLRGGGSPSPQ TPNWPNNKAAFVLP PPPPVFGNPKKKK KKAVAFSSPNRR
3397	17298	A	3420	3	253	RGCREMRLCHCSSAWAIGVSEKKKKK KNWQ*CLLGICSYLDLWLPGLFKWLSQI GRIVELQLELQYLRGITKQTLKILH
3398	17299	A	3421	1	393	RTRTIKTPAITQYQTPLEFVGCALITAA LLLSLPVLAAGITILLNRYLNTTFFDP VGGDPILYQHL*LFYYPGDYIVILPG FGIISHMVAYYSKGKEPPGYIRMD*AMI SIDFLRIIV*AHHIFTVEN
3399	17300	A	3422	142	377	LSKNCYKPSYGVFCQCKFFNQLSKFLE VKLLYCMVKLC**EG*MAQPL*KQFVLV ALKLNIVLPYNKAISLPGIYSTD*KTYT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DTQNLHTTVYSSSLIIKN*KQQRCPVGE* INKCFIYTTEYYSLTKRNKLSSHMKA
3400	17301	A	3423	2	435	LILPGFGIISHIVTYYSKGKEPFGYIGM G*AMISIGFLGFIV*AHHIFTVGIDVYT RAYPTSATIIAIP TGVKVFR*LATLHG SNMK*SAAVL*ALRFIFLFTVGGLTGIV LANS*VDIVLHDTYYVGAHLHYVLSIRA VFAI
3401	17302	A	3424	2	436	LNTTFDDPAGGGDPILYQHLF*FFGHPE VYILILPGFGIISHIVTYYSKGKEPFGY IGMG*AMISIGFLGFIV*AHHIFTVGID VDTRAYTSATIIAIP TGVKVFS*LAT LHGSNMK*SAAVL*ALRFIFLFTVGGLT GIVLS
3402	17303	A	3425	1	193	PTRPPTRPACSELRSRHCTPAWTE*DS VSKKKKKKKFSPARGAHVCTPTFLGGQR GKKFCFAP
3403	17304	A	3426	3	446	HKKFLFPKSFNNRVPPPTKKKNPRGPGF FFFFLKKIFFPPPGGI*SGGFGSLQLFP PRVKKFFSPPPEKGGFKAPPPGPGNFF FFLKKRGFSFFGGGFLK*NPGFPPPPPF KKWGVPKGGAPPPPPFF
3404	17305	A	3427	202	1	FSPGRMLGNTIKLPYTHSFIILMNQNNL EKYKVGIGIPLSNFKTNKATAIKIMWYW HMNRYMD*WNR
3405	17306	A	3428	159	1	NPPHEKNPSCFFQMESHSADQAGVQWCD LSSLQPSLRGFKRFS*VSLVSSWDH
3406	17307	A	3429	22	298	ESYASTAKATERDMSDRMLSASGMPPRY SDYDAYTT*NILSSVGSFISLAEGILI IFMI*EAFASKRKVLIVEEPSINLE*LY GCPRLRGR
3407	17308	A	3430	267	26	GITFFFFFWLEI*LYYWLFLANKLYPHE QIWFGLVFFFGLLLFDFSFDYFPLLL CLGSFSNF*CLIHCFFSVIVLLF
3408	17309	A	3431	274	376	NKG*ISCSISPPQHTVRRGLTSLPRLEC SGVISAHCRCLCPGSSDPPASAS
3409	17310	A	3432	177	47	FYFFFFFFFFFFFFFFFFGLLFFFFFFFFF FFFFFFFFFFFFFFFFQINRSFIASFYHK*V LIFKKKN
3410	17311	A	3433	379	83	FKRHFTKEDLRMVTEHKSCSSSLATRA MQIETTMACYTFMRLAKIKKYQTKCC *R*RVGTGLTYCWCEKMTQPFWKTIVR RFLKQYIYHVGIV
3411	17312	A	3434	214	3	AASTFFFFTRSTYYVCIFLKSIRMINK* NYIKLKSCTTTTKINKMKRQPTDWEKM FANHINHEGLILK
3412	17313	A	3435	1	353	GGGQPGQ*SETLSQ*KVSWAW*LQLHR RMRQDNLLSPGDQG*SEPC*CYTPAWA RVRLCONRSVNEKSLHDICNDKK*QNI* IISVPBGKQRMKGLNLFNEILDENYPS LARDL
3413	17314	A	3436	29	394	VFMEVDFFFFFFFFFFFFGKRNFPPPR GGGGGPP*IFGPPPPRGKGNFPPPPGK GGKKGPPPPPGFFFF*KGGSPPGGGG FLTPLWDPPPPPPQRGFGV*TPWPGP GSDFLNFFFF
3414	17315	A	3437	108	2	PVAVAHSCNPNTSGGRGGWIS*GHEFQT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SLANTVK
3415	17316	A	3438	215	3	LLLLREFFFLPKHREVFIFVFYFMRQGLT LTEAGVQWRSHGSLWPQTPLGK*SSCLS LPSIWEYSAYHHIR
3416	17317	A	3439	1	186	QTSFSFRRSVITNFFKLKDDV*TH*KE AKNLEKRLDEWLIRIKSVEKTLNDLMEL KTSTRP
3417	17318	A	3440	290	3	PGLGGGPRYSRFSGGGLGPKIPLNPEGEG SIKLNPPPPAPPPGPN*DSFLPPPPKKK KKKTHVLFAGSGNLLQPLQPGAFTEVN GGLAQSPKVL
3418	17319	A	3441	163	2	PAGLPVKPPRFQDKLNFFPGPPFFFFF *I*DKVLLCHPGESATVHSSLGDR
3419	17320	A	3442	131	1	RPRRPLTIKSIHQWY*TYEYTDYGGGLI FNSYILPPLFLEPGS
3420	17321	A	3443	162	2	PGAAHSTGHLPLRFLRLGAVTHAGNPR TLGGQGRWIT*QGEFKTSLAKRVRP
3421	17322	A	3444	2	130	WEKIFANHVSDKGLIYRIYNELQQLYK* KTNGPIKKRPKSTRP
3422	17323	A	3445	2	117	LALGLKPKGLK*ATCLGLPRYWDYRHQP PHPACFSKGI
3423	17324	A	3446	350	101	KAFSSSLGSSRRKGDSDAGFCIHFKTVP FGFFWTLELKKGIPFFLNFFFFPFLRVL KGSKNPF*KRGPPFFFFFDFNYIWN
3424	17325	A	3447	106	1	LLQPNGQLGPGTVAHGCPSTLGG*GER ITTSGVR
3425	17326	A	3448	28	333	GQQEQNSISXKKKKKKKKTPFKKGKRR IPGGKKKPLGKSRAAPPPLGGGKPNPPG KRAPEKIPKKKPRGNWETFKRMEKGFLLK GQ*PGNP*KVKPLWGGK
3426	17327	A	3449	81	339	PIVSSCPGVAGALKQAMTLEFKVYQHHV VANCRLSEALTELGYKIGTGRDITGVQ QALLVVGLRLAS*PIVSSCPGVAGALKQ AMTLEFKVYQHHVVANCRLSEALTEL YKIGTGRDITGVQALLVVGLRLASQFV QPGCGPGSAAAAAM
3427	17328	A	3450	166	322	RDFSTTVLITDRTSRQKIPTDVSQNLNI DIYKTL*PTIGKYTFSSSTYRSLR
3428	17329	A	3451	257	354	KFLSFFRDRVLLCCPGWSAVV*S*FTAA LSSW
3429	17330	A	3452	286	3	TDPPFIKRAKEREMLOITKIRSIRENFI TDQOKTKEL*EEQLYAHVRVDNLDMDKF LEGYK*PSMTHGKIENLCRPITSKDIES VIKNLLTDP
3430	17331	A	3453	358	353	R**KLMMPC*IBTNKT*NTCTVIKEEK GQPGTVAHACNPSTLGG*GGRIT
3431	17332	A	3454	108	353	THLGCNPVRLYAWLLLHVASYRIFSVS HCKDQTYLPILL*NFLMELGTVAHTYNP SILGGQGRIT*VQEFETSLANMVKC
3432	17333	A	3455	342	50	GPVTNIPVPPPLGGQKELFFPKKKKF* KFWGSPPLFFPKPKPNPRETPPESCPKP KKTPIPVKV*GKKTP*TFSKKKTPPI ELFLLKKKKLIN
3433	17334	A	3456	343	2	KAPFFFFFKFWSQKKRGLFFFFKNNF IPGFFPGPTFFFWGFFFFFKGPPVF*LKK FFGGPLPPLKDPGVFFPSPF*FWDFFP PPPPPPPPFFETVSLCRPGWSAVSRD C

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3434	17335	A	3457	2	259	LTKPTESGTEDEKKGDRDSKESEGKTERTE SLRSQNGGENSV*SCPSTSSSTAALNTAA AANPLALNPQVSLSSLSCCPISIKGSFV P
3435	17336	A	3458	186	334	AGGNKKMEKRNM*NKEIF*WFKKNWPGA GAHACNPPTLGGRRRIMRSG
3436	17337	A	3459	207	1	YFKPTLKINDKGVLNETIDKDFPRDINR TSNLT*EHALFPSTCGIFMRDYEIGH EVNLNQFORIRTQ
3437	17338	A	3460	268	3	PLNPGPKQSSPPGLPKPWPFRRGEPLPLG PWFFVVKNRGR*AFFGTNPLAFPLFPL *DRVLFCHPGWSVVVQSQLTVQPPPLRL KQFS
3438	17339	A	3461	350	2	AETAHNINNAFGPGSANKCTVRWFK*L CKGVKRLLEDKALGGWPSKVAINQLRAII KGAPLKPTRKVAKELNIEPSAVIQHLKR IGKVKKLHKWVPHELHENKRNRFVWSS LIIP
3439	17340	A	3462	312	1	HIVTYYSKGKEPFYIGMV*AMISIGFL GFIV*AHHIFTVGIDVDTRAYFTSVPII IAIPPGVKVFS*LATLHGSNMK*SAAVL *ALGFIFLLPVGGLTRIVLA
3440	17341	A	3463	181	3	FLPLLAASFGLLLFSGFLGVFLFCFFET ELPRECCGTISAHCSL*LLGSSDSCAS GTH
3441	17342	A	3464	176	263	VGHDAHNPSILGGPGGWIT*GQEFKVDA A
3442	17343	A	3465	239	336	EPGEVAYS CNPSTLGGRRSGWIT*GQEF TSLT
3443	17344	A	3466	88	326	QTSLLNTI**PLH*KNIFLPPPPPLPPTL TPPFSPPPPPPPPKKKKRKRK
3444	17345	A	3467	4	345	EEERRRERKKRRKKKEKKKEERERBEK ERKKKKKKKKKKRRGRQEKRGKTG*IE RKQ
3445	17346	A	3468	265	335	QMNDRHLQF*DKVLLCHPGWGTVAR* LTATSRSSCLSPSGWDCRRVPCLASF
3446	17347	A	3469	115	342	INKQINKIKDPTSYNILLSQSLI*FKAL TLNSVKAQRGSKATEEKFEKGSIS*FMR FKQINHLVNIKVQGEKPSD
3447	17348	A	3470	56	328	RTYPTKPKMRDPEDPTSRPRYIPRHL ITDEVNDPSLTIKGIGHQWD*TYEYTDY GGLTFNSYILPPLFLEPSDLRLLDVND VEPATRA
3448	17349	A	3471	3	329	RIGARDESSLAVTHKPKIHRKLTWVF VNDSLVMPRPDKNHQWAFNKNCFPLVDV GIDPYLVYHLRPHQAQGIIFLYECVMGM RMNGRCGAILAD*NGLGKTLQCISL
3449	17350	A	3472	154	2	PNLLYPKSYWKKKDINTPMFIVALVTIV KIQKQPRCPLMDKSIR*L*YIH
3450	17351	A	3473	132	340	ALKTENITLCLDF*LIETVR**MCVFK KKKKKKKKKKKKKKKKKKKKDPKKKKK IK
3451	17352	A	3474	3	345	VIYSSIFAGTLITALSSH*FFT*VGLEI NMLAFIPVLTKKINPRSTEADIKYFLTQ ATASIFLLIAILFNILSGL*TTNTNTN QYSSLIIIMAIKLGIAFFRRRGREFQ IY
3452	17353	A	3475	1	254	FHHVGQAGFTPDLR*STRGLPKCWDYR

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						REALCLVHLLLYLPMIGPFRIQKLLKAA VFVFLQLHQAFIQSLLTLFYFISFPCNS
3453	17354	A	3476	351	186	SVLSADNTEMGFHHVGGAGLELLSSSDP LAPAS*SAGIRGVRHNTWVLTITLN
3454	17355	A	3477	330	3	GEKVFEIPLTRDNVSEILRCFLMAYGVE PALCDRLRTQPPQAOPHQKAAPVLAFLV HELNGSTLIINEMDKTLESMSRYRKYEW NVKERLRLKKTARA*RLGRSQVKK
3455	17356	A	3478	373	248	NRLNPGGGGWSEPRSQHSTPTWVTEYDS VSKK*INKNKNWK
3456	17357	A	3479	3	92	EGQGCSEP*SRYCSPA WTE*DCVSKNF F
3457	17358	A	3480	380	2	VEVPLINTSVFFASGVST*AHHSLEYN NRNQIIQALLITNLGGLYFTLLQASEYL ESPPTISASIYGSTFFVATGFHGLHVI GSTFLTMCFIRQIIIPHFTSKHHFPLEAA A*CWHFVDVVCIFL
3458	17359	A	3481	225	1	ERAERVVEQVMIALFSPNYIRLSFPISP TPVVRHKFRFHLKGYIWPGTVAHTCNPS TLGSGGGQITRSGD*DHFG
3459	17360	A	3482	332	1	IKYFLTQATASILLIAILFPNNILSGQ* TITNTTNQYSSLLIIIMAIN*GIAPFH F*VPEVTQGTPLTS
3460	17361	A	3483	277	1	LSMSSFSISSIPASINS*ALLFSSAES NSLECTFSSSPNSSESFSSSPSCSC AS*FSNSQLIKASSSTEASPLNSSASC FLPLPLVG
3461	17362	A	3484	404	209	ALSVQPLWRPQENGVNPGGKASR*PRF PPCGPAWATKGBLVPKKKKKISFLGHD QSLLELLQR
3462	17363	A	3485	31	347	FCILERKAFLYV*CWKFFFFFFFFFLE KGFFFLPLLVPFWCYHLKGASLP*VFL FFYLHCYSSLFTLFFIFLQSLTPHFFLV *TFYYDPLMFFFLTLFLELV
3463	17364	A	3486	327	161	QKKVRDPYEQ*ANKFKN*BEMPRFLEK HKLPLKTQEEIKNQ
3464	17365	A	3487	311	3	PRRGRFQLTQNFALPFLNKNKTKIPFKK KKKTEPLCPCTCVCAAFVCLCFHCT* PCDCAHDCDNICVNCVYCVVTHLH TGLCSVDCHICVGTCC
3465	17366	A	3488	245	1	RPRRLALLLIITF*LPQLNGYIEKST PYECGFDPISPARVPLSIKFFLVAITFL LFDLEIALLLPLP*ALQATNPLIV
3466	17367	A	3489	2	400	AAPILGMLGLRQGRGKYRQRQLCLWSA ILLFLYFLNKL*LTKKKKKKKKKKKK KKKKKKKKKKKKGGPRGNPQILKGKIG KPPGGFFKGGGPKKIFFKNRGALFFK KKPPQKNLGPGLKNFLKEKKA
3467	17368	A	3490	57	366	INVFAGKDQLPLCACPSPIISVESDR PDMYQCGLNHFIYLIYLRWSFALVAQA GV*WHHLGSLHPLPPEPKCFSC
3468	17369	A	3491	25	384	IRGTF*FWGGGLGGLSKNNPL*KKNFSP PKLGVLPPPLFFPGGFFFFFGAPPGF KKKKPPPKKFF*KKGAPPPFFFFF FF
3469	17370	A	3492	170	41	AQPDHGETTFLKIQKLRHGGICL*S QLIGGLSFITQKITC
3470	17371	A	3493	1	240	VLSPADKTNVKAAGKVGAHAGEYGAEA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						LERMFLSFPTTPS*FLDFFFFLEKIGFH HVGQSSLGFLTSRDEPSAYNSLLGS
3471	17372	A	3494	359	204	TQWLMPVILAPWEAEVGR*PEVRSRLPA LNSPFFKRLVVIMYIMNIILS
3472	17373	A	3495	1	178	DRLSPGV*GSSEL*LCHCTPGWATEPDH VSRKKKRRKVGKGNKAKQKHPRGYR AEL
3473	17374	A	3496	361	1	LGPKLLKKPFWISIGIKGVAGLPGFFPT PPQ*G*NFGKLRGGFFFFFEAKGWFT PGGKQRPFRSLEPFPPRVKLFPPNLP NNWGHKGAPPKPPFFFLRWSFALVAQ AGVQWCDL
3474	17375	A	3497	276	79	AEVYKIKCELGAHAHACNPSTLGGQGG ITRS*VSASFKKYQQLALMKELLNE
3475	17376	A	3498	3	476	FGTSMSTIITLTPRLARGNNLFCFPPT FTFDHLATPLLILT*LLPLTSMASQRH LFREPLSRKKLYLSILNSLQSSLIITFT GTELIIFYIFFETLIPTLAIITR*GNQ PERLNAGTYLLFYTLVGSPLLLIALIYT HNTLGSNLILLTLVSAQE
3476	17377	A	3499	581	2	AHACNLNTLGGCRGWIT*GOEFDTSAN K
3477	17378	A	3500	380	135	RHQSGQIGKTPSLVKIPKLTTPKGGV* SHLTKRARQEKGLNPKSKGFN*PKLRPC PPTIVAKKQNPVSKKKKQTRQEPSA
3478	17379	A	3501	1	386	GSR*GNHPERLNAGAYFLFYTL*GSLPL LIRLIYTDNTLCSLNIILLTLTGQELSN S*AHNLI*LAYTIAFIVKIPLYRLHL*L PKAHQAQPIAGSIVLAIVLLKLCGYGII RLTLILNPLKKHIDYP
3479	17380	A	3502	2	389	EKQL*KDKQVYRATHRLVLGAGESGKS TIAKHMRILHVNGFNCGEEDPHAARS YIDGKATKVQDILNNLKEGIETIGAVM SNLVPVVELANPENQFIVDIYLSAMNVP DFDPPSEFYEHAKALWE
3480	17381	A	3503	2	379	PFGYIGMV*AMISIGFLFIG*AHHIFT VGIDVYTRAYFTCATIIAIPGVKVS *LATLHGSNMK*SAAEL*ALGFIFLFTV SGLTGIGLTNSSLDIRLHDTYYVVAHFH YVLSIGAVFAIIGG
3481	17382	A	3504	281	68	FKMRFGWGHSTVSENYKPLLKEIRENP NK*KNIPCSWIGRISIVKMPPLPKVIYR FNAFFIKLPSPPFTL
3482	17383	A	3505	139	263	ETGSHYVPOAGL*LLASSDPPATASQNI GITHVSYYVQPL*PIFWEAVAGGSLEAR S
3483	17384	A	3506	2	427	LKTSMTMISTTLLT*LRPAWH*AQYQTP FFV*SALITAGLLFLFLVLAAGITVLL TDRNLNTTFDPAGGGDPILYQHLF*FF GHPEGYILILPGFGIISHIGTYSGKKE PFGYIGMV*AMISTGFLGVIG*AHHVFT GG
3484	17385	A	3507	343	3	GWHSRSSGGASSPSSPSHRSLRVSSGS LGRL*WSKSSKTSVSCGVVARDTEKPL SKIEASSSDSCSVMAKANAVFTSTTG EKPASSASLSLVWASGSSPPGAANSSS S
3485	17386	A	3508	3	363	GPGDKAARRIALENLDIT*KWGMRTKRC

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						AKQLLSKQPF*SSRTGDLKLELQIELVR ETKRKC*RVL*IDRALTSYSLQTD ALGDASADLIQKTS*LQEEFGYAKTQK LLCRNGET
3486	17387	A	3509	3	434	GPGDHVARGISGKKYDIGQKWMGMYTC TKELLSQRFGLGSPVDELEL*LQIELLR ETKRKYESVLHLGRALTAHLYSLQTDH ALGDAFADLRQKSPQLQEEFGCYAQTQK LLCKNGETLLGAANLFVSSIYTLGKTKM EDTL
3487	17388	A	3510	1	401	GTRKNSFLHDSQTSFCFSDSIPTPSNME ETQKSNLELLRISLLETPWLEFVRFL KSMFANNLVYDTSDDYHLLKDL*EGI PTLMGRLEDGNRRGTQILKQTSKFDTN SHNHDALLKNYGLLYCFRRDMN
3488	17389	A	3511	117	2	FKFIFSEMESHVA*AGVQWRNLGSLQP LPLWFKQFSC
3489	17390	A	3512	491	90	KKVKIVLAGFFFKPPPPKN*KKRGKLR KGVGPRGYTVNPHPCGYKFFGGPGVQNP PGQKGETPFFQKKNKPGGGGALIPPP KGGGRGVPLSPEKFKLFPFGPP*GKK KNRFQKKKKKKRQN*PKRSQC
3490	17391	A	3513	2	31	GKGAPTTSLINVAGTKIATKVVEDNKL GAICSLTCGAHIGTPMARDERNLLSF TGSTQGGKQVGLMVHERPGRRLVELGN NATIAFEDAHLNLYVPSTLFAAVGTAGP KCTTARRQLIHESIHEA*NHFP
3491	17392	A	3514	2	390	KEFHKTHPLENITLAPDPEGPDPGLPPVA YNPMDIRQREDGQTLNIREBPYGPVVD F*RKIRQSYFASGA*LDQDGRLLSALD DLQLANSTIIAFTSDHGWALGEHGEWA* YNNEDDDTHDPLIFYDT
3492	17393	A	3515	3	410	RGTGNNAWQGHYTKGAELVDSVLDVVRK ES*SCDCLQGGFQLTHSLGGGTGFMGTL LITKIREEYPNRMNTFRVMPLEKV*DT EGEPYNATLLVHQLVGNTDETYSIDNRA LYDICFRTLKLTPTPYGRHHLVS
3493	17394	A	3516	1	396	GEDAANIYARGHYTIGMENIDLGLDRIR KLADPCTGLQGFLVFHSPGGGTGSGFTS LLMERISCYDGKKNKLEVSIIYPAQVCT AVFEPYNYILSTHTTLEHSD*AFMVDNE AIYDICRINLHIERSTYTNL
3494	17395	A	3517	2	399	EKIGYNPDVAFVPISGWNGDNMLEPNA NMPWFKGWKVRKDGNASGTTLEALEC ILPPTRSYTDKPLRLPLQDVYKNGGIGTV PAGRVBTGVLPKGMVTFAPVNGTTEV* SAERHHEPFREALPGDNVGF
3495	17396	A	3518	1	402	GEDAANNYARGHYTIGTEIIDLLDRIR KLADORTGLQGLVVFHSPGGGTGSGITS LLMERLSIDYGTSKLEFSIIYPAQVST ACSEPNYSILTHTTLEHSDCAFMVHNE AIYDI*RLNDIERSTYTNLR
3496	17397	A	3519	1	408	GSCLGQKLYNSTTKTAT*WSSNHTKKNP FSKFPKLQNVWTHPESHRTWTAPTRLVW ICGHRPVVKLPNQWAGSCIIGTIKPSFF LLPIKTGELLGFPVYASHAKRSIAIGNW KDNEWPPERIIQYYEPATWAQDGL
3497	17398	A	3520	3	162	ETVLLCCPGWL*TLGLRQSSCLSLPKCS

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						DYRHATVPGQKYRFFNRYVGSYS
3498	17399	A	3521	184	354	ETGSSLLP*GSSELPVSHPYFFNTHSLSLSHTHTHHTHTNSSLNHYHCPLYTNMSCQRLVAVYRQKGSFKDQCTDI
3499	17400	A	3522	2	313	YYLSPPMGDQPGQHGETLPQKLAG*GGARLRSQLLRRLRQENCLTPGIQACRELLGWYKSNCAFCQKPKQLLCVNLTLYSSLDKARDSVSTTKKREGREK
3500	17401	A	3523	13	127	LGLQARTTSMFSS*GYRRAPPPCPALLYF*VETGFHHVGOAGLELLTSTRP
3501	17402	A	3524	148	1	VCMFLEESCSVAQAGVQWYHSSSLQP*T PGLKRSF*LSLPSSRDHRLMT
3502	17403	A	3525	1	98	VNPGGEGCSEPRSHCTTAWVTE*DSISKINK
3503	17404	A	3526	138	3	AASTHDLG*LQPPPPGLTPPSCRLRLSSWDYRPVPLRPANFLYF
3504	17405	A	3527	10	206	PTTSLISFTSYSPCLKCSNVYEQVNRMRVLFYKSKQRLGMVAHAYDPSTLGGRGSKIT*GQGRG
3505	17406	A	3528	345	3	VTELIQSNKAKLKKKSKNKNBOSLQKI*DYAKQPNLRISGVLEBEEKSKSLENIFEKIIENFPGLTRDLEIQIQAQRPGKFI AKRLSPRHTVIRLSKVTKGRILRAERQK
3506	17407	A	3529	3	90	AVL*ALGFIFLFTVGGLTGIVLANSVDA A
3507	17408	A	3530	3	90	AVL*ALGFIFLFTVGGLTGIVLANSVDA A
3508	17409	A	3531	354	3	AVINSLPTKSPGPDGFTAKSYQRYKEELVLFLLKPFQRIEKEGILPNSFYESSVILIPKPHRGTPKESFRPISLMNLNAKILNKRAS*NHQHIKKVIHHGQVGFIPRTQGWENKQ
3509	17410	A	3532	2	357	FTRPRFSFTFFVLIRKIALSCGKISIQHSY*KKKSKGKLGGL*GINFCFFERKFHSVTQVGGQKHDPG*LKFPFPGFRGFSRLSLPSSWNHKGRTPLRANFCTPNKNGGRRGRKFQIY
3510	17411	A	3533	76	365	KKKKKKKKKKKKKKKKGGAGPEIPKLKMGKSEKPPGVFLRGVGEIKKFFFLKGG PFF*KKKPLKNKNWAREBPSFKKIFKKKKKAHFFFGPKILKK
3511	17412	A	3534	7	353	FFGFGGVFLVFLFFFF*KYPFFFFFFPPL FFFFFFFKWARRPPPPFFSFFKNFFFF FPPPPPPFFFFPQKNEPLFFSPLFFFS PKFFFFFFPLTKKKKKKNKKKTTPKIHPQTQRK
3512	17413	A	3535	354	41	AGGVFFGIPPPWWGGRAGGSPKGRGFGPPWPKRGTPPPFF*KKKKKKKPGGAIPA TREGEKKSP*PWKPRVQPT*NAFPSP PGEGAKPPQKKKKSMFHKR
3513	17414	A	3536	174	364	TFNSLAFTFFFF*RETGSHFFLEAGVQGNHSSLNP*PPGLRGSSCLTLPC*KDYRREPLEPA
3514	17415	A	3537	38	368	PGRRLRQEA VNHCTLEPGQSV*KKKKK KRGGAFFKAKLTLAGWKGEKKKTGVFF*TLKIRPKIERNQGGSQQRKAELGKLQ QTYPVLNFKATFYGEQGDY*TFFKP

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3515	17416	A	3538	107	349	SVTFPPFFFLKQTGSHFVV*AGGQGGNFD*LEPKPPWLRSSLLTLPSSLDYGPPPTGSPNFGIFFEKRGFCLVPQASFB
3516	17417	A	3539	274	3	PRRWSLPLTQMGPPLPSRMGPXKLCPEKKKKKIPPRKILEPDVFTGQFYLMFKBITSIFLKLFPQQCEEFTFSNSF*BARIALKTK*DN
3517	17418	A	3540	1	374	ACALVRNDHIYYVVGPTYALGELFFTTETPIII*G*DN*LGPLVIGAHVVALLINYL*P*PPSVLLLLACAIPEARAGTGCTAYPPLAGDYSHRAAYVNLTLISLHARVSSILWDTDSITT
3518	17419	A	3541	427	76	RGSLSPGV*K*PGGQNTFFPKAPKLRPGAPRCFPAGKGSIKPTPGSPPGRRGTGCSKKKKNFRETTPPSFFWGGPPFLKNRGGFMFWASKTKNGLNKTLPNPGPPLGGLRSPFWVG
3519	17420	A	3542	234	88	FFFFFFFFFFFFFFFFFSLFFFFFFFFFFFFFFFFFFFFFFFFFW**ILYFV
3520	17421	A	3543	30	419	TFSFFPFLFFFGFLVLGGEKQKQKWDPKPGEAKPPTFSPPKI*KKGAPPPRVNFKKF*KKGPLPFSPPGGKNLKSFWGIWSIGNPLWVTPPKNPQKKPPFFKGPKNFFPKGPKPGGKKTIQIFFFLWEKK
3521	17422	A	3544	159	411	VSRDISPVRSLSPSSCFH*PFLHISSSVEGRFSSFAQFLLSCLNFCTFPLLELLLR*DRVSLCHPGWSAVA*SQLTATSTFWVK
3522	17423	A	3545	2	351	CLARTSGVES*ASLPCGQNSYIHYLKLCCMBELSPFPYLLIYSISYLY*HTIMVIYFILVL*SILLNLIYLFVTQIFPALASGSFNNWLLCLFNTTLAVHVCVCVCVCVRVCAC
3523	17424	A	3546	397	1	KPPPPCSYGKKKKIFLLVFFRTLPETKPPGAGRKIFPRGPGFFLNKPKAL*TFPAPPFIQKKGPELLQQA*IPFPVFLFKKKPFLCSP*GGIGVSLFFFFFFSETESCSVTQAGVQSCDLGSLQPLPPGLKR
3524	17425	A	3547	76	354	FLNFEMGKIFKNFRGGVFFFFFFFWGGYNI FLVELKIFFFFFFFGGFFLEFFFLKKEFF FLGFFFGKISQKIFFFFN*IFLLXGAPPLFFFFFFL
3525	17426	A	3548	197	1	INKMKQQRMD*EKIPAKHVSHKGLISQICK*LIHLNSEKTNSPVRKWAEDLNHRHPSKRDTKMVNM
3526	17427	A	3549	175	309	KSTLKVMLISISIFNFYFF*DRVLLCHPGWSAVA*SLTAASTRP
3527	17428	A	3550	3	196	GFHRVSQDGLDLT*SACVSFPKCDYSHBPPRPAHKTSLLKKNKMRVRIIMMTITYPAPVVC
3528	17429	A	3551	3	360	RAVEIFCYDVCVESGCADIQLLLCPTS IKVCFSSLSLDIVTIVPIYICIIYIIIFFFFKQARS*COCLNDKE*YCSLWPTPGFKKLSCVSLPSIWDLRCAHPHPNFCVFGKNGV
3529	17430	A	3552	326	1	KDNHRILKMLAKSGKVRHYVDFGKQIKSMSEKNIGVKPPIGKEKTKNPKKPSRTEDPKICTYVL*PDKKWRRLNT*GIQIG*KEIKLSLFADDMIVYLENPV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3530	17431	A	3553	186	1	RPRRLPIKLEPMFTFFTELEKTTFKFI*NQ KRVRIAKSILSQKNEVGGITPPDFKL*Y KDTVTN
3531	17432	A	3554	3	366	KTSLGNMVKPYNFFV*TFYI**KKEIKK NSIGVL*PGTEQSKHEFKILPSKRNKI ASKRIKYL*INLT*EGQDMYTENYKTL KEIIEDLNKYKDIPCS*IIRLDLVMMAV LTKLIYRFN
3532	17433	A	3555	239	1	GRGKMLPVSLNITRVTTFAPCSGSIIIV LIALPSLRILYITDEVNDPSLTTKSIGH QWY*TYEYTDYGGGIFNSYILPP
3533	17434	A	3556	3	123	QAGLEV*TSSDLPTSVSQSAGITGGSHR ARPANIINSVP
3534	17435	A	3557	237	2	KGFSEPTQKFGFLGVFPQKKTKKNPR PPKGLTPVS*KGMLTEPLEPFFFFFLRQ SRVQAQAGVQWGNLGSQALPP
3535	17436	A	3558	87	379	KKKKKKKFTLQKPVGFNPNGEAKSQI INELLKIKATKKKKNLKLRLKKKGKDLF RGNYNPLFKKIKDDPTNGKNFPCS*MGK ISFEKMTLLPKAI
3536	17437	A	3559	390	181	KKKKKNPGGGGPPFPPTFRGG*GGGPPQ PGGGGAPKV*ISPPPPPGGKSPQKK KKKKKKKGPFPLPHL
3537	17438	A	3560	2	101	VIVTAHAFVIFFIPIIIGGFGN*LV PVDAA
3538	17439	A	3561	2	126	INTLLALLLIITF*LPQLNGYIEKSTP YECGFDPISRRRG
3539	17440	A	3562	16	349	PAFQKITLAMEKATEAQTGAKKACQGT NNIMKFLKKKCIPTTIFWISFPLFFF FETKPHFFNWPEGKGNLG*LKPLPLGL KQFCLTLPRKGNVRHVLPPVNGFFFF
3540	17441	A	3563	6	130	TLRRILEDHFSLRS*GCGEPCLRHCPA WLTE*DPVSKNIY
3541	17442	A	3564	3	152	GFHCVRQDLDLTS*SAHLSLPKCDYR RKPPHPAGKGTIFYIDYSTIR
3542	17443	A	3565	241	3	NLVSHVISMRKVINLVEQNVTSNRSNH TWLSFIKLYFIIISIVFGEQVVFYVA KFFSDDF*DFGVPIQTQVYTAPN
3543	17444	A	3566	71	256	SVFLLTVFLYPLATSFPLNRVSLCCPG WL*TPGLKQFSCLSLPKRWNYRHEPLTP GSNFF
3544	17445	A	3567	1	392	AGAGTSGTDYPPLSGNYSHPGACVDLTI FSLHLAGVASMLGAISVMTVMNIEPPA ITQYQTPLFV*SGRNTAGLLLLCVPVLA AGITILLTDRNLNTFFDPAGGDPILY QHLKGRGIIICSHRDRI
3545	17446	A	3568	334	409	LGTVAHACNPSTLGG*GGHITRSGV
3546	17447	A	3569	3	467	PKNPPGGFSPLE*EKKYILPPPP*IWPF PGFF*KAPPPPPPPPPPPPPPPPTFQI YFITF
3547	17448	A	3570	3	420	FFDPAGGGDPILYQHLF*FFGHPEEYML ILPGFGLSHIATYYSGKEPPFYIGMV *AMISIGFLGIIV*AHIFTG*IDVDTR AYFTSATIIAIPGVEVFS*LATLHGS NMK*SAAVLSALGFIFLPTRRGLTSIV
3548	17449	A	3571	1	418	NLINHSFIDLPTSNIFA**NFGSLLGA CLILQITGLFLAMHY*PDASTAFSSIG HITRDVHYG*IIRYLHAKGASIFFICLF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleo- tide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						LHIGRGLYVGAFY*ET*NIGITLLLAT IATAFIGYVLPGGQISF*GATVITNLL
3549	17450	A	3572	3	414	SSGLAM*FHFHSTLLIIGLLTNTLTYY Q*WRDVTRESTYQGHHTPPVQGLRYGI ILFITSEVFFAGFF*AFYHSSLAPTPQ LGHWPPPTGITPLNPLEVPLNTSVLLA SGVSIT*AHHSLENNRNQIIQALL
3550	17451	A	3573	2	423	GTLVLLFGA*AGVLGTALLLIRAEGLQ PGNLVGNNDHIYNGIVTAHAFVIIFFIVI PIIIGGFGN*LVPLIIGAPEMAFPRINN ISL*LLPPSLLLLASAIVEAGAGTG*T VYPPLAGNYSHPGAYVDLTI FCLHLGAV
3551	17452	A	3574	411	117	DGGPLLQLRRARQENCNPRGGGCS*P RLCPCPPAWGAKLNSLSGKKKKKRHVE KYAQHDYIINVLCVVCVHIKWLSLYMY ITKSIDKICKKAS
3552	17453	A	3575	2	394	ALANMWEQIRSLHQYAVHRTISLFLLS KKHDRVLEQATQYLRGSLTNDVPLPDY AQDLTVIELIPMMLEIINS*LTNSLHH IPNLVYALLY*RDLEQQRTHPSFQDIM QNIDLVSVDIYYDSFLS
3553	17454	A	3576	262	418	GWREWTELIIFYIFFETTLIPTLAIITR *GNQPERLNAGTYFLFYTLVGSLEP
3554	17455	A	3577	232	443	PSVQTFPCCLSEEGPWLLCVAMTPSPG VPVPTERALYSMECAFHPLFSLTSGACR LDYRTPDNR*VQLP
3555	17456	A	3578	48	410	GGLLHRAGCWCGHADRRADQPDSSDPH SLHAACLPPGAARAAGAPSPA*TPAAA CPAPVPAPCSEHRC*PPGLSQRCLPGL PDARPPGAAAHGWSLPTRLVLHDSHP EEAPRRHED
3556	17457	A	3579	422	186	VYSKFL*SQLRLRLQENRLNPGSRGCR EPRS*HCIPAWVTQDSLSISSSTSHBI CGSHCSPGYLVHICDQPVFSL
3557	17458	A	3580	442	3	GSATSSRCTQESTYQGPHTPPVKGLRY GIILFITSEVFFLAGFL*AFSHSTLAPT SQLGHWPPPTGITPLNPLEVPLNTSVL LASGVSI*AHHSLENNRNQIIQALLI TILLGLYFTLLQASE*LESPFTISDGM YCGRSRG
3558	17459	A	3581	428	1	IRDIFMASSLGM*FHFTPTILLIIGLLT TPLTIYQ*WRDVSRESTYQGHHTPPVQK GLRYGIILFITSEVFFAGFF*AFYHSS LAPTPQLGHWPPPTGITPLNPLEVPLLN TSALLASGVSI*AHHSLENNRCIAAA LE
3559	17460	A	3582	160	415	RCLSHCLAFPMLSILFIPSQLLSLPFHV KWIFFFFFLNKKFCNCPVQAGGQGNLI* LHPPPRGLKKFSCLRITSS*NYGREPQ S
3560	17461	A	3583	399	2	STHLGLPKCWDYRCEPPRPALLAIVKLL CKTIHVRINNVCCLPLLTGAASVIGLSA SLLFSVSPGTSLOLEAR*TFPWPHMSST CVWRFIFTSLGRAQPHSDLTQTCPRRDV DLAEFGLLFNGQMLVPPGRS
3561	17462	A	3584	215	1	KSPGLLNAFSRGSQIYQASRAMGA*LNQ RFWPGTVAHACNFTLGG*GARIMRSGD GDRNSKDGVSPPCGRV

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3562	17463	A	3585	138	19	LNQRFWPGTVAHACNPRPLGG*GARIMRSGDVYRNSKDEV
3563	17464	A	3586	262	3	GRPEVFYKPPPRGEFFFFFLLFFFFF FFFFFVLFLLLLLLLLLLLLLLLLL*Q VRLYLLEKYELFFFLFYPOEISLCCPGWS
3564	17465	A	3587	381	1	KKFTPPPPRKMGPDPGFF*RAPPPFFFL GGGGGGLFFLGGPPPPGGGFFFSPPPV FF*KSPPLFSFF*KKRGPPFFKRGSSPK TPPCFFFKKNPPKKKKKKKKKKKKK GRPSSKSDAWVTRG
3565	17466	A	3588	198	1	PKSPRPLARGKEPNFFSKKKKKSI*N LNTNSWLDMAHICNPSTSGRGG*PHL RSGVRDOPGQ
3566	17467	A	3589	373	1	GIFPPPPKRGGFPPPPPKKFFFPGGFI FGGGGGPFWPPPRKGFFLKKKKGVF*SP P*KGKKFFFPGGGVGPPRGFLKGGPI IFFFFFFFPPPPPPPPPPATIFLITYK DLTCHPGTHFTH
3567	17468	A	3590	506	98	HTSRGPPPPPKKKIPPTRPFFCCFWV FFPPKKKFFFCSPRSFIHSPKKKKKN FFPKGGGPPPLSPFLTTPPPLFFFFF FFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFF*LFVSLFSI FVLLIFFFLFYNAITTI
3568	17469	A	3591	407	1	LVRGQITNKKNLNLFGEELREWRVVF LPQQRLLFFKL*LQ*KEIYLF*KMTCS RGGAGFKSSLYFFFRSPPQVVLFFFFF IFFYFF*FFIFFFFFFFPPPPPPPPPP YLYISPPPLILEKKKGGRSRSRS
3569	17470	A	3592	380	68	FRRGVGPQWPPQKGFSPKPPGGFKRP PLKGGKITFFPPGKFGPPKPPKPPPF FFLEGKTLFLGDPD**NLGWGG*RGHGK *GPANPRVPVFFFFFEYSY
3570	17471	A	3593	394	45	ALMFSTGQEGRQEKHPPPHKKKASRGE EPRGGVRKNYPPPKKKSFPKKNPPGVTP PKKKKAKLPPRPL*GGPQRRPQKTAPP PLNFYPPKEPTKVLISFFSFFFSAND VELY
3571	17472	A	3594	402	62	AMIVLLHSSLGNKARPCLFKKKWAKDLN KHFSKEDSQMANKYMKRCLISLVIRNMQ MKITVRCHFILTRMAKIKKMNVSCKRKE VQKIPTLKHWCWECKIV*ILWTNLAARV G
3572	17473	A	3595	220	425	FISGFLNLQEEERETIAFFFKVNIRLGAVV HTCNPSTLGGRRRIT*SPGV*DQPGQH GEPCLYLNQKN
3573	17474	A	3596	13	412	AEIAPLRSIHRARNCLKKKGRKGRKNPG GDGNNPQIGPAPFGGNGKTPGQKPHQP QTWGGQRHLKGGGGPKRKGVPKPKKTP TIWGGTPLAFGVEPNWGHGTGNPGGADP KPPGREK*SGGAQITGPHGTG
3574	17475	A	3597	2	293	CQLSP*ELGTPRERERERERERERER ERERLPPRDLREKRAQDVATHPNYEFV CVIRHYRGCVVYTPLTTHASIDAHKMCV CVKKRPLYKKKK
3575	17476	A	3598	243	9	ILLRQEKQCSKGRFQQLQDEQVLNT*D RTWEVMWPGAVTHACNPSTLGGGRIM

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						RSRDRDSCRIHQGGSKPKSPR
3576	17477	A	3599	1	329	PSARRDWKNIPKLPPrRGKNPTGFFFLK PGGPQRGPCKKGGKNF*SFGKPF*KGGG PPQFCPPPrGGGFFFFPGGPPGEKKGG VKGPPrPPFFFWPPPrPPNLFPPGA
3577	17478	A	3600	206	1	LRLGIMERAHAHTEVRLVFQILGSPL* YIF*QDLSPSPRLECSGTIAARCSLDL LSASNSPASASQ
3578	17479	A	3601	322	99	KRTGAFGFFFPPLFNKKKKVFLGPEGPK IVKKKKKKKKKKKKQKNRQTKKK*KTN NKQNKRETDIFGVEDT
3579	17480	A	3602	410	25	LFFFKKKTGGGGGGPPFFHPFGGVNGG VIRGELSPPCPPGGTRFFFKTKNYPG G*GGPFFPPSGGGGLGPKKTLSPRGAS L*PNFGPSLPPKGGGPPFSKKKKKKKK QSRPRDS*SLRRGIRK
3580	17481	A	3603	27	349	RSSIQCGGILLFYFLYFMVFNDFVVL* GFSAITSLISMLFSCI*YFFPKMYCLL FNFRCHWIFYILF*MKTIAQIGN*IFFR DAYLGYFFLFLFFFFFGGKLYL
3581	17482	A	3604	88	435	RAISTCLQNEQYKNLTTITSVEKSLNDL TELKTMV*ELHDKCTSFSSRFIQLEERI SVTEDQNMENMNPPLIHGFIFYGSSYSW STMVRKQDKLRVKDAGIKHRNQNKGFTA EKSA
3582	17483	A	3605	331	428	YGHYQIEATFLPAITTEKETLKRKL *SSINLLK*T*NVRPGTVGHACNLSTLG GRGGQIMRSGIRDQPNST
3583	17484	A	3606	3	294	GG*GCSEL*SCHCTPSSLG*NTVRKKER KKGKREKERKREIIPGFGPCAHHKGA VTLGNLPPRVQVSQVQRKIIITVIPD RLGEIVLVQSLS
3584	17485	A	3607	263	426	RKLAGTFPFLWKSPPFQTLIAAQRMG NDPKETRVFAGLSLSSLGK*VWKI
3585	17486	A	3608	213	439	LSWACAAEWTVTQANFPLDYILFFLL IRESSKF*RHMATOLETAASRPGVVHA CNPITLGGRGGRITRSGVH
3586	17487	A	3609	2	441	MTDLESFPLESELSANSPVQCSGLCKPV LTIQVISHKGCHSKYLLNANYNVFL HLSNSVLPRLLSGQRTETQKHFTAVLS VCLSIYLSRDRVLLCYPGWSAVM*FYSL *PQIHGLKQSSCLSLPKC*DYQHGISPP WCN
3587	17488	A	3610	102	354	EPGAWADRCWLGRVLLTHLLWPCCLYFF YFIIFILNSGDRVSLCCPRWSClk*SSC LSLPECWDYRCQPLHPACAVFIENSKR
3588	17489	A	3611	462	371	GLNFTL*SAHLGLPKCWYRHEPPRPA WS
3589	17490	A	3612	463	319	RNSHDGLELLTL*SAHLGLPKCWYRCE PPRPVLC
3590	17491	A	3613	49	476	PRNSTILLILGLLNTLLTYQGWFVTR ESTYQGHHTPPVQKGLRYGIILFITSEV FFAGLF*SFYHSRLAPTPQLGHWPP GITPLNPLEVPLNTSVLLASGVSI*A HHSLIENNRNQLMQALLITILLGLYFTL LQ
3591	17492	A	3614	223	467	TPS*PLAII*FISTLAETNRTFPDLAER ESELVSGFNIEYAGPPALFFIAEYTN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion
						MIINTLTITTTIFLGTTYDALSPELYTTYF VTKTLLLTCLFL*IRTAYPRFRYDQLIH LL*ENFLPLTLALLI*YVSIPTITSSIP P
3592	17493	A	3615	2	405	ARGLQEAGAVQNDPVSRLFDHAMLQGHR AHQMAIVTYQEFGETYIPKDQKY*FLHE SQTIFCFLNSIPTPSMERTQHRSSLEL LRISLLLLIESWLEPVRFLRSMNANLVY DTSDDDDYHLLKDLLEGIQTL
3593	17494	A	3616	328	63	PSKF*KPCLISPPPLGPGPPN*TPGFLK KPKFPFRGGGHP*SLLLFRVRPGDPLNP RGQGFP*PKLPPGPPTRATKPNFVSQKK KKKB
3594	17495	A	3617	1	379	GTSVGIPITGGQEF*FAALHGSNVK*SA AAL*ALRIMILFTVRGLTGIGLANSSLD IVLHDTDYVEAHFYVLSIGAVFAIGG FIH*FPLFLGYTLDTYAKSHFTIIFIG VSVTLFPQHFLGLC
3595	17496	A	3618	494	17	GSANPRNPRRSGSKTRETSPRNVMSLMS PMSPTLPMRPTSPGTPMHLTNSMGPMQP PNSSRPVNPASSATPVSPASPARPRKPS CFFAPQ**SPPL*SPEPRHGLSCLSWVK KECETWHVVMHIVEDRHSKPYHGPOMV AHACNPSTLGG
3596	17497	A	3619	350	480	LGSWDYVCKEPHLLAVLLL*RQSFVLLPR LVTNS*AQVIHLWP
3597	17498	A	3620	2	400	AAABPHGCYAKVLDEFKPLGEEP*NLIK QNCELFEQLGEYKFNALLGRTYTKVPQ VSTPTLVEVS*NLGKVGSKCKHPEAKR MP*AEDYLSVVLNQLCVMHEKTPVSDRV TKLLTESLVNRRPCFSALEVK
3598	17499	A	3621	3	476	LGYSVHPPQPLAQVLSPPPLFGASRAGWL LRMRGPPSPHPPRTFAGLQAPHALVPA RASPTPPCKLREWAPALASPERGSHSA VGG*RAPQMPKWEPRQGRQCQEQARALR TASMLSPLSFTHPVTLSLLNFPTSLPPR NSPSWPVVSVR
3599	17500	A	3622	40	390	MKGALTPQGRAGGLGSQSQMDMASTPKP SPDDQGCSTHLWGFFFLVSLPPSLSPS PPSPPRHSVGTHCAP*VLPRPLGALRVP HSSVPRPHAVPVVGTTRYRSRGANPLSL DFRGL
3600	17501	A	3623	52	475	AVEFHLLFLQPLET*TNLLSVCMDFILA NSPK*NQIICDLFVFFHLA*CF*DLFML EHVSVLHFMAL*FFFFFF*KGVSLEFSPG WRAGAQFWLTKTPPHSPARLKQFSCLT PGSWNYRRAPPSANFFVFSGKRGFTIL P
3601	17502	A	3624	333	466	SIIGKIRLWKMRFPWGAQAACDPGTLR G*GKRITRSGVRDRPG
3602	17503	A	3625	2	138	LRRGNRLNPGGGGCGEP*SRHCTPASST E*DSVSKNQKTKNSQWH
3603	17504	A	3626	3	337	LSLREPALPPCPRRLLPTPGQGHGPGSAG FPGRFTL*RLPPLDPDPPSLGLSPGDDP GLAREELKSPCPWGPPLCHLPFP*CW SSQPSINAYEWRKKKKKKKKKKKKKK
3604	17505	A	3627	2	393	LGTDLSLIRFELGQPGNLLGNHINYV IVTAHAFVIIFFIVIPITIGGFN*LFP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: In USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LIIGAPDMALPRINNISL*LLPPSLLLL IASAIVEAGAGTG* TGYPPLAGNYSHPG ALVDLTIFYLHLARVCSI
3605	17506	A	3628	2	379	QDATYPIIEELITFHEHALIITCLICFL ALDALFLTLTKLTNTNISDAQEITV* TMLPAIILILIALPCLRILYITDEGNDP SLTIK*IGHQWY*TYEYTDYGGLI FNSY ILPPLFLKPGDLRL
3606	17507	A	3629	1	400	PTRPPTRPPTRPMTNTLNSIHPPLEPR*K KKKKKKKKKKKKKKKKKKKKTAAGGGA *KKKNRGAKTHRGSKKLNPFKKRNKKK PPVKIEKKTFFLGGKKKKPPQKNNAK KKKNYFEGESESLLLL
3607	17508	A	3630	416	1	SQLGYSGVRDPLEEATCLFSDLKLHAGR TTPLFOAVRQGHILQRFLOPPA*LCPA PRGGVYRGRQASLSCGGLHPVRASWPLC LPTQFSAMEGAPPLALLPRSSSIDYCA SNEQGSVGIGPSEPCTGYNLLVCHLL
3608	17509	A	3631	275	83	RWGSYVVLQGLQLGSSDSPALASQSA GITGVSHCTQPKNVI*KISHLTVAGPAA DKTPQTPR
3609	17510	A	3632	186	3	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFLVQCQVPLLCNL*HLVYLF YML
3610	17511	A	3633	3	235	GIISFLLIR**YARADANTAIRAILYN RIGDIGFILALA*FILHSNS*DPQQIAI LPHPSDSKKVLYLSHIQLKKA
3611	17512	A	3634	1	428	RTLKTTLFNPDGG*DPILYQHLF*FPGH PEVYIIILPRFR*ISHIVTYYSKGNEPF GYISMV*AMISLGLGVIA*AHHIFTV* IDVDTRAYLTFATIMIAIPTAVRALS*L APLHRSNIK*SAAKL*ALRLIFLFTVGG QT
3612	17513	A	3635	2	129	PVIYSTIFAGTLITALSSH*FFT*VGLE INMLAFIPVLGFW
3613	17514	A	3636	2	422	DR*LFSTNHKDIGTLYLLYGA*AVVLGT ALNLLIRAELEGQPGNLLGNDHIYNVIVT AHAFGIILFIVIPIIIGGPGN*LDPLII GAPDMAFPRINNISC*LLPPSLLLLLAS AIMEAGARTG*TAYPPLAGNYSHPGASV
3614	17515	A	3637	14	479	QNCKINNFPYFLPHQSEFFRKSCQQN TICFRLSNQNTMKKTENHALLWIRKQ T*KQCKSNSGYTPSTPSRAKKKKKKKK KKKKKKKKKKKKKKKKKKKKPGGGV LKKL
3615	17516	A	3638	2	449	IIIIICFVGLCALVLTTLTKLTNANILDA QEVETG*AILPAILMLVIIALPCLRILYI TDEVNDPSLTIK*IGHQWY*AYEYTDY GLMFNAYILPPLFLKPGDLRLLDGDNRV VLPNEAPIRIVMTSQDVMHS*AVRTL SLRTDAIPGRL
3616	17517	A	3639	347	98	HFFLGGGKGGGFSPPFPQFFFFLGRFF FGGGGPNFPKKKGFFSKKPQGVF*TP PKKKKKFFFFPRGFWGPPGIFFGPPP
3617	17518	A	3640	2	426	DR*LFSTNHKDIVTLYLLFGA*AGGLCT ALSLLIRAELEGQPGNLLGNDHIYNVIVT AHAFVIIFFIGIPIIIIGCGN*LVPLII GAPDMAFPRINNISC*LLPPSLLLLLAF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AIVEAGAGTG*TVYPPLAGNYSHPGACAD
3618	17519	A	3641	94	294	GRGGGGVAGGRGAMWSKGRQRGRNGFVR GREGGRKSHFRKEG*KEGRKEPPPPPKK KSRGEKNQREG
3619	17520	A	3642	1	405	RTRGFDLERFVLFDDVAQQMVESGYVCEG DHKTMANAIIIDRVSLIKRKRQRLVRE EQEKKKQEESSLKQQVQSSASQTGIKQ LPFADTGITASTTSASVSTQVEPEPE AD*HEQLQYQQPSLSVLSGDTVD
3620	17521	A	3643	34	405	HLGRKONKAI*FLEAEKKKKKKKKKKKG GPLKKNPGGAKNNRGGEKKIFSP*GOVK KTPLGIFEKPPYFGGKKWANPPKKIKT LKKKKF*RGKGGKKPENPWGEKDESS PK
3621	17522	A	3644	430	81	EFAQLSPQIKGFPPSPPPNPLPPSLFGF FSPFSP*KFFPSLKGFI*VGGFFPPFSP PKKSFFSKNPQLVFISPPFKKIFLPP PLNFGPPRVFFKRPPPPPPPPPP
3622	17523	A	3645	399	2	AAAAKKKKKEFFPPPPKNNFFFSRVFF FLGGFFHFFPPQKKIFFLKIPRGFFLT PKKKKIFFFFP*FLAPPGFFL*ABPPF FFFFFFFFFFFFFFFFFSPCSWSCHQV FPHASNRIHNPSNSYPLQQY
3623	17524	A	3646	49	326	KKKKKKKKKRGPPFKKTPGGAQKNPGG EKKFFFL*GGHKKPPRGIPKKKPPFGG KNWTPPQKNKAFGGKKKFLGGKGEKPP PKPRVKKK
3624	17525	A	3647	327	94	QKKKKKFFPPPPPKNFFFSRGGFFGGG GGPPSPQKKGFFSKNPGGVFLPPPKK KIFFPPGGGAPPGFF*RGPP
3625	17526	A	3648	2	301	TSSVASTFIMSLFPTTIFMCLDQEGTIW N*H*ATTQTQLYLSFKLDYFSIIPV ALFVTWPIIEVSL*YINSDPINQFFKY LLIFLITILILVTGC
3626	17527	A	3649	2	406	STNHKDIGTLYLLFGA*AGILGTALNLL IRAEKGQGNLVGNNDHIYNVIVTAHAF IIFIVIPIIIGGFGN*LVPLIIGAPDM EFARINNISF*LLPPSLLLLLGCATVEA GAGTG*TVYPPLAGNYSHPGACV
3627	17528	A	3650	3	418	HAYADAWVHFSITLLILGLLNTLTIIY Q*WRDVSRESTYQGHHTPPVQKGLRYGI ILFITSEVFFAGFF*AFYHSSLAPTQ LGHWPPGTGITPLNTLEVPLLNTSVLLA SGVSIT*AHSLIENNRNQIIQALLI
3628	17529	A	3651	526	2	WGGGEKGRAGGAGEETPHQESQRQGCAL PQEPPLYPCCPAIHPPPLPLGGLLLFPS LPPLP*AAWFPHPGQPGRNNGESPTTR EKRLWGPPLPTPLPWPTQPTPLSRRTG CPPCPREVPTSPPPWAEPPPLPGPPSEI AHLTTVRRGAALANVNHENISDTDENKL NAFVTA
3629	17530	A	3652	464	297	RNSFHRVSQDDLDTLL*SPCLGLPKCW DYRCEPLLASYIDVS
3630	17531	A	3653	162	467	NSKKQQFVLLSEITSYVYWLHKRDLDSH TIIMGDFNTPLSTLDRSARQKVNKDIQE LN*ALHQADLIDIYRTLHPKSTETTFFS APHCTYNFLQSYFSSQF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515, I 26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3631	17532	A	3654	372	1	LMMLSI FSCVHLAFVCFLWRREMSGVSL CCPDYSGAAVHRCNHTALQPQTPLK* SSCLCKRHLQLRPQVYTTMLGYLFLFLF LRQSCSVAQAGVQWHDHSSLQP*TPGLK RSNSPTLV*DL
3632	17533	A	3655	444	341	VGQDGLLDLLTS*SACGLPKCWDYRRE PPRLAY
3633	17534	A	3656	466	315	VGHTGLELPTSSSELPA*ASESAGITGVS HCTQSGCAFCYSTMIPTKPYTC
3634	17535	A	3657	40	276	EFDTAHAFVIIFFIVIPITIIIGGFGN*LV PLIIGAPDMAFPRINNISF*LLPPSLLL LLASAIIVEKKKKKKKKTGAPLV
3635	17536	A	3658	351	470	FTTLPVTSASLPLKTLAWPGMVAHACNP STLGG*GGRIT
3636	17537	A	3659	40	182	GIRKENHLNLGGRGRIEFGSHHCTPAWA TK*DSVKIKKTRIQKTPLI
3637	17538	A	3660	160	461	INGKDTDTPGMVAHAYNTSTLGGGGGGI A*GQEFQPSLRN
3638	17539	A	3661	145	437	YFSLSLCLLELMNSVILFFFLVLERGFY PPPLVEMQGNFPG*LNPPPPGLKQFFCL TLPKSWNNRPPPPRGGNFLDF*KKRGFN YVGRVDLKLRTSG
3639	17540	A	3662	255	451	LLSFNPPPPPPFPCKGGPPSLPPGGKGG GLNFI*TLGPGQKRNPPPPGEPG*RG PTPHPLFF
3640	17541	A	3663	185	66	PLEQPLRK*LYLFRDGVLLCHPDWSAMM QSRLMATSAEF
3641	17542	A	3664	42	193	FQLLTRLRQENHLNAGGTSCSEPRSHHC TPA*VTETQSQKQKVKVLGFSL
3642	17543	A	3665	216	2	KSKGKCSFLHSRVNRGNSKELLFLRDGV WRYCPAWS*TPGLKQSPHFNIPKCWDYR REEFHHPGLVVYEF
3643	17544	A	3666	43	267	GRLWSAMTPGKLLTCKIDWPALEVWGP LEGSLDRSLVSKVWHKVTYKPRNPDPFP YRDT*LELVLDPPPPTHSG
3644	17545	A	3667	212	2	SQLLGRAEARGWLEPRSLRKINKTSQVW WYTFVLPSSCDYRHTPPRANFCIFSRD GVSPC*PGWSRTPD
3645	17546	A	3668	104	334	TVLFPPCFLLHIDFCMVLDFFSNFFVLN YF*NYRRVQKMYEFPFFLEFFLIFSF FLFFLSTFNFFLCPLCDLWYH
3646	17547	A	3669	369	260	DGLDLLTL*STHLSLPKCWDYRHEPPCP ANMPSFKN
3647	17548	A	3670	111	342	NGVSFFPPKGGIWANGNFRFPKPGG* RNFLA*PPQKFGMAGPPPPQPVGIAGP PPHARRILEFFFFFCKKGV
3648	17549	A	3671	377	3	FAIIGGFH*FPVFPGYALAQTYAKIHF TIIFIGVNLAFFPQHFLGLSGMRRYS YDPAFTT*NILSSVGSFISLTAVILIIF MI*EAFASKRKVLIVEAPSINLE*LYGC PPPSHTLEDVY
3649	17550	A	3672	39	348	AKIAPLNSSLDERMRVSKKKKGHGLTP KPFLKKKLGNFPLSQLEBGVKKKQKPF GFKGLELAPFNGKNGENPNTWRWG*T MSFFFFFF*DSHPFIQAGVQWRDLGSLQP RPPRFKRF
3650	17551	A	3673	327	3	SKDPVFFKVFKNPPTPNIGVFPFALPL KRGQFQPLFNPKGFFFFFKPVQLGRGK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						ISPQFFFKRFPWG*TKSFFFF*DSHPF IQAGVQWRDLGSLQPRPPRFKRF
3651	17552	A	3674	379	267	EPRLSPCTPAWATE*DSISKONKTKKPK LALNKKKMF
3652	17553	A	3675	2	270	FCRDRVSLYCPVRS*TPGPKGSSCLDLP SSWDYRHAPPGLAKIGGLHVFCLPCCGS LLVCWSSHCSLAHQELLLENKHTDVWVG GWMDR
3653	17554	A	3676	3	54	PVYNKKNKRPDAVAHTCNPSTLGGRGGQ ITRSGDRDHPG*HL
3654	17555	A	3677	291	30	YSLVLLIFFFYCFYSYFISLMNFCHNL YYFLLDFGLVCSYFPIILWHNEIYFIG SMFFIFSIV*IFPCWEMSCNIYKLHQE MF
3655	17556	A	3678	1	298	RDFSASASQVAGTTGMHRAQLIFVFRV CVCVCVCVCERERERDGVLLCRPDCC SVAHT*VQGRDLGSLQPPPFGFKRFFCL KLPSWGHRCVVDAP
3656	17557	A	3679	20	376	VPPPHLANPLNFILFVDTGSYYVAVAG FKLLAPCNLSASNS*SVGTIGVSHALL LLALKCNOLFQFVIFILLHAVCIYDFIM VRFSLQCFPQFYDFPFCFILFVSSKAQF CFLRLPY
3657	17558	A	3680	110	334	NTTDYFKLP*ILSGTR*DMYKQPL*HLN TVREYTSKYGWRPGVVAHACNPSTLGGQ GERITRSRDQDQCQHGET
3658	17559	A	3681	326	511	LTMMLOMKISVICCLLRNIFWPGALAHA CNPSTLGS*GGRIARSRLNPSPLLGS QPSS
3659	17560	A	3682	448	248	AKDLNTFFFTKE*TPLANKHMKKSARFT YRNVIQITT*RCLGTPTRVTGV*MRNSA RHR*GCGGLV
3660	17561	A	3683	486	176	PAPINPPQLRSLVQRSGIRFC*AGQVGF KLLVSSDPPTLASQSAGITGVSHQTWP* NYS*NSGMPHPRQASSWRLREQWYHVS LLPCAYYKNGRQNSLLI
3661	17562	A	3684	238	27	NKHILCYVGQEMGMGWGSHSHGWKPHFK SFQVCPSAVAHACNPSTLGG*GGQITLV QPGKHGKRRI PALF
3662	17563	A	3685	1	299	LITQTCVHGLKIKCI*TSKKKKKKKKK KKKKKARGPLKKKGPLKTPKPPGPPK APPPFWGGPPPRFFPGGGGAPPPVFLKKK KKNSPLWGGGGFFFR
3663	17564	A	3686	494	91	PLGKRFPGGDIALTKLSRPWAWAPPGIP PPLGGPGGGVP*VTFKPTPFRPGEPL PLKNQTFFGVPGPPPYFPPLGGLGPEIP FTPGGPGSIKLAPPPPPGAPKRNFFP KKKKEVMKMLCFHFNLLVQNI
3664	17565	A	3687	17	249	YSRFGRHFGHDPGLYFQILRLRWENHL NPGGRGCSKL*SHCTPAWATE*DPVS* KKNVTTIAKRWKQLTCPLADG
3665	17566	A	3688	296	461	FWLWVSSVLKHMNWPVVTHACNPNTLG GQGE*SA*ARV*DQPG*HGETCSAKEK
3666	17567	A	3689	149	422	ASGRQGPDRGCWGGQAPRHPARGAKPAA DMGMSGQGYTKQAAP*GDPSQRAGVRLP REPTSRKASGGSGGHSRASGGAVPGQRV AQPSPAR
3667	17568	A	3690	1	415	GDPAGGGDPILYQHLP*FEGHPEVYILI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						LPGFGIISHIVTYYSQKKEPFGYIGMV* AMISIGFLRFIE*AHHIFTVGIDVDTRA YFTSATIIIAIPTGVKVS*LATLHGSN MK*SAAVL*AL*FIFLFTVSGLTGIV
3668	17569	A	3691	1	393	GTRKYSFLHDSQTSFCLSNSIPTPSNME ETQQSNLELLRISLLLESWLEFVRFL KSMFANNLVYDTSDDYHLLKDL*EGI QTLMGRLDGTRRTGHILKQTSKEDTN SHNHDAIVKNGYLLCYCFRK
3669	17570	A	3692	402	2	FLTQRWGAPLPPIPPFWEAPFGPSP*APG FKPPLPPRGNNPPFS*KTQIYPALGARPV IPPSLGGGGGESFLPPGGGFP*PRLFP PPRGAKPNFFQKKKKCLFCKAPQAQ HRSACLHECLPLGNLLKLCPR
3670	17571	A	3693	3	434	IFYIFFGTTLIPTLAITR*GNQPERLN AGTYFLFYTLGGSLTLLIALIYTHNTLG SLNILLTLTGQELSNS*ANNLI*LAYT IAFIVKIPLYGLHL*LPKAHGEAPIAGS IVLAAVLLKLGSGYGIIRLTILNPLTKH IAYP
3671	17572	A	3694	452	208	INKSARHGSMNL*SOLLRRLEREVCLSPG VQGCIEPWSHHCTPAWETE*DKTLSQKQ TNKKTQCHLYDHRPSALEATFRLSH
3672	17573	A	3695	464	146	LKQTRATKGNLFLP*KPKLTPPGGFRPP FQPFWKPRPLGPPKSGVLDPPGPGKTP FVLKKNLLGGVIPTLFFPLSGGLGRKI PSPRGGGGAKKRPPRQKKKKK
3673	17574	A	3696	2	465	VTRLRERPALLVSSTSWTEDEDFSILLA ALEKFEQLTLDGHNLPVLVCVITGKGPL REYYSRLIHQKHQHIQVCTPWLEAEDY PLLLGSABPGVCLHTSSSGLDLPKVV MFGCRLPVCANVFKCLHKLHVDENGLV FEDS*ELAAHLEKL
3674	17575	A	3697	173	51	TFISVVFGQVVFQCMKFFSGDF*DFG APITQG*SFLSI
3675	17576	A	3698	380	26	KQRTNFFLFFFKGTGAFWFFPPFFNKK KKVFLGPGGPKIVKKKKKKEKKENQKN RKQTKKK*KTNNKQNKRETDIFGVEDE TWRQRWGLGGGRVANSSAEMGKGNSTTR PSVNS
3676	17577	A	3699	11	414	RLVVTAILIOTP*SFTGAVILIIAHGLT SSLLFCLANSQQKKKKKK
3677	17578	A	3700	1	401	SSSLTSLNNKSPFLNQVTFNEMWILVD NW**PAQWLDQEA PKHFPKPNLDQKKVM FAVWWSAAGLIHYCFLTPGETITSEKYA QQFKEMNRKLQPLQSAMVNRKGPILHDN A*SHITQLKLOKLN*LGYEVL
3678	17579	A	3701	395	140	TPPKKKKKIFPPPPKIFPPPKYKPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPSIYIDFNLCIDNL*LQKTLVFL E
3679	17580	A	3702	407	371	SPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPFLWYKDIIIGKNEQNV*CS
3680	17581	A	3703	36	409	LLKCEGIWKKEGKKKKRREKKGGPPFR VLLGGPTFRGGAHKSLFRGVFFNLGG FFPEGPPFLGGALLGPPPPPIFTPLGKK KIFKGRGPPPLIFLFF*IRGPPPPSP PSTKPPPPPPPTP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3681	17582	A	3704	56	415	QAPWGGKKKKGKEKKKKKKKKKKRG GPLKKNPGGGPTMGGGKKYFSPWGGEK KNPGGNLGGKTPGGGGNWAFFFFKKKG AGGKKKI*RGGGGKTPLIGGGKNGGPP RTSPR
3682	17583	A	3705	108	1	NLAK*IQ**IQTIMHHDQVSFIPGIQGW LNILKGIN
3683	17584	A	3706	425	52	PFPH**L*KVDPIPLPPQNFLHPSNNI YFSPSPKFFFSLQFFFFGEIFPFP PPKKNFFS*NPNLVFISPLKKKIFPSP PPPNFAPPKNLFKSPPPPPPPPPPP FSGKNTLYWVDK
3684	17585	A	3707	117	421	VLLVIAEYLLPEVFGTRSVSDFGFFRF WNICIIISG*ASLI*KSEI*NALKNISS FKKKFIFILEPRSHSVTOAGVQWDHGS LQPQTSGLKLSHLSLP
3685	17586	A	3708	308	3	RSPPPWFFFGFFFLFFFFVFQLFSS KYNITLYIKKKTETFTETNDNGNATCQN LWDTAKAIPREKFLAISTYI*KVGKHQI NNLMKHLKEIBKQKQTK
3686	17587	A	3709	94	420	KKKKKKKKGGGAFKKKPGGAKI*RGKE KKNFFLKGGGKKKVGNGFKKPYFGGGK KREKTPKKN*SLGKKKFLKGKGGKTPP KPWA*KWSS
3687	17588	A	3710	413	184	LGECLSLRSKKLWSGPAGGGVCL*FQQV RRRKWEDHLSPIRG*RALSSHSRIPAW TAEQDPVSRGLVWGLEGGSW
3688	17589	A	3711	3	104	GGCSELRSCHTPAWRQS*TSSQRKKKK KKKMY
3689	17590	A	3712	2	393	GLFSTNHKDITLYLLFGA*AGVLGTAL SLLIRAEKGQPGSLGNDHIYNVIVTAH AFVIFFIGIPIIIGGCGN*LVPLIIGA PDMAFFRINNISL*LLPPSLLLLASAI VEAGAGTG*TVYPPLAGN
3690	17591	A	3713	424	1	FFFFFLRRSLTVVQAGVQWRNLGSL*A RPRV
3691	17592	A	3714	2	130	GRVGGRVG*NLKLYSQRLEKKKKKKKK KKKKKKKKKGGGPF
3692	17593	A	3715	3	197	FHHVGQDGLNLLTL*STRLGFPKC*DYR CEPPRPAAFFFFFLKKKTLAPKKFKTL DLTTRERS
3693	17594	A	3716	3	497	RSPPSGFAPGPAGPWEAGAAAAGQPLG ARPHSPCTGGCRSAGTTP*PAGPAGPPP HAPAAAERKPRGAEQSQRVQETGPPPT RAESNPSGLRGREVPGSAGCWSGSQESD FGAGCPAVT*GTYPYRIAGQVSSRAPHP AESRGCTAGLSIGPDGRQ
3694	17595	A	3717	40	379	AITSPRSPPAVHGSCLARTHPNSPQCLP LSGTLPLPSSSLSLSHPATAGE*IWDA EKKKKKKKKKKKKKKKKKKKKKKKK SPGGALKKKNPGGNPPGGGKNISSPPR G
3695	17596	A	3718	445	286	KKK*METRSCYVGQSGLELLASSDPAT LASQSVGITGVSHQAQPVNKLPRVQ
3696	17597	A	3719	15	383	GYFLEASCLLHPLHPMYQNCGHVACLA AKENGKFMQAACGQLNSPALSNGRLS AAYGGSDCVLFFPMKMLGTQ*ALNKY TLNGPGAVAHACNPSTLGG*GGRNLRSG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						VGDQPGQHGET
3697	17598	A	3720	14	472	RSCARNPGLTHASAQYQTPLFV*SVLIT AVLLLLSLPALAAGITILLTDRNLNTTF FDPAGGGDPILYQHLF*FFGHPEAYILI LPGCAIIHIVTYYSKGKPEFGYIGRV* AMISIGYLGFIIVRAHHIFTVGIDRDTRA YFTSATIIIAIPT
3698	17599	A	3721	3	298	EAAIKYFLTQATASIIILLIAILFNILS GQ*TITNTNQYSSLIIMAIKLGIA PFHF*VPEVTQGTPLTSGLLLLT*QKLA PISIIYQISPSLNV
3699	17600	A	3722	86	505	AGAVTYIVTYYSL*KKDSFWIHSVWC*A MRVNWES*GLSV*AHHIFTVIDVDTRA YFTSATIIIAIPTGVKVS*LATLHGSN MK*SAAVL*ALGFIFLFTAGGLTGIVLA NSSLDIVLHDTYVVAHFHYVLSIGAVL
3700	17601	A	3723	432	48	FKTSFLPFLLPSCFSPFSFSLPFSFS CFLSCPSSLSFLFFLLSFHPPFPPTLL ISF*VFLF
3701	17602	A	3724	2	406	HHIFTERIDVDTRAYFTSATIIIAIPTG VKVS*LATLHGSNMK*SAAAL*ALGII FLFTVSGLTGIVLANSSLDIGLHDTHYV VAHLHYVLSIGAAFAIIGGFH*FPLFS SYTLDTQYAIHPTMIFIGVNL
3702	17603	A	3725	174	158	KFFGGGFFHFFPPQKKGGFFPKNPPRGFF TPRLGKNFFPPPPVNLGPPRGFF*GP
3703	17604	A	3726	2	392	LFSTNNDMGTLYLFGA*AGGLGTALS LLIRAEQGPGSLLGNDHMYNVI VTGHA FGIIFVPIPIIIIGGFGNRLGLIIGAP DMARPRINNISC*VLPPSILLLLASALA EGGAGTG*TAYPPLAGNY
3704	17605	A	3727	48	474	KKKKKKKKKKKKKKKKKKKKTRGPPP KKTAPAGPPPPPPREKKNPPPEGQKKPP PAH*KKPPPPRGQPPPPPPQKNPPPE KQKTWGAEGGTPPPKPPKKNKSQQIAD PPSNAAKNRHPTQEPQQSCIPPPPTP PP
3705	17606	A	3728	387	53	PPPKKGVLPSPNFTYPPK*GVFSPPLPP *KFFFSKGLIFWGGGGPNFPPKKKFF SKKPRGGFFPP*KKKILISPPREKLG PRIFLKGPPPPPPPPPPPPPPPP
3706	17607	A	3729	1	397	PTRPLQPLSPFKRFSCRTSPDVAV*VS LPSPPPSGRSFFVFL*VESFCVWIKKRF TMLARLVLD*PSDPPAWASQSAGITGA SLRASLLYIY*CFSIQGLLPBFLIQV QLLIVYPRIHHLVLSVPHLH
3707	17608	A	3730	407	0	TLKHTKKKKKKKKKKGGLLKRTLGPK *NGGRKKKIFFLKGGKKQTGEILKKKL ILGGEKKGNPPKKKPLGEKNFKGEK GKKNLKMFGVIKLTSSKKIIF
3708	17609	A	3731	3	200	GGSELRSRCRTLAWVTE*DSVSLKKKK KKKGPFKVLRGRGPGSNKREGAKKKIQG KPCPFWESF
3709	17610	A	3732	3	380	TNHKDICTLFLFGA*AGVLGTALSLLI RAELGQPGNLLGNDHIYNGIVTAHAFVI IPFIVIPPIIGGFGN*LVPLIIGAPDMA FPRINNISF*LLPSSLILLASATVEAG AGTG*TSYPPLAGN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
3710	17611	A	3733	6	394	AMISIGFLGVIG*AHHIFTV*IDVNARA YCTSATIIIAIPTGGKVFS*LATLHGSN MK*SAAVL*ALRFIFLFTVSGLTGIVLA NSSLDIVLHDTYYVRAHFHYVLSIGAGF AIIGGFH*PPLFSGYT
3711	17612	A	3734	27	238	GIPGSSHASAHIG*IIAIVLPHYLNITIL NLTIIDIIILTTAPLLLNLNSSTTLLLS RT*NKKKKKRGPF
3712	17613	A	3735	402	249	ASAHASAPLPV*SVLITAVLLLLSLPVL AAGITILLTDRLNLTTFDFP
3713	17614	A	3736	100	430	VTWPKSDSYREVKI*LEPRQTDLRALGF CLSPTGKKK*KKKKKKKKKKKKKKKD KRG
3714	17615	A	3737	158	306	FLSSVFSLVQGVLFSSLCIDRNLPDMQ LWSEIFNK*LYLQELSILGVY
3715	17616	A	3738	279	3	PGHCYFNFNLFYFQIFPQNVLANSGSL LFLYQTLILSFNIPYILYLIQISIVFQ SVIL*FIFNSYSWYGLVCLMTFEGK KQCAHV
3716	17617	A	3739	268	388	HFFFEADSVAKAGV*WYDVGLQPP PPGVKRY*LSL
3717	17618	A	3740	395	153	GWLMRFKERCGLQNIK*GEAASADARA AAS*PEDLAKIADEGSYT*QWIPYVGET AFYWKMPSTRFLAREKSMGPFL
3718	17619	A	3741	271	386	TCPPPLKLWVYELGLL*RNMRQGAHAH ACNPSTLKG*GGRISRSGR
3719	17620	A	3742	406	190	QLLKRLQENPWRWGG*GCSKPRSPRP QAWVTERDFVSKSTKTNPQKQNGERKV FFWFFFLRKPQVFEI
3720	17621	A	3743	272	408	MGLQACANSPL*YVDIAPCNNGAHSV GLMWWMLAREVLRMRGT
3721	17622	A	3744	211	407	KGKRNILFGPVKNI*FCDQFTSCVNFR EEVSLDCPGWSQTPALK*SSCLGLPTCW D*RRQPR
3722	17623	A	3745	405	189	CVSQDGLDLTS*STRGLPKCWDYRKC WTNQLFVNGQKSLNSFVCYSFVLDITG FKEIVMLVVHLVPLF
3723	17624	A	3746	120	362	LKA*EISWNGTIQTHQEKPEVQNOVIL EENIVFLGPQDRIFECQAVTAELEPEKK AIVAGCSDSHLYPSTLGGQDGWIT
3724	17625	A	3747	401	233	NSGGRGCSEPRSLPCTPAWVTRDPISK NKNKTNHQ*QKKCKR*TKVIFMTRSL
3725	17626	A	3748	353	109	LGLANFCIFSRDGVFPWPWGSRTPDLR *SAHLSLPKCWEYRA*ATMPGLLMCFI KALDFQGCVRWGGGSWTDIKLCQM
3726	17627	A	3749	412	221	HGLKECLVYPKWCQNSNISLQGHFSEV AM*QRAHNHGIHWFYHDSFPRKIWINWA RRGGSCL
3727	17628	A	3750	1	355	FHHVSQDGLDLTS*SPRLGLPKCWDYR REPLRPAENTVYVHFSSWSFTNHSGKIN *TLDQWKEQLPGWL*ILRGVFFFNPSIW NS*QKKASIYVFLCWKRDIFLYHFPVS GTFRGF
3728	17629	A	3751	423	125	QVCEKVLISLITEMQIKTTVRYHLTPVK MAFRQKTDNKCWRGYGEKGTVPVHCWWK CKVQPL*RTAWRFFK*RKIELPYDPAT PLLGI*PKERKSGQV
3729	17630	A	3752	3	171	FQPIAFLYANSEQSGKEESTSYSSYEE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						YLGINLTKEKMDL*KENYKTLMEKIELD
3730	17631	A	3753	2	247	FHHVS*DGLNLLTS*SAACGLPKCWDY RHEPRRPALTRFLFVFLYLQRLDHLIRI NSFFIMSVNGMFTFVVLLKLFNLIIHA
3731	17632	A	3754	3	197	GLELLTL*SAACGLPKCWDYRHDPLCPA QYLSFLYAINKLFSSTYLEIHNRLVCCI VTLLIYKP
3732	17633	A	3755	2	103	VSQDGLHLLTL*STLLSLPKCWDYSCEP PRPAW
3733	17634	A	3756	103	2	FRPGMVAHACNLSTLGG*GGGITRSGVQ DWPGQ
3734	17635	A	3757	394	244	ASTHPANFFCRNGVLLCCPGWSQMPGLK QSS*LSLPKC*DYRCEPPHSAS
3735	17636	A	3758	341	2	AEIAPLHSSLGMRDVSVKKKELKLNK QKPNNPLKK*AKDMNRHFAKGIQGANEH KIKCSTSTNLREMQIKTTVRSLLI*VRM AIIKSTNISCW*ARREKILITWWECK
3736	17637	A	3759	2	322	PPRPTPLNNTINOMETICMYTRCYLII AE*TLFPSAHGTLIKIGHILGHKASLNK FKRIKIIQSAFFKHNGIKLENDKRIKIG KHPNTWKLKHTSKPMSQEMFF
3737	17638	A	3760	444	422	VRLPHRPSPPDPVRVRFHHVGOACLKLL TSSDPPTSASQSAGITVPSLQ*QP*SVR LP
3738	17639	A	3761	266	1	GGGVPLGPVIPPRLPPQVRVGOALAPQP GPGSKIF*IFFGPOFKNRVFFKGRNLVF FPPLFSLLPFFFFFF*DGVSLSCHPGWSLE CSGM
3739	17640	A	3762	70	381	HSITSYI*AFINGFFLFCFVFFLIKEME SHYVAQADHELPASWAPPTSASQYAGIS GGSHTQHYFIFYWIFYFTVFCGGGFLR RSLAPSFFAQAGAQRDLGS
3740	17641	A	3763	229	390	DIPYSFCFFFFFFFWKGSFVFPQAGGKGR KLG*LKPPPPGLRGFCLTLPGSWEN
3741	17642	A	3764	119	1	QTSCRPGAVAHTYNPSTLGG*GVDHLRS GVRNQPDQHE
3742	17643	A	3765	400	200	ITAYCSLDLLQPHFLFFSRDKVSLCCPV WSRTPELK*SPCLSLPECWD*S*ATASG LKHFIKSLPL
3743	17644	A	3766	376	44	TQPIFLGPGFQAPPFGMG*PNFLF*EKK LVFFPKPKPTAPAGGGPKFPPLPRPKQ KKGPHPGSQNFQKPRPKFPPRPPTWGKK REFFSQKKKKKKRERDVKITDLNTST
3744	17645	A	3767	403	3	DHFFFKGPPSQKGEFPLFLKTFPSPLGG FG*ISLFPFPIFPPPPKKRIFFGPPLSF FFFKKKKTYPAGKGLLPFPFKKPGGGF KRWPGPPKKFFPPPGFWACSPPPFFFF FFGAKVSLVAQAGARSRSRTS
3745	17646	A	3768	407	177	FHHVSQDGLDLTS*SARLSLPKC*DYR HDPPRLARCIKNFCRGWRCNLRKSPLS LPPSAGELRAPFLDFLEDAQ
3746	17647	A	3769	292	391	RPGVVAHTCNPSTLGG*GGQITRSGVQD QTGGY
3747	17648	A	3770	395	198	LDMGFHHVGOAGPELLTSSDLPASASQS AAITGMSHRAQPY*VISMCCQCYKHFI R IFFNLHNNV
3748	17649	A	3771	1	241	RTRGRTRGRTRGLLSAHTGRYQKHPRIR

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						TPQIFSTGTTKARAGELLEPGGACSEL RSCHCSPARATRVKLHVKKFKKIK*KHP RIRTPQIFSTGTTKAEAGELLEPGGGAC SELRSCHCSPARATRVKLHVKKFKKIK
3749	17650	A	3772	112	406	FFFFFFFFFFFFFFFFQGEVPPPI*KPPPP K*FMFPKKKLPPPPPPALKLFFSPPPP FFFFF
3750	17651	A	3773	24	197	IFSVMGFCVVGQCDLLGSSNPPASV S*SAGVIGVSHHAWPLVLFVVRNKL SYV
3751	17652	A	3774	85	201	VNFFHLI*FVNKRKIKLEKKKKKKKKKK KKKKINWKKKKK
3752	17653	A	3775	1	382	WENHLSPGSRGSSEP*SHYCTPA*VTE* DSVSKKKKPNLQAEKRLTLLLIKKAIF KNRGSPCFSIKWAGFKKIKQGWFFVATR MGDRSRGTFFNLGENFLKSFLSFSIKIQ FYVLGLKNSPSRNIY
3753	17654	A	3776	1	181	IKMATVTATYRFCVIPSKLPMLLFTKL ETKILKLIWNLERA*IPKAILS*KNRMG LSNS
3754	17655	A	3777	70	385	LNKMOTKTFTSDTHTSICFTLHFIINTKL QFIPLLAIYLLFVNPPFIFINFFEEPGF CFDDLSSCFLFY*CIP*PYFFSAFFRL HLFFFYRFLSLTLDLFSFLI
3755	17656	A	3778	2	406	KDDRNTHEQVHPNASDQDEAFDPYENF FEDSDSPKSSSTEPSPHIHVPDIQMTI FHCADNFARQYIILAKKKKKKKKKKK KKKKKSSSPGGGPKKGAAPPPPRGEKN FFFFGPPLIFSGGGF*NGGGGGP
3756	17657	A	3779	403	176	FLFPIILFFFLRQSFTLVTTQTGGQQRDLG SMQPPPPPRFK*FNEGKGRKLWGGA
3757	17658	A	3780	3	248	GLNQTLRKILAYSSITHIG*YIAYLPY NPNITILNLTIIYIILTTACKKKKKKKK KKKKKKKKKKKKKKKKKKGGGGA
3758	17659	A	3781	3	330	VDRLRTGVQDHPGKHSESPSLPKKKKKR *KILPKRGGVYLNPHFFERLRGENNLTP GGEGQRETESPPCLPAGGKNKIFV*KIQ KKRGGPFKGNKFFPRGGGKKIFF
3759	17660	A	3782	399	187	FPPPAKGDFLPShLFGLPPGFSPPVPK PRPRNLILGPP*KKFYLPFPPR*TWFL* NGPPPPFFFFFLDF
3760	17661	A	3783	392	11	KKLKVNLDPHFAVPPPLGIFPKEMKAGI* RAICTLMFIAALLTIEK*WKQPNWLLVD K
3761	17662	A	3784	324	80	PGPPPPPPPAKRGFFPPPPFLVPPGFF PPPLF*TPPPDFFFLAPLKFFFSPPPA LNFFFFKGGPPPPPPPPPPPPPPPP
3762	17663	A	3785	354	24	PPNKIFFSPPQKKYFPYKTPPTFFFL SSFFFFFFFFFFFFFFFFFLC*MVH FIVKYRKCKRGTRIILHTPTLRQLVLC LSDVLLGCCIFIYVTMCDLCAPKLG
3763	17664	A	3786	3	369	SCRGLVWVYGEILLHPCRGNQISRVQK KKKKKFGASPPREGAPPGEP*RG*P* TQKEPPPLKK*APPPGPGGRPPPMGLGG PAPPPFFWPKAFKKGPFSGQBFGLK GLFFWKFPF
3764	17665	A	3787	1	125	FRHFRSRDGLDLIF*SARLGLPKCWDY RREPPRPAHSIII

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3765	17666	A	3788	427	251	LTPKGRGCSEPR*CHCTPAWVTEGDSVS KKKQAKNRCSLRMKYERNEFTSSPC
3766	17667	A	3789	250	2	GFPPVEKIKKNPFPIF*KKPGFFFPFNP FF*ISGGKGIFFLGPFFSFFSFF* DRVLLCHSGRSAVAQSQTATSTFRR
3767	17668	A	3790	412	3	GSTPITTPFWVGVALPPGGVPPPPAP PGGTPTFFFKKKKKKQNFPRPCSRYN GGLGRKNFFLEAKGSINPNFSPAPPPG GQNKTPFPKKKKKSR*MTLQSFPRPGTA PGAAM*PVSPPEPCGPPAPALSTK
3768	17669	A	3791	10	187	GCSL*LIHCTPAWVHSETLSQKKKGRG KGGFKKNGIPCFGKNKGKRFKSGFHF STG
3769	17670	A	3792	1	331	FRVPLGRLSRGEHQQQ*QQQPPPPPPP GPLRLPAGPSRKGSFKIRLSRLFRKSC NGSGGGDGTGKRPSGELAASAASLTDM GGSAGRELDAGR*DRPGAGRQTSFSW
3770	17671	A	3793	1	431	FRKGSARCRAKPKAGADGVHGHIRASP QTAQAPPVTCSSARGSWMDFSHASGPDR DLHSPSPVCPRGWAPGTHSPTGASGA*G RTPVGGGK*VAGVQRIHPGLAPG*LVL PGIAVHITKKPGSKGTITPGTVAHACNP NTLG
3771	17672	A	3794	342	48	KRENMPGVAYNPSTLGGCNPSIVGGFCN RVCNPSALGGCNPSFLGGFCNHVCNPS LGG*GGRISRSAAQDHPRQHGKMSPOK IQKISQACFARVG
3772	17673	A	3795	2	189	LNPGGRGCSEPRSCHCTQAWATE*DSVS KKKKKKGSRFQNTIPALPGFPVSGELI LGGPNL
3773	17674	A	3796	1	401	LNPGCKGCSEPRSCHCTPVWVSE*DPIS QKKKKKKKKK
3774	17675	A	3797	279	3	ILAKVYPMVNSFLEKIHYFLLVLCFL QHVLYLTFTTETGSRSSVAQAGVQWHD RSSL*PLPHGLKRSFFLSLPSWDYMH PPCLATE
3775	17676	A	3798	229	394	VFVKSLLCQPGMVAHACNPSTLGG*GGR ITMSGD*DHPGKHGEVSTYNTKKKGG
3776	17677	A	3799	380	206	AGHM*S*LLRRLRQEDPLSPGVQGCSEP *S*PCPPAQVTVRISLKKRLHERDKSS AS
3777	17678	A	3800	450	3	IYLLRGRHSLHYSRPSFYFSNYRGACSY MRPPQATLLGRNLQGITREGPAIAHSP AVRPRLSLAHAVRRLCLPRPGAPEFP AFFLPCLLVAQAGVWRDLGSLQPPPPR FKRFSCLSLPSSWDDRRPPLSS*FAFL VEMGFRRV
3778	17679	A	3801	301	10	KKQPFKKKKRCFPPLFPFKGFKGSPFP FFLTPLPLKNLPTLKPQLQIFLRTFFF FFFERGSPSVTQAGVLNHDLSLQ*TP GFKHMPSCPULLC
3779	17680	A	3802	420	51	SASSPPASFFFFPPKKKIFSHPPFFFF PPFFPPPPFF*PPPPFFFPFKKKKIF PPPPQKIFFLKPFPFPFPFPFPFPFP FFFCGFVNCQFSVLI
3780	17681	A	3803	253	73	QTTPSKRYSYVLNCCNN*ITTCRKIKLD PFLTDLKIN*KSFADLNVRKTIIDTIK KVKG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion
3781	17682	A	3804	385	55	AGTRPVFAALAAAPAPRLPLAPHGSA ATGFPFPPPCPHGEGLRGAPAASSPPLA HRSQTPNWVDCGESPIPDQFPL*NGP PALCLPQGLETVNVESLALCFTSHGN
3782	17683	A	3805	191	2	QKHLKALNPLPRCVVCVCVCVCVCNV TF*ACKICTCSDFPGPSRKRYLEFGTKI INIVDFN
3783	17684	A	3806	1	367	KLRQVIYLEDLPTIIDEGSYTKQWIFNV N*TAFYWKMKPLKTSVTREKSMGPKA SKDRLTVFLGANVVSDFLKPMPYINSE NPKAIQNDAKSTLPMYKRNKACIAAH LFTAWFTEYF
3784	17685	A	3807	3	145	LGPGGGCGCSEPRSCHCTPAWATRGKLC QEKKKR*RLDPEAEVAVSRGRAIALQP GQEGNSVSRKKKKGRDKVSLCCPAGF
3785	17686	A	3808	362	86	NPPFICSPPPFPPLWGPRQVVPWCEG* TPPGPPCEIPLPPKKSKSPGVWGPFF FPPPWGGGAPKFFLPPKWGFPOQTICPL PFGLGEKN
3786	17687	A	3809	245	377	FGYMPSPFFETQSRSVTQAGVQWHDLSL QLPDPGFK*FSCGLPL
3787	17688	A	3810	3	268	KRNFLNLIKRREKPIANFVFNISKIVNT FHLRSSTS*GYLLPPLLNLKVLNEI RQKEIKGRKNKGKKTISVYSIMLSANT EKPK
3788	17689	A	3811	2	388	SAENCLNPGGRGCGDLRWCHCTPAWVTE RDCVSKTNKKETEKYMRN*TGNMLTIID AGRRYMRCHQTITFTFFFWRGSLLIFLAP PPSQGEGIFLPHPPKWKVKVRIITPTY FCFLRTDGFPLCPGPGGF
3789	17690	A	3812	292	136	PPTVIARKGKPRPKLSSEPWFSAEQLG LPSFLCFFVCVRCCCLLFLLLFCRDEV SICCPGWS*TPGLKQSSHLSFPNCWDCR CEPLCRAIF*FFCLCTLLLFVSAAVL
3790	17691	A	3813	359	52	KKGRFFFFEKNPFGDLVPKPKKKKTPPP PNPKKKKRGAPPPFFFFFRH*VPLCC LGWFRTPGLKGSSCVGLPKPWDYRHKPL PLTKDDYYVYGLPFVSLQ
3791	17692	A	3814	382	1	GGPGMEAPLGYHIKTPFPLKPKQNNP GAKPVVPPPPGG*AGKMGLPPRQRFPLT QKGPPPPPLGGKREPPQKKKKKRVAM GDP*NSECR*GCHLRVQKEMRLPLGRNS PPHYIPNRNTDMCSC
3792	17693	A	3815	472	340	TGFHRVSQDGLDLLNS*SACLGLPKCWD YRRGLFTIIFNMGEWS
3793	17694	A	3816	247	378	PPPPGGGXGNLGLLKPLPPG*REIPPP PPRGGNPGGAPPPPG
3794	17695	A	3817	25	465	TPPLGG*GKRFPFRGPGFSPPPPKGNPP FF*KFKKKPRPGGAP*FPPPGGRPKN PLPPGPKGSH*PKFPPPPPPGETKRKPP PPKKKKKKRKKKKKEI*AYKAYICFDC PLTGPDLKSDKTLAFPSVIGLPRPCTC LSPR
3795	17696	A	3818	475	147	PPKG*RHPPGPPFRFRGPNPPPHRFFF VLRTFGYSFF*KKRGPPPTFFFTLPGP PGFLKGPSPGGGGQKIPFRGGGGPLK *IPPPPPPGKKKDFFLTKKKKKK
3796	17697	A	3819	461	57	TNQKKAAPPPLLKKKFFFFFKHTGGAP

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						PGEKKKRGGGGEEKKKRGVYRKGPAPRSRG CAPPLYRGGGLFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFHVKNILFVF*DYIVIIADL IQSLRHKDPQELLRR
3797	17698	A	3820	1	418	HAYHI*KPSP*PLAGALSTLRMTSALAM *PHFHSITLLILGLLTTTLTIYQ*WCDG TPESTYQGHHTPPVQKGLRYGILFITS QAFFFAGFF*AFYHSSLAPTPQLGGHWP STGITPLNPLEVPLNLTSVLLASGVSI
3798	17699	A	3821	385	1	LQPPFFSPLLFQVQRPFFSSFPSCPWG PVPSKLLPLQLILGRGFYQKSLLVSLG FFFFFLLI IKHRNEVLLCCPGWSRTPE LK*SSHLGTPKCSDYRCEPHPPDPWDI CSYVPFLQSTHFGILNY
3799	17700	A	3822	72	424	KKKKKKKKKFFPRKKGAPPAPPLFGKAG GEXLFPFRGLIFKKPKKAPGEKKKILFK KKKKRGGP*KKKKLKAGGGEEKKIFPKGA QKKNPGAGFKKGGRGKNRGAPQKKGGEG SSS
3800	17701	A	3823	154	2	GHHTQHTEPQRLNNSYRAELKHLNNTK NNPI*KWAKDMNRHFSKEDIQM
3801	17702	A	3824	422	212	MGSSNPSPTASWVDEPTGICQHT*FYVE MGFCHVSKAGLGLLGLRDPSPASQSAG VAGVSHCTRLWII
3802	17703	A	3825	2	417	KRVNTRGFPPPPFFKTPPPKIFMGPQKK KNFSPPPPKIFFF*KAPPSP
3803	17704	A	3826	423	65	ACGRGKYFKSGGRVKPFCAVDFPPSGKK ANQPTPKNPRKKQKPSGRGMSPMGKPPG CPCMPKASEPGPVSEFNKGVAPATKDFC PIGTA*IPSKKKKKSDPG*VKKGKPN LYSIYNK
3804	17705	A	3827	285	136	FFFLFFXFLFFFFFFFFFFFFFFFFFFFF FFFFFFFFFSGA*KIFIATIH
3805	17706	A	3828	425	316	QDGLDLLTS*SARLSLPKSWDYRHEPPH PAQTFFKQ
3806	17707	A	3829	3	169	LSNS*ANNLI*LAYTTIPIVKIPLYGLH L*LPKAHVEAPIAGSIVLAAILKLG
3807	17708	A	3830	6	452	IGFCQGFADFCSSKKFQNRVRSPPRGE GRKFLLFKGGGFQKFPPLPPGWGAKTPF LKPPPKKKKKKERKEKKKKRNPGPP VSPSSWSVP*APSEQRSGPQLPPSRGD *VVRLSPPPRFRDCVRRSATRGNSPPC RGSQGP
3808	17709	A	3831	45	387	NFGVKVFS*LATLHGSNMK*SAAVL*AL RYIFVFTVGKKKKNNKKKKKKKKRGT PPGGEKKRKFSPKKKKKKGFLKNPQPK NFFWGPQKKKGKTPFWGGGKAPKKT P
3809	17710	A	3832	463	288	DGLDLLTS*SVRLGLPKWDYRHEPPRP APCILMATFFQFEVLFSEFLETIVKSVL LH
3810	17711	A	3833	294	90	FFFLFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFF*AGIYFI TCAPPPAYPRS
3811	17712	A	3834	427	37	SYHFGRLRRADHEVRL*NRKGRPGAVT HACNPITLGG*GGRIMRSED*DH
3812	17713	A	3835	499	53	AKLMYFQSRENVAKRSYRRNQKASMVHP

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						NQEPAVIAGQGTIALLEVNLQVK*LSSYH CRLLVGMYHGCLLVSSVTPFCNIFSGLK VH
3813	17714	A	3836	304	3	RLKITKTNNNQTEINS*YIKDLNARAET IRLLEENIGGKPHDIRFAMIFWI*HLKK TKNIYKLDYTKILDPCISKDTINKVKR* PLEWEKIFANHISDKG
3814	17715	A	3837	475	135	MEGLFCPAPMVHPFIPPPPLGG*GGGSPG PGIQTTPPGYPGEPPEPFFFTLKKLPRRGAV FFPPPLGGLGPKNVFTPGAGASLEPGW APSPPPGGPP*NPFPKKKKKKRLKIGWH F
3815	17716	A	3838	415	245	ETGFHHVGDGLDLTS*SACLSLPEKCV DHRREPPHPDPQVSFIRALFPFMRAPLS
3816	17717	A	3839	460	413	WDYIKLTGFCCTAKETRVKRPQTEWDKTS AKYISDKGLKTRLHKEQ*KMTNLI*NVW K*LGRYSH
3817	17718	A	3840	2	470	GGDAPHFPDGVAAARRRGSSLLRWGCQA QGLLTSQTGWPGRDAPHLPDGVTAGPRR SPHLRRWAAGQTRSSLPKCDGGREBALL TS*VGWRPGRDAPHFPDWAARQGGSSHP RRWAARQRRSSLPKRGSGRAEAAISNSA SLQVSVKVSVCRRPGG
3818	17719	A	3841	54	332	QFGFHHVDQAPELLTSDHLPSSASQSA GITGVSHRARPSLAHSFTHSLAL*PTPA HSLIHWLTHSLTHSLSPFCFSFSSPFSHT HSLARPLGV
3819	17720	A	3842	208	468	ENPTPPPLWCFALGVL*EDGFSLYLSA HVCEIVFLYCPVLESARPLMFLWNLAHV CYYEWHLFSVSLFHTVS
3820	17721	A	3843	406	2	PSSSSSSSSSPPAAFFLGCFCGVFPSPFF LKPAPGFFFWGPKKKNFFSPPRGVKFFF FKGAPPLFFFFFFF*DGVLCHPGW SAAHAS
3821	17722	A	3844	370	253	VGLLEPRGQCSELRSHHSTPAWATE*D PILKQNETEQK
3822	17723	A	3845	369	73	LRQNGMNPGRACSEPRSHHCTPAWAT E*DSISKRRKQNSVFTESYFASEHCYS LTGGGVAILEGPTGPDGAI FMCHLRNL CRCSPILPLALQCDH
3823	17724	A	3846	198	388	FRKSINVRVHVNRLKNHTIIPIDAOK P*EKLQQLTMKYSIIMNSRKLSQPALR NLF*KPS
3824	17725	A	3847	391	20	GFPFPRVF*HGPANFFLGPPKKKIFLPP PR**TWFLKGPPLFFFFFF*DGVS LCPGWSAVSKN*QTNKKSILPIRGKLN L FVHSM L I K G F T C D L L I F K N R K V K E S T K T IDHIFSRQLMA
3825	17726	A	3848	227	2	KRRNPFHKAIAAIDSSDGR*SKLKNFW RGSIAIAIKIFRDSWEVKISILTGFNK KWILTLMDDFEGFNRTGR
3826	17727	A	3849	373	2	SSPQKYWGPGFFPPPGFKTPPPPPFFW APTKKKIFFGAGRENFFFLRGPPPIIF FFFFFFLFFFFFFFFFFFFFFFF*YNSF I*DIKTHVFLHSGVGRVLVYKTRLYFT LYHSFLKNELG
3827	17728	A	3850	394	2	EACSVTQAGVQWRNLGSLQAPRRQSFCL RGSLLSPQH*EDRT*HIGGTQQTSMNE*

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						MNLYLQWLCPLLYQLCSTSYT*EVIQLN IAFCVCLVGFFCFVFFLFFETASQSFA* AGVQWCHHSLQPLPKL
3828	17729	A	3851	3	164	NHLNLKGRGCSDLRLCHHTLANATEGDS ISKTKTVQ*RKLQNNIPHEHTCNL
3829	17730	A	3852	35	390	NFVSNSEFFFFFNGAPRGPRGGGQGN LG*GEPPPPG*KQFSFLTQPRGGNNGG PPPRVNFGLRKNVPPGGPGGPPDL GTGPPPPPEGSPPPGPQFSKTKRTAPGQ PKGGPF
3830	17731	A	3853	6	437	PNK*KTPGLPPPPFFYPFPPPPFLSFL KPFSPPPPPPLFFFLPPP
3831	17732	A	3854	1	236	PTPLRLWLRLQENRLNPEGQCGEPRSCY YTPAWATE*DSISKKKGGRLKGPTLT SGGGQGLFFLRGPQKSTSGAAF
3832	17733	A	3855	52	351	TVGIMEPQTIDVVVKLHKCTDFLLPDYI FNKQHYPKKKKKKKKKKKKKKKKKKK KKKKKKKRTKQKKKKREKKKKRGGAPQ *LTLSPPPPLYFFFF
3833	17734	A	3856	72	420	NTYGGKKKKKKKKKKKKRGGREKELW EAGGGGTTRGL*KENSGNMGPRIKKK GGKARGAPLGVSTQLL*RGEGEKCLSP GGGGCSEHKTTPLAYPGLGKKKETQSGK EKK
3834	17735	A	3857	410	107	SSSSSPLARYFLGVAPGFPLPTLFTKGP RIFFLGPP*KTFSLPTGR*T*SP*KGP PFFFFCRDRLW*PGWSEMGKQSSC LCLQKCWRYRYKPPQLA
3835	17736	A	3858	419	239	TTRSQLLFLVEMGFHHAGQAGLKLTL R*SACLPCWDYRRESLYLADA*GFYNL EDPL
3836	17737	A	3859	262	1	TAAQEFNFGGPIKKIFRCQPGEVKLDPF KRPPFFFFFLFFFLFF*RRVLPCCP GWS*TPEFK*STCLGLPK*WDYRHEPPN PAS
3837	17738	A	3860	357	133	NTFPPGAGRNKENPLFPKKKPRGVGLF PPPRKAQTEEWLYPGPK*FFFFPPPPG GKNTKKKPPQKKKKKSL
3838	17739	A	3861	253	375	TLSFQG*GGPPPPPPRGGGLEAPPPPG LFFVFWGKRGVSP
3839	17740	A	3862	3	482	YITDEVNDPSLTIKSIGHQWY*TYEYTD YGLIFNSYILPPLFLEPGDVRF
3840	17741	A	3863	1	129	LANSNYERTHSRIILSQGLQTLPLTA F**ILLASLANLAKEG
3841	17742	A	3864	289	372	NHLVKKWAKDLNRHFS*EDIQIAHREMR
3842	17743	A	3865	266	31	KICFIFSPQKKSVFFPKVRFQKRKFP PALLFSAYFFFAESSSVTQAGVVQ*CN LGSPQPPPGFKRFSCLSTLGG
3843	17744	A	3866	1	395	NTSDFCIKPRAYNESEHHWDMVRRL*G KEDNLTLDISKLEQIFETSKAQLNVS ETAMVKAVDSLTNLPVTWKTIGNST IANFVLILGLASLLVVYRIQQLRRDS DQREGAMTMVAVLSKRKG
3844	17745	A	3867	137	2	APLIKKEHCLRAVAPACNFSTLGGRGGE ITR*GV*DQPDQHGETP
3845	17746	A	3868	1	108	ENRLNPGGRRCEPRSCYCTPAWATERD SMS*INN
3846	17747	A	3869	198	302	LLNINHNVGGV*GCSEL*SHHCTLAWAA

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						ASLHPKKKKKKKKSVKSGQAFVSHYA MAILNYIREKKLFLKWK*LLNINHNYYG VLEKKKP*SYTYNLKKSQNLPLQL
3847	17748	A	3870	237	419	KEIQSKQGLRAICIPMFIAASLMIDKG* RQPKCPWREE*INKLWYKHL MAYHSALK RNEIL
3848	17749	A	3871	239	232	KAFLEHTRVKRGIQPGAVAHACNP SALGG RGGIRITRSGDRDNPA*HGFSWKGKCLGIE LVGHMFNFLRNCQTVFQSGYIIYILPMP LDS
3849	17750	A	3872	417	219	CHVAQADLKLSSSDPPASASQSTGIAG ISHRAWPRGTNP I HKGSTLMT*LPPORP HLLTSLSPRGF
3850	17751	A	3873	45	414	NILFFFFFWKSNLVPQGGGQGGSLG*W NPPPRGLRGFFNLTPRTGNKGGDPP PQ ENFGF*RKGGVTQGGGGGSKTPALGGPP GLTPQRGGNGQDPRPPAKKFGLGKKKK NRQLFFLGFFR
3851	17752	A	3874	278	2	LISIVYSIIYLYHSGFQLSKISPPQGQL AYLSIYLSVCHFLIYBIGVITMPASKID K*DLIKIKSFCTAKETIIRANR*PTEWE KIFAIYSS
3852	17753	A	3875	233	379	QCDVFNELLRMEILGPGAVAHACNPNTL GGRSG*ITRSGV*DQPGQHGE
3853	17754	A	3876	6	247	MLITSASYPEDLAKIIDEGGYNKSQIFN VDETALN*KKTPSKTFTARDKSMGPKA SKDRLTLLGANFKLKPMDLIL
3854	17755	A	3877	411	3	AKIPPLTSSQGHRTVQCQKKREREREKE KEEGRKERERERKKGRKKRKEERKGS* VRMLFLDKVDFRSQKIITDKEGHYIMIR E*MQH*DIILNMYISNNRALKYMKQKLT ELIGRVGRPGRSGTVPGRRNGVQ
3855	17756	A	3878	174	375	SFQQ*TAELEIKNTTSFTLTPPKLYLG INLTQYVQDLYK
3856	17757	A	3879	1	106	PHRVSRDGLNLLTS*SARLGLPKCWDYR REPPSPA
3857	17758	A	3880	383	24	FALNNFPQGGAFSGPLTSLPQVGLFFAP GPPPPGGGFSCLPAQSFFRIFPQKSGPP ALSFSPLFKKNPVVFFLRTQPLPLFPQ PRVFFFPFFFFFF*DRVSLCCPG*SAVA QYGSLLQP
3858	17759	A	3881	400	71	RIRQENRLNPGGGCYSEPRSRPRTTAV TG*DSISKNNKNK*NLSEIYFYFFLR WSLTLSPKL
3859	17760	A	3882	282	3	IFNFCGYIVSVYIYEVQEIF*YKHAMCN NHIVENGVSIPSSIYSLCYQSNYILLV ILKYAGWAQWLTVPVIALWEAEAGGSRS QEMETILA
3860	17761	A	3883	1	175	LYKNFFKLAEHGGVYQILRRLRQEDCLS PGG*GCSEFKSCHCTPAWVTQQDPVSKK FF
3861	17762	A	3884	415	233	SQDGLDLLTP*SARLGLPKCWHYRHEPP CPAANFFLKARYFWMVARYFWLWCNYS ALPS
3862	17763	A	3885	237	367	GPVLGPGMVARTCNPRIIGGRGRWIT*G REFETNLAMAKPCL
3863	17764	A	3886	359	108	TGQGGGGPPPPPLGRLKKKNGVNPEGKN SNKPKLAPSPPPGGKRPSPKKKKKKK

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3864	17765	A	3887	245	377	G*HLPMLPRLGSNSWAHDMILPPYPK QFIKNISWPGAVAYACNPPTLRG*GGWI KRSRV*DHPDMVKPHL
3865	17766	A	3888	406	2	SLNIFFFFFFFFFFFFFFFFFFKGRVFP LKNFFFFFFFFFKGCRIPFPPIFPLWLKVFP GPTPL*NRPG*KEGFCPPPPPPPPPP *GRVLLCRPGWNAVAQSRLTATSAHAS
3866	17767	A	3889	3	114	EFHCVSQDGLDLPTS*SAHLGLPKCWDY RRKPPCPA
3867	17768	A	3890	395	1	MVLIS*PCDPPTSASQSAETTGISHRAR QFPMLLSQ*LVCHSVTEVFLIFLLKLFY IYDILLYIIYNYILLIIYLLFLFLFFFE TGSCSVIQTGVSSITTAHYSLSKSHPSGL KRSSHLSLPSSQDYRCAPT
3868	17769	A	3891	2	189	GRVGERGGTLL*SQLLRR*ENHLNLGGK GCSEPRLLHCTPSWATEQDSISKKRFS IKALHM
3869	17770	A	3892	410	258	GC*GCSEI*SRPCTPAWATE*EPVAQKE KRKKKRKKKKHVLATLAISSLICL
3870	17771	A	3893	244	412	GIEEACGNFRVIVLKSSLALEGEPSGR DSS*EASGGRARWLTPVIPALWEAEAGG
3871	17772	A	3894	208	2	RISPPITPFPWPVTKTKG*PGFFFKN *KSFFFLRWSLALVPQAGAQ*LDLGS LPPPPGYKPFSC
3872	17773	A	3895	407	18	PLLGHPPKKAGAPLIFNLPRRPK*KPEF PFPPLSPTQPPPPPPPPICPAWLPPPGV PSSFKG*MGGPP*RPEV*GPINPFWAPS LPVWPQNPIFPKKKKWBIHCMVCPLS FNETFSFFKMESLRDGG
3873	17774	A	3896	82	401	KGFLKNSPKGEGFLFSFFFFFLFLATW LWPRKCSGAI IARCSL*LLGSSNPSDP PTSTFGEAGITAAGHAQFPDPSPPKT RAHVTQPGKLPS*SSPPASA
3874	17775	A	3897	263	396	VWWPGGLG*Y*TPPLGGQGRITRSGD QDHPG*RGKPVSTKNT
3875	17776	A	3898	2	386	KTGLELLGLSNPPASASQAGIIGMSHC AWPNLFLYWNHLYPHKK*VWPGTVAHA YNPSTLGG*GRIA*AQEFKTSL
3876	17777	A	3899	140	33	IFFFHL*GRIGFTMMLDIGGGFTGTBF QLEEVNFSVNDINKIIAFFVT*GVDV*S RIPTMAKTKPYNISLKLS*KTF
3877	17778	A	3900	377	2	TPPKENGGLPKIKVPYFRGNKFKFPLC FSKVPPISTMWVLKNQFPPIPFLLKNF FKTPKKGVSHPYFPQPKS*GVFFFSKK KNFYPPFWREQKQKQGPNAFLFLLKKK RAARPTRDPTRP
3878	17779	A	3901	2	123	RVSQDGLNLLTS*STCLGLLKCDYRHE PPCPALRCVFG
3879	17780	A	3902	188	3	LRCTWCPGTDGWSHLAHL*FKKGRPGA VAHACSPSILRGQGSWISRSVQNLGQ HVETP
3880	17781	A	3903	422	238	ILHVQLPSSWDSKRKPPFFFL*R*GFTM LPKLLNS*GSSDPLASACQRLGITGMS HYTWP
3881	17782	A	3904	414	1	STHLGLPKCWDYRHEPLHPASMSYL*I FFIYLFTHWSVSLTARMQFAEDRDLIFL LHCYISSDSNSTSVVL*YILVFVHSPWL VTTIALILGFYVVFVFLFFFTGSRSV

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						AQAGVQW*GLSSLQPSIIPPGFK*FSC
3882	17783	A	3905	396	236	DRVSLSPRLCNGTISAHCNLCLLGSS NSPGL*NRGHQIFSI EGQIFLQAMLSQ LLCSALVVQKQPYTMYKGMEMAVCL
3883	17784	A	3906	377	57	RGLVFFFPQNPQA*KNLGRGRVFFPSGAQ KNPQKGGWAFGRPPRPFGRPRPGGAR CPLNLTGGGPKGKALGPPPWGWSKFQK GVPLQWVGNSGLFFSKKKHKL
3884	17785	A	3907	341	3	TRFFFFSPLGKKGFPSKGFGLGTPRVFP LPPFLNPGPGIYFWGPIKKKTPFPFPGV KPGSFKRAPPFFFLMFIAALFMVVKTW KQPRRPSVSE**NKLSYL*TTEYFYSIK
3885	17786	A	3908	3	162	MMRKAIRGHL*NNPALEKLLPHIRGNVG FVFTKEDMAFPQKPALLOHHSQYI
3886	17787	A	3909	1	421	PTRPPTRTRWGFTMLVRLLLN*KHSQAG AVAHACNPSTLGGQGRQITRTGVQEQPD QHGETPSRTGRTRG
3887	17788	A	3910	2	424	PRVRTSPGLALSGLTGLKFSKNQKKKGK KPQTTKTQKKKSPKKKTPKKKGGAP LKKKNFNARGGENFFFF*GPKKNPGAR FKKGGGKTRGT PKKAVGKTPFFRGGE KKKESPSQFYKKIKKKVFGKKIFP
3888	17789	A	3911	3	236	GFCHVGQADLELLATDDL PASAPQSAGI SGLSHCAWV*PHVMSSSLKSLATRPSL HRVKLQKNGLRKTRRELYMKNS
3889	17790	A	3912	304	2	VAKKGKSKPGGLKKNPKIGLYPQGGP QNQIWEKFFFLTPKNRWGAPL*GGGGPP SLPKKRGPPPGWSNPPPPFFFLRQ SCSVTQTGVQWRDLEL
3890	17791	A	3913	91	344	HAAPVCGRRTLKVHPHAPSPPSSWAHP PPTWPEPSGTTWAPEGTVVTLGPPQELS LRRGVSYHCPPP*PLIWGRKWPPPLPCL
3891	17792	A	3914	328	402	KSWGWPXAVAHVCHPSTLGG*GGR
3892	17793	A	3915	16	179	GGGCSERL*RHCTSAWVTRARLSQKKEK KKKGPRKGEVATGSVWTRGELKSWAL
3893	17794	A	3916	229	46	AGPELLASSDPLTSASQSSRITGPFPLT GLYSKDHIIETANISYTNA*AL*ITLRT RGSTR
3894	17795	A	3917	42	383	AFPCFVIGRVISKGKECTLYFFLPLFFF FFFEKKFFFFSQGGKKGGEFGSMFPFS GLKETPLPHLLBEGKFWAPPPPVYFFV F**KRDFTLVARVVS NRLPSREKGLDYR P
3895	17796	A	3918	402	286	PPPPF*TPPPPKIFGAKKKKNSPPPPG ESFSF*KRPPP
3896	17797	A	3919	349	380	KKSPFPQ*RNFGSLQPPFGLKPSSPLS FPSSWVPR*TPPNPANLFFFKMRISHV AQ
3897	17798	A	3920	28	327	KTLLNQATIIQAKAGTWGHPPPLSPRE NKQKQKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKNGGGGP*KKKNFSGGGGEK FFFFWGAKNFGGGGF
3898	17799	A	3921	414	1	NFPKVS GPKLMSPPPHFFPKSFPPP PLFLEKKNRFSPPFPEKKV*F*KKPPF FFSPKKKPRFPKVLKVGKKRVLKNLG PGLLSKKGRTPPPPPLFFFFF*DGVS LCLPGWSAVVRSQTLTVTSASQVQVE
3899	17800	A	3922	1	169	LRSCHCTPSWATE*DSVSKKKKKT LKN

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						LSPOKLNRRAGKIFLRVFPLEKKSGTQLL *NRAGKIFLRVFPLEKKGGTQLL
3900	17801	A	3923	263	74	LLSVWRIPCAQKKERKKRYECEFLIVF VFDLSEENSSYISFKPILCVCVCVCVCV CVCVW*VKNFRKS**SSDRSKTKIKKH SHSYLFFLSFFCAQGILQTERSHELLPHL EVSLEKE
3901	17802	A	3924	3	129	TGFHHIGQAGLKLTL*SACLGLPKWWD YRHEPPHPAPFCD
3902	17803	A	3925	281	10	NLEPLPGATDYPASGGGGCNEMRSCHCTP AWVTGAKPHLRKK*KKKRQMLKTIKEM GNFNMVYILDKITK*FLYFKQLILSFLM GELGVK
3903	17804	A	3926	110	1	QLGAVAHACNPST*GGQGAELHRSIGQ DQPGKHGK
3904	17805	A	3927	180	368	EINFITNYIILFFNRQGLALSPRL*SG GAIITHTLKLHDSSEPPTS*VAGTS GTYHHA
3905	17806	A	3928	92	2	VRPGAVAHACNPSTLGGGBG*ITRSGDR DH
3906	17807	A	3929	2	146	HLNLGGGSCNELRLHCCTPAWATE*DPA SKKKKSFKITSAFTCQIVML
3907	17808	A	3930	221	3	KERAIWGTLELMVSKIFPI*LKQRKNL* PPNICKYNNLLRP*LGPGTVAHACNPST LGSRGGRITRSGDQDH
3908	17809	A	3931	1	102	GGRGCSEPSHNCPTA*VTKRDSISKNI NNKIVK
3909	17810	A	3932	351	69	GQGGGFRFIQPPSSRGKRFPPPPPPPIW G*RIGPPPRANFFFLFF*KRGFLEGRE IFFPPPGVPPPPPPQNFQGGGAPPPP PPPPPPPP
3910	17811	A	3933	401	94	RGPPPLNPPLWEKNHAGPPKVG*KKPP PTKKKPLFS*KTKIFPPGPPPLIPPPR GGKPKKFLYPPKFRFREPCKGPPPPRG TKKKTTPPKKKKKKKVS
3911	17812	A	3934	184	2	LKEFFPSRNSRSLHTSNF*HLFI*LII YFFEIESYSVTLAGVQWSDLSSLQPRPP GLKQ
3912	17813	A	3935	2	393	KILIKVEIEGTYRKITNAICEKPTANIV PNRKKLKAFFLRNGTR*GCPVSPVLFNI TLEVLARVIYSEK*IKGTIKIISIATME NSKKFPQKTENKTTICSSNSTTGCISKR KEMHISKRLHSPVYCNT
3913	17814	A	3936	291	2	FPFPPQTRGPKSSRAHSPPGPGPGSTT GAR*PFRPLLVRASLRPPLGLPTPTGP TGMQRPEA*RTPATDKPQNSRRGP*GA WGRPGCRCRGA
3914	17815	A	3937	382	1	QWTAQTWSVQNELLLFCLKPHPPPSLLP PSSCPGPHLGTPWTPAFPSHPTSTLKAH PIGSGPSSPLLTSRMPPEIQTATG* PASSLTPTVCSQHGNRFFKKGVRAGRS SHLESQHFEPEAGG
3915	17816	A	3938	398	2	PPPLLLNKIGAKKKAFFCFSPFGPRRTP CGQTKKSVFFFRVP*DKSTFDCLCPI VYVKKQIWLAPLHCVFSGRVAQGSKKSP LCLSLPFFFFEMESHPVTQAGVQWRDFR SPQPPPGPKPFSCGLPSS
3916	17817	A	3939	240	385	KLLFLFLFIYFF*DGVSLLCCPGWSAVVQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						TLLETPSAIPGAGGTPVSP
3917	17818	A	3940	230	381	LISSSYREYLAKDLRFSSKQS*WLCSKE FRGLGAVAHVCNPNSTLGGQGRW
3918	17819	A	3941	1	107	CWFWVS*TPDLKQSTCLGLPKCWDYRQA QPHRNLL
3919	17820	A	3942	2	95	DLLTS*SACGLPKCWDYRRKPPRPALF AFS
3920	17821	A	3943	163	404	CRHKAQWLPQLPGHLLSEKTLKYSSPK GLRSQH*KLLFLFCFG*TESRSVTQAGV QWRNLGSLQPLAAGSKRFSCLSLL
3921	17822	A	3944	3	200	GLDLLTS*SAHLGLPKCWDYRRPRLA YFTFIKKKKDGGCELLNLFNNSCMDTAH VHPAHLTGG
3922	17823	A	3945	423	2	LFFFFSEV*SHSVAQAGVQWYNLGSLS S
3923	17824	A	3946	209	413	TTCTEQCNKTRRLGAVAYACNPSTLRG* GRWITRSGVRDRPDQHGGETTKNTNISTT KKSTNTKISQA
3924	17825	A	3947	425	3	SPSQGLRDKTPIISLGQSTWGKGQMAQR QQT*TSWPDGSESSRSPTFEQQISER SSSAKGQTNSSSGSLNSVSPDWETPPSR SQQTPHTGELQLASGRCSGMMNLPEEGT DSNLCCSATHAS
3925	17826	A	3948	299	3	ASQTTTFREGCFLFFSFFISVCLFVCLFE MEFHSRCPGWMECNGDRARLHLKTTITT TIEIVKDDTNKWKHIH*RLPNIKMSILP KVIDILFNALPIKI
3926	17827	A	3949	331	374	NAPKSERASKAF*ATLEENKEKLPLDYN PVVHPHGHI*FKCVAPPHCLGWDLSAVPA SHALGFPQPNASAHVARSKAASCLGT AVTSAGSGVLGTPNKMPPQVRERARLFW R
3927	17828	A	3950	439	69	TNQKVVVPPKEKGLFKKKQLRPRVGGPA FHSPPLEGGQS*FP*GQRFKPRPPWVK PLFSKNPKNYPGGGAPFFPPSPGG*GG KFPPTPKAKVFFIQISPPPAQAGGPTQV PFPKKKKKSH
3928	17829	A	3951	422	3	CFFALGIGPPHPPKRVG*KGGTPPPGLF FGKFLKEKNFGKNPGPGQGGPFFPKKQ RGPFNNGRPGKVKKGAPGPGVPPKKPP RVPPPPGFFGNPPGAPPKFFFSRGGED QKRKNFFFFFLRWSFTNEAQAGVQWR
3929	17830	A	3952	223	3	ALFFWGRGTLPRVKGLNPKGGGKFFFF FFF*ETESHVAQAGLQWHDLG*LQPPP SRFKFFSCLRLPGSSLS
3930	17831	A	3953	1	388	EKGVSPPGRTCSERQWCHCTPVWATERD SVSKKKGMSNNFSLILRSWNNKGGQGT FQQKFIYPCFLKIKGHSYNCKIPKK** NLSLHVHVTDVNVRILQLDCQIHWD FNFELNILQCQGLGGCK
3931	17832	A	3954	1	396	KLRPKDQDTWPTQSAIVVEFVPPSVYF VKSISEILFFFFLKKNFPLGPPQLKGRGQ ILVKNPCPGGKKKFPAPPPQRGGKGG PPPPQFIFVFLKKTGV*KIGPGGV*TPA LGIAPPPFPKGG*RGGPPF
3932	17833	A	3955	2	199	PGGGGCGEPKTRGCTPANATERDSVSKI NK*KLKLKNSWLYAKSLASSPTGR*EE WGCFINEHI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
3933	17834	A	3956	393	2	KEFPLFPFGAPPNPLSGPFSVLERPKCG GGVVPGINTPPGGGGFPQGSILWAGDFP* PLFSPQIPFFKKQKFFFLPRGGLWAPF FPPFGGPLFSQNF*KTGF*GGFFFFFPG DGVSLCYPGWSAVAPHAS
3934	17835	A	3957	278	390	LVYIFKIRTCWPGAVAHACNPGTLGG*G GRVTRSGDQ
3935	17836	A	3958	385	311	GPKNPASASQEGETTEV*HAWLIFFL FFVELWSSHVAQAGLKLPASSDQS*TLY I
3936	17837	A	3959	410	119	SPPPRFKTPPPEFIFGAPKCKFFSPPPR PLNLILLKGPPLFFFLPKAPKPHINFV FPPQKKKNV*INLYFPPPKKENESS*GK HFALHCNPSCISK
3937	17838	A	3960	77	400	TALPLPKKKKKKKKKKKRGGPLKKKK FKAPGEEKKNFFKGAPKKKFRGRV*KTG ERKKPGGNKKTFGKKPPFPRGEKKKKP QA
3938	17839	A	3961	2	194	CL*SQLGLRLRWEDHLSGN*GCSEP*S PHCTPAWVTE*DPVSRKRKKYPVUNQTL RGFLSPA
3939	17840	A	3962	52	409	NSKTSQEKRRVIRLSLRVRVGDTRKV NTRRWGVFGWHLKNLPTTLVLKMEKIL ETYPMTDLHDPTTSYFNGCQLQAIKV GGTITDLIVE*IVSKPNAAGLSLNNVN AKFNDLI
3940	17841	A	3963	382	96	LSSQLLREAGERNE*TGWLQOPLQMIH KNPCIEPRRYCTPAWATEQDPVSKNKQ TNKQTKNSLHL
3941	17842	A	3965	3	169	DAWELRSHRCPPAW*QSETPSQKKKRG KKKIFRFYLFNKRKKFLNGGNLGVIP
3942	17843	A	3966	1	121	AGFHRVSSDGLDLTS*SARLGLPKCWD YWCEPPHLAENS
3943	17844	A	3967	200	2	PPFRIYWGEVLTPLFLRVKPKFFKPWGF PFCLFFFFFEMESRSVAQA*MQWRDL SLHPPPPAFK
3944	17845	A	3968	471	440	MELRFYHVGTGLKLLTS*APPVMASQS AGILGVSHSTW*EAPNSLAITFLSSHLS PRQP*THLGC
3945	17846	A	3969	214	2	EGQPECQLQAGDWVSLWNLVCSGLEVRA WREAPRLEWSFCLFFVSEM*SHSVI*DR VQWHNIGSLQPLPP
3946	17847	A	3970	53	398	GDLPKKQQQKPLNFCQLLLYARLFGP IFLV*HLATYNNKHLLECVGKVMINCOA DILNKMEISKVGAQKKKKKKKKRGG PLKKKKFIPRGGEENFFFLGAPKKKTGG GFK
3947	17848	A	3971	396	160	KRRIKEKEDNKEEKDKEKKASGKKERK KEKIRDRESKEESSNLLQEELSLCCP SPGHPPNSSL*DPYFATGNSLRC
3948	17849	A	3972	416	3	FPPFRVPEGVPGGEGVFPFGFGKSGVP FPRPRGGGAPI*KPPFPFGPPNFFF*K KTGPFSPPGGAPPAKRAPPPFGGGGG KIPTPLKKGGLFFGPPKKGVPFGPKKT LFFPQKKKKKKGRPPRSHASAHAS
3949	17850	A	3973	232	381	YKTFSLIF*LFFFRDRVSFCHPDRSAVV LS*FTVASISWAQGILLAQPLE
3950	17851	A	3974	396	141	CCFFPPPKRGFFPTPIFGGPPGFFFPF

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						F*NPPPKIFFGAPKKKIFPPPGGKNFF FLKGPPPPPPPPPPPPPPPPPPPPEDG
3951	17852	A	3975	286	422	RKQLISPHSQDNSKQKEQSWRHATCLQ TILQGYSNQNS**APIAKTILSKKNKAG GITLPVKLIYYKATVTKTAWYWDQK
3952	17853	A	3976	3	116	GFHRVQNGQFDLLTS*SACLGPKCWDY RHEPPRPAP
3953	17854	A	3977	223	399	EGPRTQSFDDTEVHSVTQDGVRRRNLS LLPPPPGIK*FFYLSLPSNWDYRRLPPR PVN
3954	17855	A	3978	227	422	SFPSPCIFSSLVDLGVSIYCLGWSQTL LKSSLSFSFPKCWDYRQ*ATTPGLPVYP FPPFVTFEF
3955	17856	A	3979	519	313	KKNLLNPGDGGCREIKSSHCAPAWVTEK DCLKKKKKTSVCVCVCVCVCV*NHL SSLGLFPEPVLN
3956	17857	A	3980	217	414	IYIFCGDGVSLCCPGWLKQSFCLSLPKC *DYRHVP RPPTS FHLLTNIGVLQFLKQ ATLSFTLELL
3957	17858	A	3981	2	409	KLTFAY*DY*EKLLLSLASLTSQAALF PEHPYTVISNCPSPANYIFTLSSGTTFF QFYAKS*CVTYE*KKNLLSPPTGDKPN *GRSQTKKIQT KY*SBICFFVHLFETGS HHVAQAGLELLSSRDPTSAQST
3958	17859	A	3982	234	416	SVLPSTPLNKL*KSKKKKKKKKKKKKK KKKKKKKKKKKKKKKSRGGAPKKK
3959	17860	A	3983	414	291	GGRACSEPRSCPCTPAWATERDSV*KNK QPNKQKNKKDLL
3960	17861	A	3984	192	415	TNANKLDNLDMDRFLFETQNLRLNNEE TEYQNRPVTRBIE*VKNLLTEKKNPG PDGFTGEFYQTFKEKLI
3961	17862	A	3985	403	145	AFPPPPPPPGKEGDFSTVLPFGGPPGFS PPPVFKTRPRNFFLGPCKKYSFPPPGP KNWFP*KGPPPPPPPPPPPPFWKLGIEV IS
3962	17863	A	3986	255	425	GGRFKGSNFTSAGLQGFXXXGPPKFTS RPGV*QRGEWKNPGVNLFALSTSPFGR N
3963	17864	A	3987	247	2	EEAVRVSNLYTKLDEEQ*VVKQLNYVE RLKK*ELFLQDLYRKVPLKI*IF*VKNL NSEFWDDVAHACNPSTLGGRGWIT
3964	17865	A	3988	1	394	HHHTWIIFFKFFCKDGVSLCCLSWARTPG LKRSSCFRLTKCWDYRHEQLCPAFKHFF LY*HNFMSTEMQE*HRNS*YPSPTVPK GVTFYYISYICFIILILSAITYKFVHTY IVSLNHVCYSNEAPLSLNI
3965	17866	A	3989	208	402	ETDRRLKSGGSLSKTLIKCMTCFVVFRD GVSLCCPGWIQTPLGK*SSCISLPSSWD YRHMPCPA
3966	17867	A	3990	2	408	THRPYHATPTYLFPFTNNLIKGGKKKKK KGGKKKKKGGPPFKKHFSPPGGEKNFF FYGPQKKKSRGRV*KRGEKNPGAPQNK PLGKNPLFPGGGKKKKPRFAS*PPPPPF SFGKKRAPPTKYPGAGLHP
3967	17868	A	3991	81	406	KGGLFLLPRGKGKGIWVGKNLGLKNKK NFFA*PSEEGEKKGGPHQAGKILKPGGK RGLNKGKGTGQKLKPGGIPPPGP*VGE KKEKPAPGOKLFFKKRKGOKNF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3968	17869	A	3992	396	64	YSSPEPTKKTDDSDASRGPPFFPPPEK RGFFPNDFWVPPGFFPPPGF*TPPPVF FFWAP*KKIFFPPPRE*KFFFLKGGPPF FFFFFFFFFFEHLQVLLIC
3969	17870	A	3993	367	193	KLWEKKKILWKKG*GEIKSCHCTPAWAT RVKLCITKKKKKKKKGGEGEIPKKKS SFLGKQKKRGPAPF
3970	17871	A	3994	188	2	KRANTLPDFKTYKATVLKTLWYWRKDK HRSMKQN*ESNEVELLYHNIRNKLKMD HRLKCO
3971	17872	A	3995	2	147	QENHLNPGG*GCSELR*HYIPAWATE* DSVSKKNYI**TSHIFSGDF
3972	17873	A	3996	23	329	RNSFIRSAFNSVLNKKVVLTLTSEKKKK KKKKKKKKGGKRREYLTRRGAGENNKYF YK*KKKKNTCG*KKKGWGRKREREKKRL GGKKKPPPFEEEGKKKPG
3973	17874	A	3997	164	392	KPLGRAGLVPCLCSSFTGFLM*KTEPCS VVQAGVQRGHLCSLQPSMPFKRPSLLS LPSSWDYRVLRLRHSWSAVV
3974	17875	A	3998	396	3	FFFFFFPPGGKGGISDSPQLFFSGVKNF PPPPVNWGLRVWPPPKNFFFFFF*KKV FSFFWGGPPNPPFFSLLGGPPPPPIF SGEKIPPSLFFFFFFFEMESCSVAQAGV R*RHPGPLQPPPPWLKQF
3975	17876	A	3999	383	2	VPSPEKVGIIKKIQPLDPFF*FLGDCQRK KKSPS*RP PPPPGKKLN*IRLMGPPFN SKEFFF*KP*AFKPPPPPKGEGI*GFF SRAHSFPNQALFWFFFFEMESHSITQA SMQWHDRLSLQPPPL
3976	17877	A	4000	213	1	RGRQNTLPLTKPNQTKPNQTKPNQTKP TTFL*SVIEIRVKKKYKTRKTKTKNPTT SLTRSLGRYKSPTRP
3977	17878	A	4001	412	129	GSLSSPRLECSGTIPAHCSLNLPGSSSP CTSAFPRVAGPE*MGQACMPCLPVNFFF WGGGGILVETRSC*VAQADLELLSFSDP PASASKVLEL
3978	17879	A	4002	411	293	RDTRCLPP*LDNFVFLVEMGFHHVGOAG LELLTSERIA
3979	17880	A	4003	46	392	QDFFFFFFFLGKGAPPPGKGGTFFPK KKTGGGPRGPPLEPPPLGGPGPPPEPGG GDLKKPWPQGTPL*KKPKMGGGGGGP P*TPGTGGGGEKNPLTPGGGPKNGPPPP PPG
3980	17881	A	4004	360	1	KCLGFQFFFRFWNICIIFISQLSIASQV QKSEIQNAPMSIFFEHHVSFKQFQILEH FGFWIFILGMLSTYKTLILLKLN*RFNA MPINIPVVFMEIDKLILKFTWKYKEPR RVKAILRN
3981	17882	A	4005	152	408	NKPVSHFYWMGNVLSRYPOFT*QFSFCH VRLPSVF*YLYTRNKILIFFAHKAFFLD AKYVCVCVCVCVCVCVYFGIGEGNLP S
3982	17883	A	4006	411	67	YLPPSSPTPGVFFFFFFPPPKKEFFPNPF ILGTPRFFFPFPP*KPPKFFFLGPKKK K*FSPPRGKKIFFFRAPPPPPPPPPF FFFFLLGGSLSFMYFHIKTYK
3983	17884	A	4007	217	2	PLFFFFKHLKAYSDVIHISFAILRYLL F*DRVSLCHSGWSAVARSWLPVAGQNTF

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3984	17885	A	4008	235	406	ITRQEAPYLLAIPRV GRHRVSSNPISI*RRRGLSLLPKLECSG VSIACHSFDLPG*SDPSASASRLGLRLR Q
3985	17886	A	4009	833	237	SLDNRRAPCLVSFIFPKGRSTAERCAP GTTSPFPFRLSERGHPIIPS*RGWERKS QLCSHLQSSRDPSGLGRAGCGGGDLRE SPGTFPGNGGSDLVPVPTAFPIBPOIC QATCAVMKLSFDEEYRRAMNELGECPRS SGKPSSSPRTGGSSAAKGTQAGSSELG LGIGARRGTDLSLHSTSHWTVTLGPL SP
3986	17887	A	4010	276	2	VEVKGNNSPSEGSITLIPNDKQPKETT DQPLMSTYAKIESPGKNPSHDG*LIFDK GAKIIQ*VKNSIFNKWCWNNWDFHVKT MNPHTLI
3987	17888	A	4011	188	27	REKFQIYTIKNDKGSITTDTER*KIIR DYEHLYAHKLENLEEMHLIGIPP
3988	17889	A	4012	1	202	CLHQKVIISN*L*ATTQTTQLSLSFKLD YFSIIIPVALVVTWAIKFSL*YINSP PKKKEAEKDLN
3989	17890	A	4013	1	403	CLDQEVIIISN*H*ATTQTTQLSLSFKLD YFSIIFIPVALFVTSIIIEFSL*YINSP PKKKKKKKKKKKKKRGGAPLKNRGGP NFWGGGKNIFFFPGGDKKPPRAPWKKP LFLGGGNLGP PPPQKFTPWGKK
3990	17891	A	4014	67	439	TELIIFYIFPETTLIPTLAITR*GNQP ERLNAGTYFLFYTLVGSLPLLIALIYTH NTLGSNLILLTLTAQELSNS*ANNLI* LAYTIAFMRKTKKKKGGGLLKDPWGGQ ILAGREKIKFFP
3991	17892	A	4015	3	260	LIVPTIILLPLT*LSKKHII*IINTTHS LIISIPLLFNQINNLFSCSPTFSSD HLSHPILLKKKKKKKKKKKKGGGA F
3992	17893	A	4016	258	3	LKKIFSPPTINLFFPPFPLKFFFLSL *FFLGVFSPFFPPPKGFFPKIPGVFF SPPFKKKKFFPPPPFYFAPPRVFFKGGP
3993	17894	A	4017	287	2	KKQKNFIFFFKNLSFFGRGAFFPLFP ILRGKGGDFYPRLKPALGNQ*NPFSR F*IFFFFFFFLRRSLAPVTOARVQWHD PSLQSPSGFK
3994	17895	A	4018	228	487	SYDVKQEKENG*ASKYWAYVFHSPFLS FFFFFKKNFFFCQGGGQGNLSLRE PSPPGVKLPLGLNLSKSW*QNCPPPI IF
3995	17896	A	4019	35	228	EELNHLNQGGEGCSEQRSHHCTPAWATE *DSSQKNKFWYIHCNRIVTTTNTPMT ESPKHYAE
3996	17897	A	4020	2	402	ARGNLNTFFDPAGGGDPILYQHLF*FF GHPEVYILILPGFGIISHIGTYCGKKE PFGYIGMG*AMISIGFLGFI*AHIFT VGIDVDTRAVTTSATIIIAIPTGV*VFS *LATLHGSNMK*SAAVL*ALG
3997	17898	A	4021	1	420	TRGATELIILDILVETTLIPTLAITR* GGQP*RLNAGTYFLFYTLVGSLSLMGL IYTHKTIG*VNILLTLTAQEL*NS*AN NLI*LAYTIAFIGRIPFYGLQL*LPKAE

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3998	17899	A	4022	409	3	VEAPIAGSIGLAAGLLKLSGYGIIRLTL LEMASCLIIICNNNNPFFVQIVTCDEKWI LYENW*LPAQWLH*EEASKHSPRNLHE KKIMVPVW*SADGLIHYSFLNCPETITS E*YAQQINVMH*KLQGLQLTFINRKGPI FLHNNTKLHVAQPMQLQNLNELA
3999	17900	A	4023	464	374	HLPPWEDKARRHLPDARTFILAFASRN VRNKFFSLQATQFLVLYASSTKITKPLK TNQKKRLKKSEQSLRNMWTPIKRTNICI VGIIIEGKEGKGAERIFBEIVPQTF*NL VKDIK*KVQ
4000	17901	A	4024	58	323	RHKLLCEHVKKCSAVLIIREMQTKTTLK YHFLLVTLAKIFNLIHF*RSVGETLICQ WAGRNAKS*PFWRRISQYLTKLYVCVCM YTHS
4001	17902	A	4025	480	150	RNSLLRRLRQEDGMSFGCCGSEL*LHH CTPAWVTEQDPVSKKKKKKAYDPDPIPK KTDKSNKGKGPDSRKNPKNPPPPWQ RSTAFRGRAAKSCPTH
4002	17903	A	4026	204	1	KKKFGALFFFFMQGLTLLPRLEYR*WCD HGSL*P*PGSSDPPTSVSQIAGTMGVH HEFLRSGVVLSEK
4003	17904	A	4027	116	472	MPPLPKPVSGPRPHSCSPLGGPQLSTPL TGPRPASLSLPISEGICGCITAILWAVW YLVQLMLGLSLFMA*RGAGSSCSAHKKW WLGLASPSC*TFPKNRTKGRARNLTPVI PALWEAE
4004	17905	A	4028	355	444	VSYKKK*SRPGAVAHACNPSTLGG*GGR IT
4005	17906	A	4029	410	181	ASTILLIAVFFNNILSQQ*TITNTTNQY SSLIIIMAIKLGIAFPHF*VPEVTQG TPLTSGLLLLT*QKLAPCF
4006	17907	A	4030	49	474	PXRXKFCHIVTYYSKKKBPFGYIGMV*G MISIGFLGFIV*AHHIFTVGIDVDTRAY FTSATIIIAIPTGVKVFS*LATLHGSNM K*SAAVL*ALGPIFLFTVGGTIGIVLXN SSLDIVLHDTYVXAHFHYVLSIGAVFA II
4007	17908	A	4031	274	427	FFF*RMESHVSTQAGLLGRNHSLLVLPQT PGLKRSSLSLLSNQYRSGPHT
4008	17909	A	4032	205	393	TWGGFKNPSPGEG*IKKMHDFNEMFLQN CWKILFFGGGPTGQIFPRAAPPINKNI LVWGGGK
4009	17910	A	4033	2	386	SEPLSRKKLYLSILISLQISLIITFTAT ELIIFYIIFFTLTIPTLAIITR*GNQPE RLNAGTYFLFYTLVGSPLLIALLYTHN TLGSLNILLTLTAQELKKKKKKKKKK KNIGGPPLRAPSGAPN
4010	17911	A	4034	3	169	GLFLAMHYS PDASTAFSSIAHITRDVNY G*IIRYLHANGASIFFICLFLHIGRGL
4011	17912	A	4035	3	317	HASADAWAFIGYVLP*GQISF*GATVIT NLLSAIPYIGTDLVQ*I*GGYSVDSPTL TRFFTFHILPPIIALAALHLLFLHET GSNNPLGITSQKKKKKGPPF
4012	17913	A	4036	446	194	KKKNQPGGPPPPFAFPVGGLIKRFPPPT PGKKFKFR*KFFPPKGGFFVRDPPPKPG CWEREKKKKPLNTDKWVILEGSEAGLF
4013	17914	A	4037	213	1	GMAKVKARFLPQKRGQRVLPNPPWGWKGF

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						PNSGTTKETPFFFF*DRVLLCQPGWSAVAQS*LTTASTFWAQAI
4014	17915	A	4038	307	36	RKGFFFSKCGEFKKLPFGPPLGGWYLKLI FCQKKFFHPKFPFP*IFLPPPKIFFI FSFEMEFCSCCPGWSAMGRPRLTATSAC WAQANS
4015	17916	A	4039	2	372	NDTSLTVKSGHQWE*TYEYTDYRGLVF NCYILPPLFLEPGDLRLLDVNDNRVILPI EAPIRIINTSQDVLHS*AVPTLC*KTDA IPGRINQTTFTGTREPVYVYGCSEICGA HRRSMLIVLELI
4016	17917	A	4040	107	279	LLLLFFFFWRKSLALAPRWECROKI*GH CKLRLPSPCHSPA*ASPEAGTTGWTYGCF
4017	17918	A	4041	3	351	GSHVIAQAGLKNPGSSHLFASAAHSAGI TGVSHHAWLKIFFKESVSDYSPHLNSRK NAVYVSFFFFWKSFVFPVQAGGKGLNL GSLKFSPLRLKQFSCLTLPRS*FYGLAP PPFV
4018	17919	A	4042	1	385	RPRRPDIE*QERRTOEVLQAVAKVKKE SOLPGTGGPKNVLPVPRAKAERPCKQA EASGLKKETDVVLKVDQAQEAKEPFTQG KGGQTTPESEKAPQVTEI*SSSELT TCQARTLAGVKSQEMV
4019	17920	A	4043	3	282	TAILIQT*P*FTGAVILIIAHGLTSSLL FCLANSNYERTHSRIIILSQGLQTLPL IAF*LLASLANLALPPTINLLGELSUL VTTFVSVDAA
4020	17921	A	4044	2	407	GTRLRIMSRNHGIFPFTLEIFKDNFEE PYREALPTLKLRLDSLYFGIEPEHVS* ESLEESCFATPTSKIDEVLKYLIIRDG* VSDDSVKQYTSRDHLAKHFQVPDFKFEG KDHKEVILH*RDLCVGVMDERSR
4021	17922	A	4045	4	380	ENWLTIIQAWHEADRNLTTFDPAGG GDPILYQHLL*FLGHPEGYILILPGFGI ISHIVTYYSKKPFGYIGMG*AMISIG FLGFIV*AHHIFTVGIDVDTRAYFTSAT IIIAIPTGVKVFS*LATLHGSNMK*SAT IIIAIPTGVKVFS
4022	17923	A	4046	2	94	ADRNLTTFYFAGGGDPILYQHLL*FF GHPEGYILILPGFGIISHIATYYSKKK PFGYIGMV*AMISIGFLGLIV*AHHIFT VGIDVDTRAYFTSATINIAIPTGVKVFS *LATLHGSNMK*SIPTPILIFRPP
4023	17924	A	4047	376	138	LLARQROENGVNPGGACGEPRSRHCTP AWATE*DSVFLWREALLTQTAPFNRLQ LLALPSEFFHFRILIVLQPHHSQ
4024	17925	A	4048	145	226	EPIQACSSRRVCETPQACSSRRVCVCVT PSRHALPGVCV*EPIQACSSRRVCVCV RAHPGMLFPACVCV*EPIQACSSRYVCV RAHPGMLFPACV*AHPGMLFPACVCVCD PIQACSSRLCVCV*ERAHPRLLF*ACVC VCESPSRHALPGVCVCVRAHPGMLFPVC VCESPSRHALPGVCVSPSRHALPGVCVCV
4025	17926	A	4049	2	414	ADRNLTTFPDPA*GVDPILYQHLL*FF GHPEVYILILPGLGIISHIVTYYSKKK PFGYIGMV*AMISIGFLRVIV*AHHIFT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VGIDVDTRAYFTSATIIIAIPTGVKVF *LATLHGSNMK*SAAVL*TLGFIFL
4026	17927	A	4050	472	228	LTRDGGACPFSSKLFRRVRQKNPLVLGE* SCSEPKLCPCPPAKKTKDYPVSKKKKF IWIINRTKIPRKRKKKNKAYHKVKYF
4027	17928	A	4051	238	3	RRHGSFAPLPPLPLCISYIWLFTITLC NILYLYFETGSRVAVQVGLKLLCSSEPP PSTS*STEITGMSHGARGPHNIP
4028	17929	A	4052	225	172	IARYPFHIQSCNTMPSFNKSTTSKEEDN GPGAVAHACNPSTLGGGGGQITKSGVRD HPG*HGLV
4029	17930	A	4053	471	30	GPGGIKISGALFPLNKVRVPVVFPRPP LIFPQKGVFNQNGDGGGFWPGETPGR VPPPPGVFFVKSPFLSLPFPFPPV*KTA VKTGFPPYRPGVPPRGLVFPKKKKSVLN RPDLMSGPQPE*SLPLGPEPSVSHAGCL PQAWRG
4030	17931	A	4054	425	41	NWGSGLTCPQKLGVFPFPPPGEGGVGA PPPARLFFFFF*KKGFSPVGRGGFKPLP PKNPPPLPPQKVGIEGGPRAGPIFSPP QLFFFLTWSLTSPRLECSGAILAHCT PAWETEQDSISKQTKK
4031	17932	A	4055	312	1	IKNARAHLLPQGSPPPLIPVVIETIS LLIQPIALTURLAANITAGHLIMHLIGS AALAISTIIILP*TRIMFTIIERTILEI AVALIQAYVFTLVVSLYLHA
4032	17933	A	4056	648	123	DDPVPVSARGCVPSGAFGRGAQLKKAWD GALA*LPPCLCAQELPSFSLGTGGPAVG LSVNSERDGRGGEVSINAEFTVA AFLKG TQSRGINGMPLPQREPPSSRYCLGLGGE SSAQGTSGLTGQRV*QNSDLPELASGDD KGQRSSQGGAVSQSSPRGRQIPSSPPA ALFNFL
4033	17934	A	4057	135	464	QHNSRLMQAKKGVTVLARVIDLDYEDE ISLLHNGGKEE*AWNTIGELGCLLVLP CPVINVNGKLQRHNPGRRTTNGPDTSGMK WVTPAGTKPQPAEVLAEKGKENCBCG
4034	17935	A	4058	3	575	LRSRPLHIILSCGLLVTPRSLSPPPFPQ RLRLCRPSRGAAEFFSLRKLHFAITLP LRIEGSKTL*NCC*LYHGC*IS*IHGG LFDVAAKNI IHBEVEKYDKQYRGKELLG FATYKTFEIIHVQYIQ*LVEPALSMLOK AMETIQQAFINVANKHFGFFNLNQTVQ STIEDIKVKHTAQAEYMIQIQVR
4035	17936	A	4059	389	3	TFKGPVFRYPTFFLCPPPRGFFSKNIW TPPPPPFFGVFPEREKIFFFLKGAFLP SFRVTPFFGLKRGFFLSPTPFFFPF WPPPPPPPPPPPLRRSFALVTQAGVQ WRDLG*LQPLPPGFKR
4036	17937	A	4060	397	1	KRRGNFFFKGISLPI*TPRGRPLWVFF F*KAPKGFCAKFFFPFPLPKENGKTH RQKTFPPHFCQIFKNGFWVLHAFSLGDF PARVWGPPFKRPFKIFKEFPYGSPPP KGPKKKRTAARDLELADAW
4037	17938	A	4061	38	410	AWISI*ERPFILVRVFNFLAISGLLFS YFRINFLYVQIHIHTFRKLFVLSYVFR FTDVKFFFYILPFFPPHFLPGWICSYAA L*FFIYFCFLPFFFNQPTSP*IGLELLI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFKKPTFGFGG
4038	17939	A	4062	405	81	GGANVFPPQKSPFFGNKKGGHFFSYKILN NPGHPFFLKKKKNAPGGWGNPWFFPPWK GAL*PKKKNPPKKKKKSPPKGGKKKNP FPPKKKKKKKA*GDNFDMGTGN
4039	17940	A	4063	415	239	RPSFFFFPPPKKSCFSTFFFFLSPGFFF PPPPFFTPPPFFFFPPKKKKYFFPPPG KKFFFF*PPPSLFFFFFFFVFFFFF FFFFFFFFFFFF*GLTSPHKQIGLVLA FLALSKITHASIPVPVSSPSKKKKKKK KKKKKKKKKK
4040	17941	A	4064	95	241	SPCRSPHRVNS*ANNLI*LAYTIAFIV KIPLYGLHL*LPKAHVRAPIAGSIVLAA VLLKLGGYGIIRLTILNPLTKHIAYPF LVLSL
4041	17942	A	4065	28	288	YFDIFVEARSPYVFQVGLLELSSNPPA SASQSVGITGGSHCAQP*VTILFTCTL HVNG*I*CIKFLIHNIPILVISLQYIFG FPL
4042	17943	A	4066	338	134	PGGGCSEPRSGHYSHCTPAWQ*SETPSK KNKKKKITYFSVKNWGIRVFIEIILNSF TTVRP
4043	17944	A	4067	26	365	WVSLMTSALAMRVDFYFITLLILGLLTS TLTIYQ*WRDVTRESTYQGHPTPPVQKG LRYGIILFITSNDCEFFAGFF*AFYHSSL APTPQLGGHWPPTGITPLNPLEVLLNT S
4044	17945	A	4068	491	174	TQLKTH*GSTTDNRTEVRVEPRVRTNYK DLLKFL*SRGYDFESETETETIAKLKVKY MYDNRESQDTSFTTLVERVIQQLVLSHI FKDNYANINAEKLSGN
4045	17946	A	4069	210	402	NVSKGLRKVPSTQ*VINISCRPGVVARA CGPSTLGG*GG*ITRSGVRDQPGQHGET PSLPGAV
4046	17947	A	4070	202	1	DSATALQPRQ*EQNSVSKKKIYRTIDLR SEYFARWSFTLAARAGVQWRNLSLQPP PPGFKRFSHAS
4047	17948	A	4071	412	143	FLGAGV*PRLGPKG*TPFLLKNQKLIGH GGGALYSQYFGGWGRNNSFNPGKGFTN QNFPFSLQTWGGKGVSPSKKKKKERKTR KWGGE
4048	17949	A	4072	2	324	RRGNFCMF*SDRVSSCCPSWS*SPGLKR SSCLSLPKCDYRFEPLYLARLVLMRCY STHNTYIMYCMQRLFQGHRYLSVSTSS ATRPYLDNFFFCNKVMPCCGQ
4049	17950	A	4073	2	326	RRGRMLPRTGPRPGNDAQQPKHSLVD* LFIYLFYFLWTGSHSVAQAGGQWRNHGS LQP*PPSLKGSSRQSAGRVKGVSHCAML LLDLSFGKPYTYKKVDKVSFEA
4050	17951	A	4074	422	116	EIKQEKNPGEFFFFPPPAKRGFFFTPLI WGPPGFPSPFLKRRQGGFFLGPL*KGN PPVFPFPPKVFFFWAGPPFFFSFKKKFFF LVPQSTFIHFIFHICYLL
4051	17952	A	4075	3	294	VFCHVGQAGLELLDSSNLPSVASQSAGI TDTSHLT*PDLSFCCCKTKFD
4052	17953	A	4076	60	389	PSAQLGSKTHIHMAVQP*PPPSPELLHL PKMLCPHSAHTPRPPNPGTVCTYSPR SSPAFPQEGPSSGGLGLVLSFSSPPN

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						HVHPAPTSPESGRGRGVRVPREGAYV
4053	17954	A	4077	93	385	KPLFAPGVLFGGPGEFKREKKGGAGQGGP KKFSPPPPPFSFPKTLWVAPLQETO GLRLCPPFFF*RGKGALF*KRGGRFKP PPPPGLLGPTP
4054	17955	A	4078	2	365	RKVEGRVS*DEDLKLTELLRYMLNIEA AKDLLYRRTKALIDYDNSNKALDKARFK SKDLKSDCAHPRDC*RA*APYFLFAKNE LVVPTGEQRHFLQDVPLIVQRTLTIRTP DHTSLPLSL
4055	17956	A	4079	6	298	PLAIMGGFFTLAETNRTTDFDLAEGESEL VSGFNIEYAGGPFALFFIAEYTNIIIN TLTTTIFLGTTYDAPRP*LSPSLFYFE PPSPYTPWSTST
4056	17957	A	4080	414	154	PIPATREGKAGNSLNPEGEGCNKRSRH CTPAWQEGKTPSQKNKKVLLALKV*SI FHMES*KYLKPGFSLDLITVIPTYFDL FRC
4057	17958	A	4081	347	1	VLKPRPGNII FSPKIKKNLPPPGRNYP FFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFF*RGGLLERLKIQLPPTPH YLSNTLRGWNPEGGSCWRSEGGEGEDCL QDH
4058	17959	A	4082	1	354	STFIISLFPTTIFMCLDQEVIIISN*H*A TTQTTQLSLSFKLDYFSIIKKKKKKKK KKKKKKKRGGGGLKKKKFNGGGGKKF FFWGGKKKNWGGGVKPGGKKRGGKKK KGGGK
4059	17960	A	4083	384	85	FFFPKEFFGCPRRFFSPPGFLTPPLQV LEFPKKKLSPPPPPLKNFFFTPPPPF FFFFFFFFFFFFFFFFFFFFFFFF FFFLLM*AKKFISWR
4060	17961	A	4084	1	122	FHRFRDGLDLTS*SARLGLPKCWDYR REPPRPAFLPQP
4061	17962	A	4085	223	401	NGKLVSVFQFCFCFFEM*SRCVAQARV QWRI FSSLHFLPPGFERISCLSLSRWD YRC
4062	17963	A	4086	160	408	ALPPRRGGGAPSFNFCLLPPGP*GKKG GYGDAPSCRSGLGQHGETAAPLKAQKSF GHGGRGYQVRRRVGPPGPGRRQKLNEG APPPRLGGKAAP
4063	17964	A	4087	261	81	YDIDGRIFCQKLESSHYSPGAVAHACNP SPLGG*GGQITRSGVQAIHPSWPPEVWG LQA
4064	17965	A	4088	428	140	QPLKNPPLGGRAPPFLRGKKLPPPPPG EPPPF*KKKKKRGGGGPPPPPPPRGE PKKSL*PQKGGGKKKKSPPPPPQKKK NPPPKKKKKK
4065	17966	A	4089	1	205	FRLRQENCLNPGGGCSELRSHYCTPAW VTEQETLSQKNFFN*KTRKAKSTGNF HMPNTSIQQLPI
4066	17967	A	4090	154	410	ITGCSIIKYFYRAMREREKSEVGYFPSS SINTPLRHRLSDGVLSRITSLSHSPA PFIKSKNRPGTVAHACNPSTLGG*GGRL TK
4067	17968	A	4091	428	67	LPHPPPPPPLSSSSSSSSSSSSSFPF PPPLPGQGRTLTRPLPAPAGQLGSRES CGAPPSSLGASLHVA*NADGRQ*RAALS

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						TPHGPLTGSPPAAWRGRREQDLLLLLCS
4068	17969	A	4092	431	3	APTSNKGSTIPILQIRKLRAIPCSSIGP SPSTLPVKLEL*SVLLPGQWLNFSCFHF FFRPKCSNRPRYTLFVPKLPSSGLPPRP SPSQQVTAFFPLTSRKEPSSPSTPASDA FFFPAPVSARRQEVLCESIPSVTMHB
4069	17970	A	4093	151	1	SIMPMMMDAVAHACNPCTLGG*GGWIYK SGVRDPPDQHGSETSSPPKTKQL
4070	17971	A	4094	35	363	LQSKIYCTFFFFLGRGFFFSRVRGRGA HPGLGAKTTGVKGNPPP*PPKGGDPGGV PPPPGCFWFFFLGKGGFLLPGGG*NPG KKKPLVWPPKGGELKGGTPGPPFY
4071	17972	A	4095	376	1	LKSPFFFLGAPFFLKKGSLGLPLGKGF TPP*LGPHPLEKGPLLGQWNPQKVKW KRGFPQKGENPPFFFFFRRDGASLC CPGWPTPGLKQSSNLSLPSWDYRCLS KSLFKENTETLAS
4072	17973	A	4096	65	446	PPFLFFLNKGPLFTPKRQKPRNFT* PCPRGKKNPPPPP*GGEKRGPPPPGK FFFFFGERGFPGGVLFLDLGTPPLGFL KGGEKGRPPPGPGPKKPL*KRKNSPP TGERGRGKKHCLP
4073	17974	A	4097	34	387	IKADEYVLTRELACVFVGDMEPLSSPHR LHTRIGSSPTTCTPACPCSSW*HGAS VIPSQTAYEDWFTLYNVLYTSLPVLIM GLLDQVGASHKQGHFWTDENALEKSQAN VSMHSSGVYFFLIKPYNSVVRHQGSWL CFLFCNKERGF
4074	17975	A	4098	80	422	ILHVLTYTCIILCFVLQS*ILWFLQNYI LHVLTYTCIILCLHVLTYTCIIMCYIHV* FCILALFAGLS*DSPYHESL**SFFMEA DISLCRCVITDQLNFISSLQH*ELRMF QF
4075	17976	A	4099	74	402	IYLLSTHLHYQFSWISITFDISFFFFFF LKKESSLFFPQGGGGGNLGLLKPPPPGE SPFPPPIFRGGGKGPWWIFFFF* KKGSPPIYPGGG*IFGPGDPPPPPP
4076	17977	A	4100	3	335	DAWASAWTEYDSVSKKKKKRGGGK KQFPKKIGPRGSLFKPRGGEKPLSLKTP PPPPF*F*KPPFKKGAEPPWEPFLKPPF CLKDRGGAPKIYFFPNPPGAPRGAAFIK RGGGK*GPPGGLLL
4077	17978	A	4101	406	1	RFPKFPFPKPKMSKWLFP*KGFFPPRE LLIGPPPPPPKKKKFFPTLFFAKVLPPR FF*NFNQVSKKRPTFPLKVQ*PPMLV QKKPTRGFPAFLKKKRSSLVIREIKRK PTMRYHLTPIRMAVFHKSNNRC
4078	17979	A	4102	2	183	VNPGGACSEPR*CLCTPAWVTERDSVS KKRADNDKQALRSFFLGFFFLPLHPT SFAF
4079	17980	A	4103	119	391	DNLCQFFFFFWKRGLLFLPRGGGFKSTG PFSGVPGTPPPPPPGGGLTPKPPPPG *ILFFLEKGDFFLLARVV*NRQKKKNPP PSPPKGG
4080	17981	A	4104	413	64	GFKPPPPKDPFPPPPQKGGPMGWRPFR PFAPLFSPPPPRGGGGIFP*GGGGAKK FHIWPGFG*KKPPPGG*NSGGQKNPPG GGGNPPQKKKKKQPTTANIWFLCLEI

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						LSGM
4081	17982	A	4105	2	196	RGRVGKVLISLNTDLLWLLCILICFHK TQ*LCNG*CHSRMKVCVCVCARVCVCV CVCERERD
4082	17983	A	4106	1	335	FLVET*FHPVGLAGLELLTLGDPPR*ST LGDPKCWDYRCEPLDPASVSFFLCILKF IFVLLKLEFFFKPPLYSKLTRGRDNNYN YFPPPNPGPLPHWRADKSIIGGNRRL
4083	17984	A	4107	1	148	GERGCSELRSCHCTATWAE*DSIYKKK KKKEPPKFFLAGFSGGKKTP
4084	17985	A	4108	331	41	GLNFLAQKFSGRFSPPPGRVPLGPKPF FFLGKPPILEGFGP*KVFFSPILPPKE VLTFSPGGEKIGPPFSGGACSGFPKPG AKKKKKRPWSN
4085	17986	A	4109	137	3	TKKERNINRGPGAVAHTCNPSTLGG*SG RITRSGDRDHPQHGE
4086	17987	A	4110	3	269	GFHRVSQDGLYLLTS*SACLRLPKCWDY RHEPPHPGFLGFFCFFFRDSVQPGQQ SENPSHKKKKDEGPFWKAGAKIFLPKPN SSAL
4087	17988	A	4111	196	330	GAIARGRSNCDCT*GSVGHVL*NDPTLN CILDQDTLYGSIMINEYYBRASDAWALL PDEEQLEPGDQTVIA**A*DMSGGQHR VSLARAVYSGADVLLDDP
4088	17989	A	4112	426	241	LLKRVREHILFTIRKGFSEPRSPPTCP AWATERISVSHKEKKRVLVRP*VDLSN SSLSVL
4089	17990	A	4113	394	1	GGVFSFSPGCLYHARAQYFWPHKKKYF PHPGQKNSVFLKGRPLFGFGFLLIFFFF LVEMGSCCIAQGLELPTSNPLTSASQ RAEIKDVSHRSQ*FFVFLFETGSCSVTQ A*VQVCHSSERTPLKQF
4090	17991	A	4114	328	2	KKRAHPIWPDGTGIEVPNSPSPNIRFLGA PESFFFKRNLEQGDPLEKPNPCYFFFG VTTPFPPLFPFPPKIFFFFD*DGVSICR PGWSAVARSQTLTATHLPSSSDSP
4091	17992	A	4115	220	3	FKKGEPGDPPVWFGLGWVWVWGFFFF ERHSFTLVTVQGVQVQCNFSSLPQPPRGL KSFHSLSPSS*NYRH
4092	17993	A	4116	342	2	PINFLYLSFNPNQV*RSNFSKILHFCF KILSFFYTALPLPSSQLIRQSFFRVYL INTICFLQDLYLYILNLYLILFLFFHL ASRLDCLFPVFETVLLCHPGWSTVAQ S
4093	17994	A	4117	124	352	TSGFT*TRMKSKIPT*RSFIIDLEAKM KEKFLKAARETQLITYRGTSIQMPVDFS WRKTEAKAQWNLMEVLKEKNCETRLH PATMSFRNEGKTKMFSDERKLDRSVTL PKD
4094	17995	A	4118	11	387	KTGKLLATSAPGDGIMVMVETFCVVVSF FLSVSKKKKNPLPQIKNPLPKPCWVFK RAPTPNH*KAFPGPKTPP*KQPKQIP CRPPKGPFCI*PNPGINPSLPFEKKN KGKAPPFKNSKQK
4095	17996	A	4119	2	407	NTFQDQSGSSSNREPLLRCRDARRDLEL AIGGVLRAEQQIKDNLREVKAIHSCIS RHLECLRSREVWLYEQVDLIYQLKEETL QQQAQQLYSLGQFN*LTHQLECTQNKD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						LANQVSVCLERLGSLTLKPEDST
4096	17997	A	4120	157	2	LTGSESVT*AGVQWCKHGSLLPRLGSK RSSSLNFLYSWDHRCGPPHSANF
4097	17998	A	4121	3	168	IALKSGRKVDIRELGHVVCPGWS*TPEL NQSTCLGLPRCWDYRREPPWALNMF
4098	17999	A	4122	2	376	ETGFHCVSQDGLCLLTS*STRGLGLPKCW DYKMRPPRPADGFINIRDFNPLLRST CCCHVKDIFASPTMIVSFLRPPQPCR TDPIQNTLPLVIMSPVALLGCDSPSAPP VLMNLPFSSDCTK
4099	18000	A	4123	11	221	GTQLLLRLRGEDLLNLGRGGCTEPRLHH CAPFWETEDPV*EKKQAAKAKNSLLTA ALLKTQVKKDSVAW
4100	18001	A	4124	2	125	AITKKTNSNRW*GCR*RGMLVHCFWKC KLVQPL*KAARL
4101	18002	A	4125	425	152	TPVILALWEAKAGRSLEPRS*RSAAWATW QNPIS TKKKYK*GGRITSAWGG*GCNGL *WCRSTPASATETPSQRKKK*EKNLFT LILKVIK
4102	18003	A	4126	3	99	COAGLELLTL*SDSLRLPKCWDYRCEPP RPA
4103	18004	A	4127	396	58	ENCNPLSWSGGIISGLLLVSGYSNKPPS FLVCLLPVIGPPENTAGPSLVPGTKWHD HSTL*TSQTPGPSLVPGTKWHDHSA* T SQTGPKLSSRLSLPSSWDYRHKTFYPA H
4104	18005	A	4128	51	549	LGQSYLLLLRKCFSPNFQVGDLDISYIN IEGTATTSPESRGCTLWQSSSKHTLPT ETSPSVYPLSENVEGTAPP*AHQSFMS PSWGGSPNLFFGGGGFEKEQSPLKKKS FTLYPLGPPSEGEHGF*PSPLCFPPGQ SPPKTGIPSGDELGF*TPGPDKKK
4105	18006	A	4129	97	362	RK*SACLSLPKRWDYRHEPPRPACSC
4106	18007	A	4130	376	279	DQDDLDTLTS*STHLGISKWDYRHEPP HRAS
4107	18008	A	4131	133	344	IIFFFF*NFVLQAGGQGNLGSLLKPPPP GLKQFLGITFRSWDHGPTSFTTRANFCI FRKKRVLLCCPGWS
4108	18009	A	4132	164	3	MNEMSYESSLLDHLKQ*NQCCLGSSSE PSPRLKQFSLSLPSSWNYRKTSC
4109	18010	A	4133	355	2	GKKQNRKTGNFKTHSASPPPPKERSSS RATEQSWMENDFDEMREEGFRSNYPBL REDIQTGKEVANFEKNLEECITRIPNT EKCLKELMELKTKARELREECRLRS*C DQLEE
4110	18011	A	4134	193	357	HHCNPSLCQNDLFWHLVLSPTGVQWYN HGSLQP*PPGLE*SSCLSLPGS*EYRH
4111	18012	A	4135	357	104	LRRL*YENHLNPEGGGCSEPNLLRCTPA WATQDSISKIIII*CNFLH*QNMOKI KONPKTNSSKILTEIKISLKGNLRELRE
4112	18013	A	4136	179	381	DTSLHIIQNRLSISKKL*TLFYTY*DR VPLCCPGWSAVVQS*PTAALTSKRSSC LSLLSNWDCRC
4113	18014	A	4137	89	318	CLEISCTKIGODLYTENYKTLGKVKCK PNK*NTTFMDQAEVSILKISFLPRLIYR LRIIPVRIAGIFVEILKPG
4114	18015	A	4138	315	60	KKLPAEIHAPLAEATD*ABLKPAGETH AEVQAPTEQTPAAEAATTIAEASVKVQP

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						PPAEASLAKFFPAETQPPADQERGSEDI
4115	18016	A	4139	377	51	GFTSPFPED*RIPGLFSCIGWTLQSFHF RNIGSVFSPPGFFFPQEMRVLLCCPG WSQTLGLKPSSCLSLNSWVYRCAPLVP GMPIF*LSCFLAIGFLEFVIYIGY
4116	18017	A	4140	413	175	NFGIFCRDGVLLCCPGWS*TPRLKPSSC LPKCWDYRREPRTVPGLPFLFLNLRKDG NSVLEIYLEYKITQIIVORLLVL
4117	18018	A	4141	1	394	EIPVTKRWSGLGVVAHASNPSTLGG*GG QITRSGV*EQPDQHGSPERRGLKERRGL MVMKATFLGLRHHLEHIVGHRELRLHN NSKKKISSHPLSTPHVPGTVLKPCLIL CFKHQKPKVRKPPNSPSYR
4118	18019	A	4142	22	376	LVNKGKTIFFFLKRGVVLPPKKGKRGIN TVNGSLNFRGQGNPLA*PPKKPGTKGGG HNPGEI**FFGKKEA*QCGPGSGIPGP RRPSGLTLQKGGTYGREPSPLPGPTKEN PRLTKT
4119	18020	A	4143	161	1	PIPAKYEHFCFFVSLF*DRVSLCHPG*S AVV*SQLTTASTFQSSDPLTSATP
4120	18021	A	4144	18	159	KHLDPGGGGCREPRSCHCTPAWVTAKL HLKK*K*VELKSPSVIHT
4121	18022	A	4145	383	109	LFFYKIQNYTGHGGPCLLTPFLQRVKQK NCFNPGGGGCR*PKLVFCPTWGKKQGF VFQRLKKPKPKPKPNWRGLFLPPFS KRPKPKI
4122	18023	A	4146	374	164	QCQLRLSLRWEDCLSWGG*GCSEP*SCP CIPAWVTARSCLQINKSLPAETVPSLY NQIARG
4123	18024	A	4147	25	375	RKKKALFFCQGGSQPPPSNLMDPPPPGE KKISWLNLPKKEKKKF*KKKKFF*KVK KNPFLPKPGRPPPEKKKGGKKKPTPQ KGKGLFAPPPKPKIKKSPHFKIPKKQK NFWQR
4124	18025	A	4148	376	202	HYNSKVFPGGPKRSFLFFLKALSFFFAP APIPFWLHSKIPFFFF*DRVSLCHPGWK LR
4125	18026	A	4149	3	144	LFCDPWTPTPGLKQSSHLGLPQCWDYRH *VTVPGLPISFVFFFFPP
4126	18027	A	4150	3	188	QLQSQLLSSLRPDHMLGVEGCGKLSL HCTLA*MTE*DSIS*KKILKKCF*KK HSFLY
4127	18028	A	4151	83	358	GWARWLTGPALWEAKAKSLEDLNA* A*QTYAPS*EESLHPIMNLIIRDPPVVT SFRVTVDSTIARHWLPCWDLLOASIGH ILILGPG
4128	18029	A	4152	162	1	TVVWVHRNKLNSQWNKI*FLELDPITYK HLVYDKTGISNHVVKDALVNTQCRAG
4129	18030	A	4153	369	20	FQLLARQREQENGVPGRGAFG*PKSRPC PPAWGTK*DSVSKKKRKKKSCFVHRIL KLEBAYHSLGSNTAQLFVSCFHKKILC LSISIPDPYLQFKMWVPPSKPLYQIDW VGLL
4130	18031	A	4154	117	2	QIFFFFFFFFKMESHSLAQAGVQWRHLGS L*PLPPRFKR
4131	18032	A	4155	369	217	FFSPPPPFKPPPPPKKIFPP*KKNPPF PKKKKIFFFFFFFFFQTP
4132	18033	A	4156	214	283	ASPSQGQLSSGP*GLIN*SDRPSVTHS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PKPHCETA*GGTSP LSSSGSSPOAPKSP-HHGPDSP LSDSIPMVISPPPEPPLRAKG CPOGPPGASWWGTT
4133	18034	A	4157	319	712	QDFVSKQHSYCLKNLKSSSLIQVAMNRA QVCLISSSKSGERHLYLIKVS RDKISDS NDQBSANCDAGNNFICIMLYKIWLN*K RLMK*HWTAI*LKIYFSNKMKFSNLNLS SVINSFDVKERLNANTLN
4134	18035	A	4158	183	369	LKRKQSQRGEVNFLKVTQPECGKAGILF IYYFFEMESHVSQGQTGVQWCNLG*LQPL PPSSD
4135	18036	A	4159	190	336	DPISIKNFWPGTVYFLIETGFLHVG*AG LELPTSGDLSTLASQSAGITG
4136	18037	A	4160	10	390	QGILLPCFSMSSEERGRISNTFSFFFF FWKGSPI NPQGGSQAKKPR*REPSPSGL TPQRPGNGGPPPPPGQNFFFKKKG*PG GPGR*TPGPRGTPPLGPPKAGNKRGGP RGRAKNFLKNQNGPT
4137	18038	A	4161	53	376	YLPFFFFFFSKREAWQGGQPGMEGAKKFP MAP*PSKGGGGEFSGLTFFPNQWNPRAQP PPRGELILILEKKRPAPNAQPGPENLGP REPSPLAPQKGGNKSENWPPPP
4138	18039	A	4162	1	356	GVFILVSFNWAFSLSPFFLGKQILVLM PQPESQGNLAPQNPFP*RGFPALTP PRTGNKGMAPQAPQFFGLKKGFSHGG QGGFKTPTLGNLPLAPQGLGNGLGPW PFFFF
4139	18040	A	4163	345	26	APGFKPALGPPGGPFFSKKSKNLPGLR GSTLQAVGPTFLGG*GKRSLKPPGG*AS RGPWGSPSPPPGGPN*IPVSEKKEREGK KKKGREKKKETFSNNLLIFLSF
4140	18041	A	4164	18	284	TLQGTSGIFEGNFFFLGTGISLYCPGW RAWGGDHGSLQL*PPGSSSPASTPLGRS WDYRHVPPGWASFFFKTLPNVGTQAGL ELWG
4141	18042	A	4165	377	30	FSGKKKFFQLGWGCGPPPLIPPLWGV*P GQPPRVGGFNPLPPWKNPVFFKPKQP GVGGASPYSPFLGKFRPRIPTLGPEGS G*PNFPPPPPPWAPKKNFSPKKKKKFYN CLW
4142	18043	A	4166	305	1	ESRQVLTSLRTLLSIHEFNILLNNSTYK HTSLPINIRQYGQDLTKLKKETKDLNK *GNIPCLGIGRINIVKMSLLSKLIYKFK AMPVKIPGELFLRNQQA
4143	18044	A	4167	394	78	EGKKQGRKKGRREGS*EGRREREKTR*K AEKEGMKEGGRGKKEGRKEGRKGRKE GRKEGQKGGRTDGGWVLRSLDTSQLI SPASGPKWREASSLVWASLCL
4144	18045	A	4168	1	431	CNTCVR*CAWCV*MCGERLCWCVCSCN RVCCV*VERVCVLVCMVVCWCVCARQ CVSVCHSRIESSRPSSGFPVAPSKCQTHL YLEKLSAPPAAGLWDLPSAATASLSGSL CQPSCPRTSRFATLVSSMYHRPVTGELQ SIT
4145	18046	A	4169	3	423	YNAREIEAAAGRDHATALQPGYRVRPCL KKKVLKLGQAWLA*P*NFPPETGSHSV PRLECSGVISACCSLNLPGIV
4146	18047	A	4170	118	402	QICTCTPKPKMKVKKITMLSNNMRYLYI

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						HLTQDI*DLIDIL*NTADMNKLKLNK*R EIHCLRI*RLNIIKTSIFLKLPRVHAI PFKISARSEVB
4147	18048	A	4171	404	285	RGCGEPW*HHCTPAWVTE*DLVSKNKM QNDNLSHLSLA
4148	18049	A	4172	274	431	ESLVGQRNWVAKYFYRITAPGRAQLMP AIPAPWEAEVGGSGGLEIETLL*NNSSR PGAEAHACNPSTLGGRRGRIITSRD*DP PGQH
4149	18050	A	4173	24	366	FLCLFHTCVLAFPPVQQLCSVGWGCKVEN ADREKQPCDSQAREEPRLCRRGFNRAP NINTRHEKLEFFVCLF*TGSHSVTQAGVQ GCGHSSPQPQLPGPKRSSHLSLRSSWD TGM
4150	18051	A	4174	397	1	TEPVLANETWGPWDRGPGLGGLSPENT DNSHAVGADQLLEPPFLSTRSIMPEM SLNAWLDSPHREMQAGTPLSLCGDTYET QVM*SWGIRGILPQQPWKMGSLSLTAS LSLSFAHTLKHKHTHTHTLY
4151	18052	A	4175	90	387	KGRWLFFPQGGGERGHNG*TAPPQTGGKE NPPPPPPKDRGKKANAPPPGGIWLKKN GFFFIGQGGPEPPPPRGPPPPAPPKGGE KRGGPPHRRPGKLLK
4152	18053	A	4176	398	280	RRLKWEDPLNPRV*GCSKP*SHRCTPAW VTE*DPVSNFF
4153	18054	A	4177	253	395	LFNFFFLVKMSRYVAQAGLKPLA*GNP PASASPRAGITGSSHHTQP
4154	18055	A	4178	366	48	PWASPGISLSFSFLRTKPTVKVR*YRVG PQRQPCPSRWAPPACPFMPPPAWVSP GSAASRPPRHAGSQVGATASPPPAQGLG APAWTAGLGEKQKLAARMRGT
4155	18056	A	4179	44	413	GDVNSAFFFFFFLEKKVWFIPPGGGPK PEFGFRAPPPPGVKKIFGFTPLRTGE*R PLPFPFGKWFFPKNGGSPMWPGGV*PS DPKGAPPDGPCKGGE*RGEPWVGWNFA LLKERKPLFKE
4156	18057	A	4180	396	235	HEVSLCCPDWS*TPGLKYSSCLGLPNCW DHRCRNHGPGKTQLEQGHROVAGLSR
4157	18058	A	4181	85	408	YTCSLRITQDHFFFFFLLGKKIFFFPP GWGAGGQILTSPTKPPGVKGIPLNPPR GGGPGGPPPPPTLFLGF*KKRGFPGGGQ KPRPKGDPPLPPKGGGLKGGPTP
4158	18059	A	4182	1	149	NHLNL*GRGCSBRLHHCTPAWVTE*DS VLKCKSYIHLGQNPTVRKVL
4159	18060	A	4183	310	3	ATAPSQFIRIN*RNHCHYIEVQSEASA NLETAVNNPENLKGIMDEGG*MKKQIWK -EMTSRIFIVEKSMFGFKTSKAQALILGA NIAVNFRLKPMILYHLEN
4160	18061	A	4184	1	359	PTRELVLDRDRPPFFFLGSGKKKNPGV FLYFGGGWTPPKKKNSLGWGGGGLKKG GGGVFFKPLPFLGGGPFKNSSGGVDKKK RAPFFFTKTPL*KKPPPPFPKIFKARG FW*KMGEPFFFCPPPSFLKKGPPPKKE GV*KKPPPPFLTPPPNQGNFFFWGG STPPQNIKKPLGFFSSQTPKKKKRAADR DLELADAW
4161	18062	A	4185	1	362	HFTKYLFI SC*K**LLCWMQDCCKKGIP MNTNVIQEKATSLYGSLLKHKEGEPKAG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EFNASKGWLNDNFRKSFSGFNKVTGEAA SANQKAADKFPDAIKKIIEBKGYLPBQI FNAGESAL
4162	18063	A	4186	366	47	AALFLVDPPGRGGVKGPPPPGPFVFF QRRGVPLSPGGFFFRPNSPPGPPKG GGSGGGPRGPA*THGVFLKKNPNOGAG KKKGFFLKKKKKPVFVFSVK
4163	18064	A	4187	394	112	KNTENLKISAWWHVSMVSAPNEAETGG STEGTGCSKL*SCHTAWVTVRETLSPR KFFIKRANYLTFR I*KVCSLYHRKTKNS FKKHTQGRKF
4164	18065	A	4188	230	372	KPMFLPPNPAILLLGIYLKEYKSF*HKD TCMRMFITALEFTITKTWNQ
4165	18066	A	4189	149	2	NRSIRFMRFKEGSHLPPI*VQGAASAD VEAASVPEGLGKTINKGGST
4166	18067	A	4190	2	159	MHQPWLLRRPKQENCLNPGGGCSEPRS HHCIPA*AIERDSLKKKKKGAF
4167	18068	A	4191	180	415	LGFLQLLFVGRSMFIFALELSHGWLGS SLSF*PVCVKQSSHLSSSDHKKHMS YPANFCIFCRDKTLPCCLGWAQ
4168	18069	A	4192	424	41	PPLLRAAPPKGLL*PKNSFPFGAPP*IPF PPKKIKIFKFTPGGGGAPLFLPRQVKA EGSLPPRVFGPPPPFFPLPSPLGAKPN PPFFFKKKKKKWLKSSSLFYSAHFVLC LKYSLSFFYQSVTK
4169	18070	A	4193	105	424	ELKRLVIKLRIGIPEKGAQCKEIQKLA QEVKGEIFMEIGSLKKQ*KIQETLDTL LKMQNALESLSNRIEQVEERNSLEDKV FKLTQSNKQPSQIKKKILYNV
4170	18071	A	4194	3	240	LCLQSQLLGRRLRQENPLNLR I*GCNEP* LHHCPTAQVTERDPVSKENKGSFIPMKI GKLVSLTLNRMCKNCKNSEKENV
4171	18072	A	4195	385	1	KMIILTKKMEIKHKDEKELQKTEVDLKI ENNTTRARLTNNIKKKPPESEKTNKNH TKKSL*DQDTKKETRPQKKKNPFKSR*V RHWNRILNLESNRNKGKPNPSGVQKRRDS VPTLITQTQETWWCF
4172	18073	A	4196	3	272	LFYLIMALKHKSSDVGNSNIYAKEKLES ASFKEIRI*KSIVVEVAKIYGKNEYCIYEI VKKEK*IMHSIYRVQYYLQFQTSLEVLE RIPHG
4173	18074	A	4197	236	379	GGRFKGSNFTSPGLQGNSTFFMGPPKLNS RAGV*QRREGKNPGVPQFNR
4174	18075	A	4198	375	1	NFKIPAPPPQNGKPLRVGTPPFLIFSEPP GSPPKSPFKAKWARRDRPF*NPGETLQK G*VFFSGRFFFFFRRDRVLLCHPGWSA VAQSRLTSSDSRVHTILLVGRGCSEPR SHHCNPANWTRVK
4175	18076	A	4199	1	270	PSRTGPQIPRRPTRSNCPNQFLGF*GCG EPRSRLCTPAWATEQDSISKERHGLLV FLKGFHYIRLLINLFAARGKRVLFPAL GGREMW
4176	18077	A	4200	388	1	PPGIINLFDPL*PPPPVVMGPPPS*KL ISPQKKKNKVPVPVPPINIFSGPPPTL VFWVLFVSLKRLIL**KSGVSAASLV RHDGAPRLTSSAGKGHAETFPQPRPTH RNACSFVLIHQSYKVF
4177	18078	A	4201	298	158	FKIVINFQFLTPIFAPSEGGRG*GRGE

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						LRSCHCTPAWVTE*EPI*KRKIKGKKRT EQESRRQNL
4178	18079	A	4202	128	358	KLMI PPSPGQPPRPGGRWGGHPPARPAA PSGR*GAPLPGRPY*EKRIPSARTPPRL GGWPSMSLRITGHDDNGGVWE
4179	18080	A	4203	406	1	FFFFFLRQSFTLVAQAGVQ*RNLSGQQP LLPGF
4180	18081	A	4204	322	2	KPRPKTPGGPFPI*GGGGAPPPRGAP KGGSPPPPPPPPPGGKKGKKNNPPGG *KPWGGFFFFPPPF*TPPKRGLPLKKK KTQNPKKKKGGRSRYRTSPRV
4181	18082	A	4205	3	127	GFHRVSQNGLYLLTL*STRHLPLKC*DY RSEPLCLACFLFL
4182	18083	A	4206	1	216	GFRRVGRDGLDLLTS*SACILGLPKWCDC GR*PPRPAHLGGNSNAKEPGLPACPLLS GHMHRVWVRWATATL
4183	18084	A	4207	427	0	LEFTTNFFFWARVFFLPPFF*NPPPGFF FLPHKKKKNPPPPGFFFFFYAPPPFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF PVVLKTVVSC
4184	18085	A	4208	2	404	PRVRLGIWCKERLFLCYFFFFLGRGFCF LAQGGGPGGNFG*RAPPPPGKKIPGPP PRGGGEKGPREGPKRIFGLKKKGGGPF GPGGVGPPKGGPPPKPPKGWGYGGKPP AQKRGFFFGKKRAPFFFNWNG
4185	18086	A	4209	40	412	PLFCLSEKPRYFEYAIYLMLSLKFLESC IMSVNSSAVSASVYY*W*KIEREPLTSW TLEKLDPEVFHQKFAFT*RAKAILRKKN KFEGTLTSGFKTHYKTTIITTVWY*HKD TQIDQWNRIESS
4186	18087	A	4210	219	392	HFFFLNYNFLGKGVSFPCQAEQGGRNLG *LHPPPPGLKQFFCLTLRNWNHRLVPP PP
4187	18088	A	4211	409	2	LERKTVFFSPPPIFFFAVFFLSPPFFYT PPPLYIFCPCPKKKKIFPPPPGKIFFFFK GPPPIFFFFFFFFFFFFFWS*FFIMYQ IVENISYNLIKVDSHLYLFKDKKILLCT ISSDAW
4188	18089	A	4212	24	399	ADAFSTTNLHGLGPDFTPTTQLYINLG MAILL*AGAVNIGYRSKIKNALAHFLPQ GTPTPLIPILVIEITINLLILATALVH LTAITAGHLLMHLIGSASLAGSTISLP STLTVFTEILLIT
4189	18090	A	4213	411	197	SWLTAPSFKRFSCLSLSS*DYRLPVPH PDNFCIGSRDGARMVISIS*HHDPPASAS QSVGFTAPKVLGLQT
4190	18091	A	4214	218	126	KEPEFLFRSSWSVGAILKNVMRRVLI KSCTPGVVAHTCNPSTLGRRGGQITRSG DRDHPG*HKSALGSCASCFTIYLDLLH IVFE
4191	18092	A	4215	1	332	MAPSLCLSNKRGFIGPGFAGAPKHPGR GQGHPREKLAFKKGPPKGLKSFVLK TPPKPPFFFLSPKGGALKTEEEP*TKKK GGAEEKPPPGKRLPGFPCPKPNWG
4192	18093	A	4216	1	185	KLYLSILISLQISLIITFTATBLIIFYI FFETTLIPTLAITR*GNQPANFLYLLV SFHEN
4193	18094	A	4217	1	388	LRFCWETLFPPLPNPFSFHSFLFFSFS

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						FFFFLGGKFCFCQPGGGPNLNRDPP PRG*KEF*APPPPRGGENQGSPPPPNG GGF*KKGGLNHGGGGFKPPPKPPPL ASQGRNKGGAPELLKF
4194	18095	A	4218	3	195	VIYSTIFAGTLITLSSH*FFT*VGLEI NMLAFIPVLTKKINPRSTAAIKYFLTQ ATASHPA
4195	18096	A	4219	261	1	EPRRRERKERKBBKKGATPSRICMKRER EERFS*ERRERGEGERGEKBERGER ERERSEERERERERPKN*MLNGRTRR TRG
4196	18097	A	4220	5	375	DEMLHLKFTYILN*TLKDTIIPKVNENL YN*DFLNSKVQGTTPPPRPSRPSSSSP DPPPGPPPAGARRARRPGRGSPGGP PAPPPAPPPRAGRAAGGRPPPARPGR GPAARPAGGGG
4197	18098	A	4221	258	267	GGGALKKKIYCGGGGNFFF*SPPPSFF FFFFFFFFFFFFFFFFFFFFFFFFFEL IYFIFILIF
4198	18099	A	4222	127	330	KKKKKKKKKKKKKKGGGPFKKKKFLPR GGGKNFFF*GGQKKKLGGVKKKGKK PGAKKKKRGEK
4199	18100	A	4223	1	377	RRFHLRRENLOEKQTMGIFFFFGVAGP PGPGGKSFSPPSFFF*GNFTFTPPPGG GGQNLVGENSNSNPPPRDPPSGPSEK I*KKTTPPFLVGPNTKNKKHFGGGSPK KKTLLPPPLDPF
4200	18101	A	4224	223	431	IRKTGPLGFGGQNNPLPKV*PPGLTFF QKGPPPPPPPPQKPRFLKFPKREGFP PPKVGLTPPPGLL
4201	18102	A	4225	173	2	RCKLHCLPPTLAIITR*GNQPERLNAGT YFLFYTLVGSPLLLAIITYHTNLGPTR P
4202	18103	A	4226	11	377	FLTVVFICISLFGRLMGI*FFVNFFCEL FFHAFPSLFLKTDIIFSIDLLEIIYAH VCHICCNLIFSLEYFVFNGLSKYIKC* NLFAIILDADVSFLIFMFRTGKRONDN QFSLKILIGF
4203	18104	A	4227	1	412	KNSKVKNATDLLKNASESPHSRIDEAEE RISELEDRLFENTKSEETK*KRIK*SM PTDLENSLKRANLRVIGLKEKVGKEL*V GSFFKDII*QNVNLEKDNIAQEAATT LSRFNPKTTSRHLAIKLSKVDKER
4204	18105	A	4228	373	163	IGVFLGGAPFFFFFFFFFPQPKRGGG KGGASGKTG*GGGGLKGGGQGWPPFF FLRTWPTFTTRAPGL
4205	18106	A	4229	392	3	PPC*NRAFGFNFGGPFKKIYSSPPPRGK FGLKGPFFFFSAPPGGPKFSKGGGFL FPGAPDF*GGFGKNYFWGQGF*PHSP PPPFSGWPKRRAPFSKKKKKRRRWGE GEGQGSNHLKHYFQI
4206	18107	A	4230	211	400	YALIWLICYILNNYALHSVFFWCCFCFLI FKFIYVFLNLLFLFAF*LVLCILKVNQNH SGSLSIYSYFPLLEACRIFPLPLF*NL *MICFNMVVLVYFKQLCSALSFLVFLF FNF*IVLCIFKPIVFCFLRRNPQLAQA GVQWHDLGA
4207	18108	A	4231	69	386	KRIFFFLGPRGGGKGMWVNGNPPPKGK

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						GNFSA*PPQGGGPKGPGPKNKVIFGFKK KRGFYGGGQPPNLGKELAGPPKGGKRG KTHPGGKFYAFGGGLFSKRN
4208	18109	A	4232	394	287	FKEKKKPPPPPLFSPFFF*KRGGGDPLF SPERGEK
4209	18110	A	4233	442	112	LLGRLRWEDGLSPQGRSCSEP*SCHCTP AWATQ*DPVSNNTNNKPNPQACSSLNP SLPWTAAVWRTLGEHCNGREALPARAKN ATKAPVLTTHICQTVRTISCALLPH
4210	18111	A	4234	415	58	SLQKGHFPPFQELDPQNPGRSGWSPVLP TTGLFFSLDFIRFT*FMAGVLVGKHCW EWTAALVLLFLRDRVSLCFPLIHTLG LKRSSCLSLSSWSYRHTIPHAST*FF G
4211	18112	A	4235	406	168	HGETPSFLKIQKLAGRGGTLL*SQLLGR WRQGNHLNWGGRSSVYIYTEKHTVHTQQ SVTTDFMSMSQTLAYSPLSLKSS
4212	18113	A	4236	247	397	TVCFSVYIYTELLPPQVK*FPCLTLPS WDYRSVPPLPAYFCIFSRDGV
4213	18114	A	4237	36	405	RLYCFIKGLNVKNKTFRIVFFFFLETNF PFGPQGGGEGANSGFPEPLALGVKKGPR PPPPGGGE*GAGPPGPGNFGLLKKKGVP RGGGGGPKPTORFPGRPPQKKKNFFG PALGKKKVVFF
4214	18115	A	4238	407	3	KKKKKLTRPGGGGPFSPLPKRVKQKGG NPGGGFSKKKKSPPPPPRGKKKKPFSK KKKRFLSGNNTGKNRLGKDPQS*PAGNA RKKPGWERALARGRAPGMTDRKPOHSG DGSQQSGTGQEPGNSGFPVKVH
4215	18116	A	4239	144	405	PTVKLVLLYLVLVLLKVAVSKNLR**GGLT V*QQRQILWKRIILSNTEFLYLRSKMMH LVL*PTVNTLKSLSQGARWLTVPVIAL WEA
4216	18117	A	4240	369	40	PLLQGTASWPRNGRAGRPRKEG*LHP RETRVPPALHHQAPAGVSLTSPGPPFW LSLQRLRGHSSSDSLPAVCQYSGSWREE KAAAEAPALTPAICTCTICSVLTVL
4217	18118	A	4241	397	1	ISKSLEFPFIPFWKKKKGFSPPLNPLGG VFFFFFLKIFEIFFLKRFFFIIFLGAPG FKIFKKYFPFPRGFKTPPKKKIFLNPF KKKGGGGGALFFFFFTGSRSVTQAGV KWHDHGSLQP*PPRLK*SSDP
4218	18119	A	4242	230	393	ADRPGLPLSPAPETGSHSIAQTGVQ*HN YGSP*PLTPGLKLSSCLSLPNCWYR
4219	18120	A	4243	434	104	KQPTFQSTTGGSPSAGRPPPPRAKKKKP PFF*KKKKSGNIGGPLFPPPPGGEKK NLFPKRGEGSHKTDSSPPH*RGKKKNL SPKKKKKKAWCWDYRRKPLCPATYF
4220	18121	A	4244	2	425	FVFKIILKNLSEIQENLQFSKIKKTIHD LNKKFNKETGNITKNQTEILELKNMSSE IKNTVKSFNNRLNQAERISELEDERSFE MTQADKKRKKGEESLQDVLYTMK*TNIL WSFQKEKRKEKGLQNLNEIVAENFPSL
4221	18122	A	4245	12	424	IYYKTLNCT*IF*FGGALACFHFSYFF IHYVGFVPSVYLFVSHVIVSVWTSGYLL YSLGCNPILSLFIFLLKLFHFGYLTIOV GIYVWILFVCLFLSNSFINI*FTYHAIP IPIYIPLKVNSMFYSIFTTK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4222	18123	A	4246	215	425	LSIQISQIRNLTYLFINIMGKILRAKRK *GTSDAVNVQITIFLRPRTVAHSCNPSTL GGRGGRIKSGDRE
4223	18124	A	4247	413	2	WVESFSLGKAFMWGCATENPGPPHPKF LLFIMKAPPPWRVGFQDCFNPKDGRFI* PRTPPCPRARGAKNSVSKKKIKIWK WPPTPLPPPGNGGTRKFPSSPPPPPPPT TPKITPPGGERQL*PQRAEGAGDTK
4224	18125	A	4248	61	281	ITWKDFDSFSLRVSKAFHLALPAFIGN CIKCHIKMGIYPEEKFKNIHKYLYLEID VCGH*TWKKIFFLFFLRQRTLPAQAG GQWLDLSLLQPPPPGFKRFSGLSFLSK* DFDSFSLRVSKAFHLALPAFIGNCKIC HIKMGYIPEEKFKNIHKYLYLEIDVCGH IRLGKKFFCFFF
4225	18126	A	4249	23	13	RVRPFASPGGREVTVCGLGREGQERRL RWHRKPFPLAATS CAVVPRSVTPSVTS GSADGGQSLAVGAGTLATVGGLELLNS NDPPASASQAGIAGVSHRANP*T
4226	18127	A	4250	182	342	KGFFFLPPGGGGGGEF*FNEPPPPRVKG IFPPPPPGKGEKPPPPFPGYIFVF
4227	18128	A	4251	2	219	PSLRKMQKLARHGGTLLWSQLFGLRRE DCLSSGGRGSQTHGSEL*SYHCIPAWAT DGDVPSKNTKFFFFF
4228	18129	A	4252	223	324	LGAVAHICNPSTLGGRGRRITR*GVRDQ PGQHGE
4229	18130	A	4253	165	336	ESDAQGHQVAARVSHVLEKDALLVFRSL CKLAMKPLGEGPPDPK*ADSSSWPPSVQ
4230	18131	A	4254	3	233	ETAFCHVQAGLELLTSSDPPASGLQHA GITGPATKSAP*WS*VSGPHLGAFDLSLA MLLAQDWRALLESARKFFPLL
4231	18132	A	4255	394	44	AKIFPPGVKKFFASTPPGGGKKRGPFP PVNFFPFKKGGFPPWPGGV*NPAPINP RPWPPKRWGFKGEAPPPPKLNLFPPQG GGGKNFFGKKKGAPTGGPPFFFFEMEFH CRFD
4232	18133	A	4256	152	2	YWSFFYCRSCCIRQGTVAHTCNPSTLVG QGARFTRSGVRN*HGQRGESPR
4233	18134	A	4257	404	190	AQLIRGWRQ*DHLSLGGGCGNEPSSCHC TPAWITEPNQSLSQKTQKQKMLIPN*YG *TVSPPKSHPELQFS
4234	18135	A	4258	288	407	ENCRPRAVAHACNPS*ENCRPRAVAHAC NPSAFGGRGEQIPRSGEQBQPVQHG
4235	18136	A	4259	406	163	GWGVQTHPGHHGETLFFLKKKK*VGGGG PTRYSPIFGGVGPQNGLNPPQGGGSKNP LNPLLPWQKGVVFSKKKKKKERD
4236	18137	A	4260	101	276	LTSIVPSLWEAEGAKLRGLGRPACRESS LCHCTLPWVTG*NLVSKKKKKRGGALGF FF
4237	18138	A	4261	2	414	WVAATPNLVFVGRGNCQDWFPGPFLTRG GWGGVLFPPVKRVIKGLVAPFSGPIPIR KNHQKVGGFLEPNKTNFKK*NFVENKNT RRGIKKNVPEKKPKQGIPLPPQIFNEN QTWGDFFDFFFAKKKKIINSLGWA
4238	18139	A	4262	337	382	RDARFLHCSLV*LIT*LQKEFFVVGQAG VQWHYFGFLQPLPSGFNQFFCLSLLSRW HYRGPPPSLGKFLVGNLVGWLVFETKFW FCWPGWRAITGFVWPATYTFRVQAIFL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4239	18140	A	4263	406	184	QLLGLRLRQENCHLGGEGCS*LRSPPCIS AWATKLDPVSEKPKTKNQKTGLGGLNQ GPASLLKKIRKLGKKRPG
4240	18141	A	4264	233	440	LPVHHGWGSLRKLTLGKGRANPSFFT WQQQKAKQKQKQPGAGAHACNSSPLGG QGR*ITRSGVQDQ
4241	18142	A	4265	2	230	GARL*SHLLVRLRKENHLNLGKGNCREL KWPHTPAWGTTKDSAAKNKNQPLPPPK GVKSPPREHGLIVTCMFVQ
4242	18143	A	4266	1	349	HKTNIHFCLVMVSNVFTFFFGKGFSPC APGGRAGPLFGLVETPPGREKAFPGPNP PRRGE*RAMAPCPGKILVF*KKTGFP RGLNFNPGGPPFFGLQGGNGGNPWP GPEFFWF
4243	18144	A	4267	2	375	RSEQFAGSASSGNEGLSTRASGCGGCTG SPNSASPPALCSISRRALAAFPRGRARD LQPMPEPPTHSVGSCAAKPPR*APPPA PRRPVPSITTQGLRSAGAQRTGRHLHLQ PQCRHWWKPGAG
4244	18145	A	4268	377	3	TPAWMTERDCIWRRTSAPGGSWPSGVP PSPGAQ*RPSPQGLGLWAAAAAPRC*T APGPRPPPHGPGSPQGASPPTRPPRCR HPRAGSAGPTGATPPGSTQQRHRHSQ LPGHHPGHRVALG
4245	18146	A	4269	1	294	LEDWGGRGARAHYDGFSLPEPESDHYLR LGQYHGDAGDSLWHNDKPFSTVDRDRD SYSGNWALYQGGCWTHACAQ*ILDAVY ATGPKYQVHCEALH
4246	18147	A	4270	2	218	TGRIITLSQGLQTLPLLIAP**LLASLA NLALPPTINLLGLSVLVTTF*SNITL LQKKKKKKKKKKKIFF
4247	18148	A	4271	32	443	LHSDVDQLAGLVFPGCPWPLASPARRAP AGPWPRRAAAPS*DAAPRLAVSAGSP AWPPFST*GLPAPAAVVASPASPTSA RSRS*ASPTARRCRPGGTAAPTSASRQ CQWRP*PCQRSPPSGTCSSAAAPT
4248	18149	A	4272	434	57	HLSPFPASAPKPLPQAASLWSSPFSIV LAQVPPMNTDPCQPQSA*PASELSPEMP PARPOAPPENWSHP*GCGAQTVAFLVPG ATPAHRPASPSPTLPLVTAGGHCIFYLY TYQIFLKFHYIKR
4249	18150	A	4273	288	424	GLSLVAQAVVQWCDLVL*PPPPRVKQ FSCLSPPRIWDY*HPPP
4250	18151	A	4274	1	429	NTRGAAGPPQMPHPPRASAFPENPCGRK N*QGVSGP*ASGSSPVKNAGPAGTWRKG GLGWGPTRVRGRGPRRRPGASSGYARQQ GPGHPGFPSPRRRLSVACALCPGQTS GTRAGLAVWPQIGLCLKAQGARSCPRDH SSD
4251	18152	A	4275	253	3	PHQFNAVIFPSPVSRGCPNNALYSFV IVVLFCEVKTGVSVTQAGV*WHDHSSLQ P*TAGLKRFSSTLILSSWDYKSTPPCI
4252	18153	A	4276	406	3	PMVSQGGVCAK*QARATPREGIFRRSAD TQVREVVQKYNMGLPVDFDQYNELHLE AVILKTFLRELREPLLTFDLYPHVVGFL NIDESQRPATLQVLQTLPEESYQVLR FQTAFLVQISAHSDQNKMTNTCI
4253	18154	A	4277	373	3	DGVSLCPPGWSAVAQSWLTAVL*ALGFI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FLFPVGGTLTGIVLANSSSLDIVLHDTYYV VAPFPYVLSIGAVFAIIGGFH*FPPLFS GYTLGQTYAKIHFPFIIFIGVNLSFFPQH NLGLSGMRRCI
4254	18155	A	4278	71	176	AGGRGCNESRSHHCTPAWATE*DSVKEK KKGLFFW
4255	18156	A	4279	2	379	SPFVPLQSSLGNKSETPSHGRKKKKRRR KRTDENQP*KHPLRARPGPGAPRAQGG QSGGGRRAGPCRKLVRHGTGNPKREP GLIPQGEGRSLGIHPSNGCHKPCPSRGR PPRPKQGRGRMQN
4256	18157	A	4280	2	338	CDMPRRKLDPLSGRNTLGFVVCVWAQTS GLK*SSCLCLPKCWDYRHEPLRPVWVYF KLWHPSPWKPFGFYFVSFFFFYLELCTTA SLFCSCLPCCSRVTLVGSSESSCLWPAG
4257	18158	A	4281	407	1	EERG VATGHTAERGRADNNEERGEVANK RGGREVQPEARMTTTATGTTAATRGAR T*TAATTATAPVTRTAAPATTASSTRIL RTPRRARTASVLWARCRRSATWRASR TCDCRTASHSRPTATRSRTARMA
4258	18159	A	4282	367	225	PCDSACLGLPKCWDYRREP RPAGVLF *ASEFS*QSKEVYVCKLTHA
4259	18160	A	4283	452	1	NTCGLQSVCRGTQRGGPKRCPCHPRE DLGDEQESSKEGRPGREGVQGGLLGAT PGAQGS*GL*AEAAMSSGHALGPGQVP LTPLSPSPNPHRPRPRGRASRQSREST EAQRAVPSQGAAPGWETDWGSSHQWQPC QAQGEGRTR
4260	18161	A	4284	436	22	CHVTGTQPIKVSWAADSREIRSGGKYQI SYLENSAHLTVLKVDDSGGYTCYAVN EVGKDSCTAQLNIKERLIPPSFTKRLSE TVEETQGNFSLKGRVPGSQPITVAVYK NNIEIQPTYN*BITFKNNCIAAARRI
4261	18162	A	4285	301	403	LSIS*PCDLPALVVSQSAGITGMSHHARP RVKSLI
4262	18163	A	4286	380	2	AQVLYSSREQERRQDLPEQVIOAEGE*V KASACQLTFEDEAMESGPAALDKDFQC TRKHHAFAEVQGSFRCMSSRYLVGDCPKT FAEAQNVCS*CCEANLVSIHAFITFILRI QWCTSTVNQAQVCI
4263	18164	A	4287	453	3	YIYEGSIMEEP RPVPKGPLGLHCPGKF QG*RN SYNHHAVRVGTRCAPEGVKDLTS SLQSVITKPEQNIQELMKHFKEKSEAE NHIRT LKAESLEEKNNMAKIHGQLEKLG SQCDRLTEELTONENENKCLKLYQCLK DQLEEREDV
4264	18165	A	4288	52	400	LDLYFFYRQCLALS PRLQRSSAILAHCN LKLGLSGDPPTPASQSKEITSMRYHI*P NL*NSMC*NCVFDTHRIGENIWESYI* *EINIQNACRI PKTQQQKTHFQNKQGLH SNLN
4265	18166	A	4289	2	263	IHGALHWSQLPGRLLKWDERRSPGSRGCS EL*SHHCTPVWVTEGDPVSKKRINICKQ NLNEKTNLTVDTPRHSPTHKIKSLNHQ MFL
4266	18167	A	4290	3	142	YLGVRHLSIDGLDLLT*SARLGLPKCW DYWRDPPRPANFYFILPK
4267	18168	A	4291	324	19	EMSKRHEQKPHRRELQMANHKVKTSLA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IREMKIETTMKYHTPIQMA*VRNNDTS QVQWHTLQVASPLVAEVGGWNEARNLRL QIVKMVPMNSHCTPAWVT
4268	18169	A	4292	2	204	IHFCDRDRSLCCPGWERTAECLKQSALLG LPKCWDYRH*ATKPGQLQSVLLGLKIFL ILLVRGVDRYL
4269	18170	A	4293	427	3	RRKTVTVPRTGERGTISNEDNGLCKAVG NIPGSPLCNVSKLNMKHPGGHARFC IWTESAFRKLDELGYTWRAASLKSSYN LPMHKMINPDLRLKSPETQALRAPR KKIHNRLKKNPVLRL*RIKLTSRHKR R
4270	18171	A	4294	24	372	FICPLQDYVICSDVTSCVVKILATTGR RLRDDSVQFSFFFFGKGGSLAPRVKEQ GGDLG*WNP RPRLREFPGLALPRCWN GLAPPPPLILVLEKRGFPLAGKMGNL LHSR
4271	18172	A	4295	1	332	IHSSYFFPQS*FFGTINTSDKPLRLIK EKKREGTN*HIMHEPWKFGIDPEDIKV KKKYYKQLCTHKFDNLEEMVHFLKKTTI HLI*NR*FE*LYKYRN
4272	18173	A	4296	407	30	WSVIYGEN*ESLGWGAHPSHVANIRVTG LRYLFSYGRHALDMLESSQDNMRSWVVS QMSSEIDVDNLGHISLCNAVQ*IRNLNP GLKTSKIELKFKELHKSCKAGSEVTKK EFIEVYHELYAVG
4273	18174	A	4297	350	1	YKTVVMNKEK*YVGYNIEQEQLALKT TVLDEWYTLDPGRIIKVGGERFEAPEAL FQPRLINVEGVGVDELLYSTIOADVGT RSEFYKHIVLSGGSTMYPLPSRMEREL KQHV
4274	18175	A	4298	623	1	SRGCAATCDGSI TAWPQRQAQKPSV HSKLEAEAKPTPGDHAASESTGFSCLP GGVHKTAHAHARNMPGDSNTGSGQSPAG RRWEARGSAERHPTOPDWTHPDALROA MARNPASSF*SF*RCCTAASPVPPTPS PVLMRGPVPGGGGGQKIRPLQEEAPP SSPVVLSR*PQAGTPSSPAVSSLYHGGL SPTGRQDRWGR
4275	18176	A	4299	469	3	PVRNCLGARFRVSGRAAHHAL*QSASTL QGDPRTKRQAISA*SSAFDVQDVSHVTL PFYPKRAQSKDLIKEAILDNDFMKNLRL SQIQEIVDCMPVEYKDSRIVEVDVG SCVYVMDGKVGVTQGVKLCVPGPGKV YEELAILYICRRPCI
4276	18177	A	4300	506	321	KPLSLLKIQLAGHGGSC*LLQLRRVR QENCLNLGGEGCSGLPKFWDYRCEPPCP DCWPS
4277	18178	A	4301	454	1	NGEKPTYSGKKYVFLF*NTRRPTLFTWG KTN*GERPRSSVYSCSSWRLSSSSLGRS *NSVGSNLIIATLTAQELSN*ANNLI *LAYTIAFIVKIPLYGLHL*LHKAHVEV PIAGSIVLAPVLLKLGGYGIIRLTLILN PLTKHIAPLY
4278	18179	A	4302	3	463	AVSLPLPLPRFGRLPPLRVGVVCPLRCH ILRTQRLEGAPSR*QTGAKQAGVWEELR SRLSLGPPLGRIRPYSGDGQVTDSSGA LASSLERGCYPAALLVGEGEEMYLGPY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						HET*DGLKRLSLAKPFGGTRLTRSGHT FWGEGIPPSAVCL
4279	18180	A	4303	469	2	FFFFFFSETESC SVTQAGV*WHDLGS LY
4280	18181	A	4304	194	3	FFFFFFSETESC SVTQAGV*WHDLGS LY
4281	18182	A	4306	517	254	VVEETA FRLIGKTGIGLVTS GDLAASAS QRGGMTGVSHCNKKEFVLMNIIVMSSGL TFLPFS PDEV*GS*GLSFLPSPLALNTG LRN
4282	18183	A	4307	276	3	KIKMEGIPLHIPNPLVNLNLGLLFYIAT SSLAVYSIL*SG*ASNSNYALIGALRAV AQTISYEVT LAIILSLT LIISGSFNLST LITTLV
4283	18184	A	4308	234	398	KKFFFFPPLEGGGPITTIWSPPLPG*RE SPAPPPERGGIKGLAPPPNLF FFLDKR
4284	18185	A	4309	403	100	SGGQKAVGPPWAAPPQYKQNTNKLGLPLP QPSTEGGAFWPTQGP KPTGLPPLPG*LN PRNPTPP*WPPPPPPFNTRSKGPHTPSP TFLCGPPPKNRLFFFF
4285	18186	A	4310	399	85	WKPIPLAPEWRGVIRFRALPPCRPLHCP TLKLTAPS VIHQRT*VHWGFLVGVSLSV FLERESCSFTQVECSGTKLALRSLELLG VSDPSISAFQRA GIAGVSHHA
4286	18187	A	4311	230	2	WTEEDTRRCLVLFSPFLSFFLFCFVLRLQ RPACCPGWSAVTQS QLTVA TSLSLAQAKR SSHLSPPQRS*DYRHTPQCI
4287	18188	A	4312	1	420	NTSWGVGELSLIVIVINMLLPYVWLPKG KFFFPQNSRFPSPAPHSPPGLRSDFSH SGGLFFHLEVLWGLPLPPPPPPASTHVR RPLGTQGCP*LAWYIHLISASYQKANA PQLSCILQDCIRSKGDILIFTFFTLCLS
4288	18189	A	4313	403	207	ESSEG*LNPLAHLAMRYKGC PFKDVREK SEFILKS IQVRKSLNTRMSLLQLDFTC RYSRCVCFY
4289	18190	A	4314	469	328	TSEGGGFNELLRLCHCTPVWLTK*DSVSI SQRIKKNLKTQSLVVRCP
4290	18191	A	4315	1	212	NTLPGEVLKRLRWEDSLNP*GQGREP *SCHCTTAWATEKDPVSKKKKKKNPGG FRPHLSQPPGPPK
4291	18192	A	4316	63	559	SNLTFWQCAVPAVETTPSSLCGPVPSPT SSATPKPIPS*AACPPDCALAAEVRL PAAGRPRFSEACLTQPNPCVLWPCLDW HSPTSCPTGSS*APHSCAFLPVPRLG MTTVHPTVHLPIHSSLTFAWE*PSPPAC LTAPRPTGHCLLSVPSSAYSSSSPS
4292	18193	A	4317	135	405	PAPPSPHPKPDSVSCVIPPSP*PAPPSPH PKPDSVSCVIPPSPSHVAGSGLPENTLLE PRGPCPPEVPPTSPFVG*AWWPHPPARR ASGRMDGRTDGRGRHLDRSTHSFLTP
4293	18194	A	4318	413	1	LYLVGRA*SFHRSFPGQERIHGGKPYD CKECGETFISLVSIGRHLMLTHRGVVPYK CKVCGKAFDYRSLFRIHERSHPGKPYE CKQCGKAFSCSSYIRIHERTHTGDEPYE CKQCGKAFSCCKYIRINERTHTGGV
4294	18195	A	4319	479	342	GVGVNDGILVLGATNIPWVLD SAIRRR *DNTVNILFLTADVTSR
4295	18196	A	4320	400	26	HSEAVTTVRSHHSPVGHISLNA PPTVA LTP*YNKPLNIFV*ARAQKIQQQLTHT IPHILLLVITRDTSRACVCVCVCVCV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CVYAYIYVCMCVYIYVCVYIYICNYTFI PTLVHLPINKMY
4296	18197	A	4321	370	1	SDRGQKAGQATRLGSRQTGQDEDKGTE KSI PSWDKGFVNNEFGKSVNVSSNLVTQ EPSPEETSTKRSIKQNSNPVKKEKSKC NECGKAFSYCSALIRHQRTHTGEKPY+C NECEKAFSRNV
4297	18198	A	4322	342	82	GLGLTTNWLITGKSAGRGCAPSSGGLWL AVGDSVYVHRETEGGKPSGPRCC*PS* AGLAPSPPPPGCPEAPGSCCLHYRCLL TAH
4298	18199	A	4323	284	3	ITKKFPRVIGGGCFSPFFMGLSKKNGLF PEGALSISLIFGPAIPPGGAQVISSAKE KKKVLSPRGVVAHACNPSTLGG*GGRIK RSRVPDQPV
4299	18200	A	4324	365	3	QVEVYVVENHPFRLEESIYQ*CRLEGAT SVAGEQISEYNISMRA SDGSGPLSTET HITLHVIDINDNPPTFPHLSYSAYIPEN NPRGASIFSVTAQDPDSNNNARITYALT EDTLQGVY
4300	18201	A	4325	253	3	PSFLSRD*SHIHKRL ECGMISADYNLH LPGSSYPPTSPSQVAGTAGPSMSLQEGR ASHDITSSSR SIGAKELLRPADHPQCI
4301	18202	A	4326	307	95	FLFLKDKILLSPRLECSGTIIAHCSLK LLDSSYPPAVAS*VAGTSGMCHYTWLRL KNHLSPGIQCSEI
4302	18203	A	4327	371	2	WAPNHISPTPRSGSTTRIWAPTPPSNSP RPCQDPGHRTDPWYPEEEFLTNPDPPR APASWSFPFQEKRLHFPALPCP*HLDSS LGPTTLFSFSPPTSI RPSQTNHSGKTP PPLSYAQHDCI
4303	18204	A	4328	409	1	RLLEARQPELEMAALIFFTLYKHVERE QKYHOLQDEYFTSAVVLTLILALFGLV YLLIFPQSVVVL LLLVLCICFLVACVLY LHITRVQCFPGCLTIQIRTVLCIFIVVL IYSVAQGC VVG*LPWAWSSKPNLY
4304	18205	A	4329	262	2	LHGAYLVLDITGAQNRKPRYSFKWRVGG FFFLVFSPRDSLTLPRLECSGTVMACH HLDLLGSGDPPTSAS*I*GTTGAYHHTQ HV
4305	18206	A	4330	1	399	NTP*FLKGMGLVNHVFTEDNLKLYVSN LGIGHTRYATTGNV
4306	18207	A	4331	408	3	SSVGIHVRTHTGKPYECKHCGKAFSCH SSLREHVRTHSGKPYECNQCCKAFSHA QYFQKHVRSHSGVKPYECTECGKAYSCS SSLRVHVRTHTGERPYECKQCGKTFRYL ASLQAHVRTHAGA*IYKYS GHV
4307	18208	A	4332	110	426	GLSPGTWSDMTGGPAVTAFFCTLTGTHA GHIIDGIDIAKLP LHTLRSRLSIILOD PVLFSGTIR*APPPLRPTQPQAGSVPSD LEHKEEGVGGDQDPRGVSCSC
4308	18209	A	4333	133	1	EPCCPSALAAPEVLGPEKYDKSCDMWSL GVFMYIL*VPSPPPLY
4309	18210	A	4334	165	1	IILTFPKNERKVVAQYQW*KNR*VDQ WNRIASPEIDPHE*SQLISDKAKECI
4310	18211	A	4335	42	440	SARRAGDPARGAFSRNNASLPDFRELTG RPAGGLQ*GNCPAPPTPQLPSPSVSRPV SGRGPPPPPSFGDPRANRPQNPKGAKVV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LTVMGEPGEIRRAACPOLSWMTFPGS LPEPKRTGPGIQKSPPSRRGG
4311	18212	A	4336	1	160	NTCGGGAQL*SQLRLRLMWEDLNSGSQG CSBLRSHHCTAA*ETKGDPLSINRY
4312	18213	A	4337	236	1	QRSLLCYIMEIRTVAVRIVAIKGVSEV YLAMSEEGTVYAKKECNEYGIF*ELVLE SHYYTYAAAVLRPVCCIESKVS
4313	18214	A	4338	408	3	CQSSVSKKERTNGAQNFGAAKQGNNELR DSTEQFQEYYRQRLRYHQHLEQKEQQRH I*QQMLLEGGVNGEDGRDQQQRNEQFL NRSIQKLGLNIGMDGLGNEVSALIQQC NGSKGNGSNGL*VNSFDTFPHV
4314	18215	A	4339	363	1	RSQSSLPKSFKRKISVVSATKGVFAGTS DT*GVQPGWQ*RWGASTATTQKKPSISI ATESLKSLLPIDIKPLAQEAVVDLHADD SRISEDETERNGDDKTHDKGLKICRTVV RARYSINEV
4315	18216	A	4340	1	353	DVFLDTLARPLRHSNFFLCYLL*DFFK FIPQFFYYWMFYFDYIFISRRNFYLLLT HFFTLPLFLVIRIQCLHLFLFFSFFFFF FGKGNPFLPPGWRARAQFWVNGSPPLRV NALLP
4316	18217	A	4341	376	3	LELEGGFLPHIADEVREERSPALDDR AGRCQGQPRIQVCLTPKSMFLAFHM*T CEHCLEQCFSTSL*PIEIRTLH*D*GCV CMCAVVICVCMVHMCAYICICVARMA KRPLESIHSTCT
4317	18218	A	4342	158	2	LAFFFFCETQSCCQWHDLSLQPLPQRF R*FSCSLSPSSWDKKHSTPHPTCI
4318	18219	A	4343	145	2	IFGEQVVFQVDMNKFSGDF*DFGASLTQ AVHTVPPNV*SVIPCHPPRV
4319	18220	A	4344	1	434	RSLIFRATAYEYRIDQADLKLPAKRS SCLGLPKGWDYRHEPPCLARFIFWQIFI AYKLR*KHYKSRQSLPSRGSC*CACDT FVSDPSSHWTMAQILGGWITLGGVQRSC LADQPLLLPLPPTLAPCLP*NDVLLFF TQSQ
4320	18221	A	4345	4	475	KHSCRSLEHLDRPLPPALQETCPVRAEP LLLVRINASGGLILRMGAINRCLKHPLA RDTFVCLLAVLGEQHSKSFLLNHLQ LPGLVRAGRGRREAGSKDGGSCLEAGS GIPVCGDKPTN*CSFSPPLQESGEGGR PRGGEASLQGCWRANG
4321	18222	A	4346	313	442	DSTLNFFFFF*TESYFVAQAGVQGHNLS SLKPPPPGFKRFSCL
4322	18223	A	4347	437	338	AEVQEFYGDYIAVNPFLSLNLTGCCQG RNWDPAQLSRTTQGLTALLSLKKCPMI RYQLSSEAAKRLAECVKQVITKEYELFE FRTEVPPLLLILDRCDDAITPLNQWT YQAMVHELLGINNRIIDLSRVPGCMRPL *RIHPGTLERSIRLLFMPSSSWTMA
4323	18224	A	4348	409	118	GLHDASFVAAPSTQVVYFFFEETASEF DFFERLHSTRVARVCKNDVGGEKLLQKK WTFLLKQALLCTQPGQLPFNVIRHAVLL PADSPTAPHIYAVFTSQW*AAGPSGRWS TSSAAAFRRPRHSCRL
4324	18225	A	4349	2	418	YTLPDFPHPHRLSHCRLLQSRTAETQ SPGACTPISQGHFGQRSSPCSSSNPAC

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						*SSSSCGSTGFRCPGSAHPGCCSYVL*MGR*RSSQAFRASPIAQGPSPAPAGRAGHPALPSPPLP*GAPPPPSAASSPGL*SPA
4325	18226	A	4350	401	276	DPLNVGGGGYS*PRLCHCSPTWVTEGDLVSKTNTHTNKKHL
4326	18227	A	4351	446	277	AQDFVLIKDGEVIGGICFRMFPSQGFTEIVFCAVT*NEQVKVSAAPRPQPQSTAH
4327	18228	A	4352	408	3	PKSSLFTSRPNKGSWSTKRPALSLAYSNENAQGSWNGDQDAGPLLVENPROYSTELSVTIAGVASLLFLNLVLAFAALYSRKOTRRQ*PLCQLSPHRGIGASELGHAPQ*ELPALLLGPIRHECEAGPPHDTLPV
4328	18229	A	4353	62	280	VRIGCLTSVPEASSCGLPPTPGCC*PLGLTPCRSRSRTRSFRRSRRTQSRSRPKTYSPPGRRRRSRSRSPTPP
4329	18230	A	4354	364	3	PVGEEGKSLVPKSPVEEKGKSPVQSFPVEEKAQYRVPKSPVEEAKSAEVLGKGDQKEE*EKEVKQAPKEDKVEKKEKPKHVPEKKKAESPVKKEAEVAVVTIAKSVKVQLEKETNEECI
4330	18231	A	4355	3	558	LGPTLLWRRGKVPKANSPIPTSLRRTLP RASGPGSRGELFMRQAGSTPMTLPRSTP SMS PML*MVWPPTAVFPV*KPLMWAPPA PLVLLVLTILTEIQEPATPAPLTQF*KPTSLMVS RPVCV VQGPRTTRSTLCATTIA PSHATLRPGLSTTSPPLWQLSLLEGGQASLPKG*NTSITLPSVS
4331	18232	A	4357	258	1	LGFDHDPGAGWSQPHGGRSAQAQ*PPQPPTVPRTSLADVSDAPLP CGHSR PQHHP FRLPHTSFSTPGLSAVCLIVHPAARVSR CI
4332	18233	A	4358	97	343	DRDLGDEYGWKQVHGDVFRPSSHPLIFS SLIGSGCQIFAVSLIVIIAMIEHLYTE*VPTLNCIMSLFLNSFNHWNLLSQS
4333	18234	A	4359	182	2	KDYFGSSVENGGEEELKQEDQLGGYSVI*ARDEDEDEDEDEDEDEDEDEDEDDDDDCI
4334	18235	A	4360	88	2	RGSRTDTG*RGS DRGTG*RGSHTGTR*RGSRTDTG*RGSRTDTGGRSRTGTGGRG SRTGTGGV
4335	18236	A	4361	2	250	ELRDEGKASSAKQRLKCAGLQKFGERAP KAWAVARLSQRFPKAEVSKLVTDLT KVHTECCHGDLFGCDEESAGLAKYIM
4336	18237	A	4362	169	456	EQLLCAGQGQLSCEPLHLSPCVGPGQTP AHRPGRMAPGPSFLSPGSPCGGLAIP CSCQPWVAGVPDHHLLFPSPMGRAGLSPS ERSAGEGVIPWP
4337	18238	A	4363	1	419	PEFKLQKLKRSQNSAFLDIGDENEIQLS KSDVVLSTLEI VIMEVQGLKSVAPNRI VYCTMEVEGEKLQTDQAEASRPQNGTQG DFTTTHPRPVVKVLFTESTGVLALEDK ELGRVILYPTSNSSKSAELHRMVVPKN
4338	18239	A	4364	375	448	PGAVAHACNPSTLGGRSGRIMRAG
4339	18240	A	4365	1	444	DFLTNHYLHFLRIAGSQLTGLGTAVQLY SAYBENNRTFLLAAVKRNNHNYVNPSPGV ATFFESI KEILLRQSGVKVBSVDHDS CV HGPCQNGRSLRKLAVSSVLKSRESLPV IIVANEPLQPFCLKCLPGYSDSWCEIDI

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						DEWLPPFW
4340	18241	A	4366	52	402	CPQEVWFHSPCHCTSAFMKDYFLCLVR FGDLKEDKVTTRHDGASSDGHIAHIFRHA AKBLFNEDVEEVTTYRALRCGAVSTACLC LWLARVHGVPVWICACGGSMDGVYTSQN QKDF
4341	18242	A	4367	119	247	WVLLSPQLHGVAVLGLIALIAMEGIEGAE MALRTFGHLLRYGEP
4342	18243	A	4368	2	430	GGTVVDGQPGPHGDSLSKAPGMNSLEQG MVGLNIGDVSSSAVKTVGSVVSSVALTG VLSGNGGTNVNMPVSKPTSWAALASKPA KPQPI MKTKSGLPPSPIKHNMDIGTWDN KGFVPKAPVPQAPSTQAC PQSQVQGT LP
4343	18244	A	4369	1	406	ETSTPEGEAGPIQRLDIPVENPVESKNI FLGAPLIICHVIDKRSPLYDISATDLAN QDLEVIVILEGLGETTGISTRARTFYIA EEIQWGHFRFVSIETEEQRDSDVYSKPG KTDLVTTSRCNARELDEKPSILI
4344	18245	A	4370	2	284	GTGTLCDLTALLSARYDGVRTCILPCWK TISTIPVALLIHYHQNASCGKRAIILE TRQHLFCADPKQWVKDAKPHLDRAA ALTRNGGTFE
4345	18246	A	4371	3	184	EDYNTILLSTMKGTTTRPINKRIEALNDTV DQLELTDLCRTLTPPTIAEYSFFSSAPKV LIQP
4346	18247	A	4372	44	304	GLPRSIGCQGLPRLPEWPTWVGCHRG IMPSVPTQVSRPLMFLDTPGVLA ESVETGLKLALCGEPGLGLGPGPLPP HL
4347	18248	A	4373	1	422	LHLFNPASAPSRSLFSGPILDPLSRAL GVGPGICGLASSPGISEGWDQIRSWTHP PDPDHLSGFCRSQVYMHPSPSPSTMIL SGGTALKPPYSAFPGMQPLEMVKPQSGS PYQPMMSGNQLVYEGQLSQAAGLSASQM
4348	18249	A	4374	2	423	NSGTHTPGLELDSKNGRLPEIKLPVNG CSDLEDSFTILQSKDLKQEPDDEPTCID TSETSLSNQNKLFSDINLNDQEWQELID ELANTVPEDDIQDLFNEDFEEKKEPEFS QPATETPLSQESASVKSDESHSPFAHVS
4349	18250	A	4375	292	429	LKISVFPSSSTEISLQORLEYIARAILTA KSSTGIASISADGESLRE
4350	18251	A	4376	544	32	ALHACACGLSPEACFLHLLQLTGTSPG PVDGQGLDNQGFRLKAILGVSPAPEPV HGASEHNADTGVSVARACVLPSTPTLAR TAAAKDESPPLAGLTMGPSREPGGSLP LPSSGLSSPTRLALPRRPPSVSVWQDAG SSGSMPTPLVQCGRHFRFYGLVSNVAVM LK
4351	18252	A	4377	378	232	PAKRAEEELLHDTRCWLNGGAMPEARH PRTGASALHVAAGYIEVMR
4352	18253	A	4378	291	1	QMLSVDVASRYRAPSTVYVNSLKEGMDG LHGESSFLGLGPSVAMNMQTAGLEMG CDGHFRQNVGCGVYLVKPDFLRDIQSSLH PEKPI SPFKQSL
4353	18254	A	4379	171	458	RGPLFLTLHIVNSLQGNFRREYIVTQG PLPGTKDDFKWMVVEQNVHNI VMVTQCV EKGRVSKQLSWHQSFAFCHLDRI LPHHQ

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						SETPQNNVGIM
4354	18255	A	4380	214	410	LDHLEPHPSPTGEIEVKWFPAVQTGLPM CILGAFFGPIRLGAQSLQVLDSELIPWA VQNGRIAPC
4355	18256	A	4381	2	74	IGDSGVGKSNLLSRLTRNEFNLGL
4356	18257	A	4382	290	119	IATVSLNIVKMPRLPKAIYRFNAIPKI PMTFFTEIDKTILKCMWNHKKIIPGNSPA H
4357	18258	A	4383	2	423	LERVCWIKDIVVAVTGENMEVMKSIQK YQHKRISLVEAGVTRHRSIFNGLKALAE DQINSKLSKPEVVIHDAVRPFVEEGL LKVVTAAKEHGAAGAIRPLVSTVVS PSA DGCLDYSLERARHRASEMPQAFLEFDVIY
4358	18259	A	4384	356	1	WYPCCLLASLICVFRGLFYLSLCLVLRV PVPLCLOFPGLSLLSLLSLLRQGLAL WPRLECSAIRAHCSLELGSNDSPASAS QSAGITGMSQCAWPLSLLSVSPRVPGLS SVPLIF
4359	18260	A	4385	1	125	SGSKKTLRSSLEETILDIEKFHRESFF YTHLINFSKRYC
4360	18261	A	4386	53	215	WQLYWTTWCQKISRNOGLAHVPRMECSS MIIAHCNLLKLGSSDPPASASQIDPS
4361	18262	A	4387	2	390	PSLAARVLARGYGNFSVFWLWRKNDRM HGECAPNVSVAVSTSHTTIIGGGIRGGG GGGYGSGGSSYGSGGSSYGSGGDDGGGR GSYSGGGNYGSGCAGSGHGSYCSGSSS GGYRRGSGGFGSCNSGG
4362	18263	A	4388	2	441	IKTRISVIHKEEFGLTPIEGAIEDMKNK TLQLAFAINQEPSDAKMLQMLKSGEGA TVNQGPLEVAQVFLAEIPADPKLYRHHN KLRLCFNEFIMRCGEAVEKNKRLITVDQ MEYQQELKNYNKLKENLRPMIERKIPE LVKPIF
4363	18264	A	4390	242	24	KLGNFLGGCVKESFPVFPQGGMQWPDFGS LQHPPSRFKQFSCPTLPGNWNFRNAPLR SGKFFFSVPFLVETGY
4364	18265	A	4391	1	244	VDQMRQNLFTTGAHHLQQANIQFRTDI ARTEYLSNADERLRWQASSLPADDLCTE DAIMLKRFTRYELGCGGEAWEECGW
4365	18266	A	4392	2	146	LDLLSQPCRAVYIFAKKNDIPFELRTVD LIKGRSSLGFGEPKSGEGR
4366	18267	A	4393	204	489	GAASEHPFKGESHGTSKASSLCADAGP AGHFASVYNPLAWTVTTIVTLTVGFPGV RVTDEAGHPVPSQVSGIQRCLQGMKAPP VTVTVSGERGS
4367	18268	A	4394	2	171	LSDGFQPSRSIIIFASWSAGDFGSGVATE WLEVFFIIPSHIGHELVLGCCPEVMFL
4368	18269	A	4395	2	197	WLELLKFYTLDCALEEYVICVRIQDILT RENNNWPKRRIAIEGEMICISFVEYFI CATHYLIOC
4369	18270	A	4396	2	285	TVDFFPQPYKCQEQEYMTKVLCECQKVN GILESPTGTGKTLCLLCTTLAWREHLRD GISARKIAERAQGELFPDRALSSWGNAA AAAGDPIGPS
4370	18271	A	4397	366	461	TSNFSCSLVLEEEASDYLELDTIKNLVK KYSQ
4371	18272	A	4399	157	3	DVLRRNFARSAYLYLFIDRVTLWNAPRL ECSGAIIAHCSLKLGSNDPPTS

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4372	18273	A	4400	2	343	DIDFKYHFDFFSVNFNEELVALYGGSLQ KQTKFVHECIKTILKLYKGQEFAPKSVA IIGHSMGGLVARALLTLKNFKHDLINLL ITQATPHVAPVMPDLDRFITGSTGWLKDH G
4373	18274	A	4401	214	430	ELGNILNYVVRWEAEAEELSNRWFNGQAV HGELSPVTDFFRESCCRQYEMGECTRGGF CNFMHLRPISONLQRO
4374	18275	A	4402	3	227	LTQVSPQMTGHAGLNTAQAGGMAKVSEL KHQYFLPNRGLSLRVMRKMGPRGPLLF FLLGSPRATHAWKRQISF
4375	18276	A	4403	158	313	NRDEFCHVAQAGLELLGSSSPPAATSQS ACITGVSYHVRPTLSNKKGCSSL
4376	18277	A	4404	3	628	HCIREGGQDVPSNKDVTSLDWNSEGTL ATGSYDGFARIWTKDGNLSTLGQHKGP IFALKWNKKGNFILSAGVDKTTIWDHA TGEAKQQFFPHSAPALDWDWQSNNTFAS CSTDMCIHVCKLGQDRPIKTFQGHTEV NAIKWDPTGNLLASCSDMTLKIWSMKQ DNCVHDLQAHNKEIYTIKWSPTGPGTNN PNANMLLASASL
4377	18278	A	4405	35	180	MCVDYHYFFCLLGPNNNNPQTSAVRTPT QTNGSNVPFKPRGREFSPGK
4378	18279	A	4406	1	438	DFQRPDDHGDVDWEKLVLLTDCSNLQ DQTYILYILYVIKGPSWDTNLSQNGVT VQNLGLGYGKTGLNQEWGLIPYISSLF RKKVDVLAEACTDLLSDQQLTVGLSDE PREKIYAPLPPKELTKLIYBASGQDII IGVLTQ
4379	18280	A	4407	1	428	TESVNAYFKGADPTKCIKIVKITGDMTMSF PSGIIKVFTSNPTPAVLCPFRVKNISRLE QILPNAQLVFSDDPSQCDSENTKDFWMNQ AVTVYLKLLSEQNPAASYNVVDVLKYQV SLNGIQSTPLNLATYWKCSASTDLRVD YK
4380	18281	A	4408	174	383	KNSWPGAVAHACNPSTLGQKGRQITRSL YRDHPVQGEIPLYLKLALAVTFLGLL TGLHDLYLTLNLT
4381	18282	A	4409	1	288	LMAEKDSLDPSTFHAMQLLTAGKGASRV PLGRPAIPGMSGPGFVPLASRPLGTEAV GSSGLILIFGSLDSTFPPQPGVGRGRIS LQWRPEGDFAP
4382	18283	A	4410	292	422	LVHSSCFQVSSKILELARKQRMNTDIRR NIFCTIMTSEDFLDA
4383	18284	A	4411	412	238	FFSRHRVSQWDQAGLELLTSLDLSALAS HSAEITGLNHHAQPLTTNFNKYCWISLQ VH
4384	18285	A	4412	1	405	VTSSDKSLKVLLDAEDKVFNEIRNEHFS NVFGFLSQARNLQAQYDRRRGMDIKQM KNFVSQELKGLKQEHRLSLHIGACESI MKKTKQDFQELIKTEHALLEGFNIRE TSYIEEHIDRQVSPIESLRMLCL
4385	18286	A	4414	2	149	GFHHVQAGLEVLTSNDLPVSASQSAGI TGVSHCAQLRSDGFKKRSSPA
4386	18287	A	4415	1	366	DICHRKLGVECPHASINRLVQVVSII TASLRFEGPLNVDLIEFQTNLVYPRIH FPMTAFAPIVSADKAYHEQFSVSDITTA CFESSNQLVKCDPRLGKYMACCLLYRGD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VVPKEVNAAI
4387	18288	A	4416	1	164	RRRCESMTMFADTLLIVFISVCTALLAE GITWVLVYRTDPFGTLAGEGPGGRY
4388	18289	A	4417	2	141	DIAIPCNNKGAHSGVGLMWWMLAREVLRM RGITISREHPWDLTSSVMG
4389	18290	A	4418	136	1	BQTKAFGQLHKVLGMDPLPSKMPKKPKN ENPVDYTVQIPPRDPMQ
4390	18291	A	4419	1	280	GNVCKYGYRGPSCEDGRLRVLKEWFR GRDVLVYLGCVGHLLTSLACKRGPSRMV GLDIDSRLLHSARQNIIRHYLSEELRLLP QTLEGDPGA
4391	18292	A	4420	3	446	TVSTSQVRQNYHRDSQAANRQISLELY ASYVYLSMPYYFDRDDVALKNFAKYFLH QSHEDRDHADKLMKLNQNRGGRLQDM RKPDCCDWESALNAMEWALHLDKNVNQA LLELHKLTTDKNDPLSDYIETHYLNQ VTAINELG
4392	18293	A	4421	6	182	DPSFCSEPRSCHCTPTWRTEQDSISEKK KKRNILKNWAKNYITLSEKERKSKQRS RR
4393	18294	A	4422	1	456	GPISYVVVMPKKRQALVEFEDVLGACNA VNYAADNQIYIAGHPAFVNYSTSQKISR LGDSDDSRVSNVLLFTILNPIYSITTD VLYTICNPGPVQRIVIFRKNVQAMVE FDSVQSAQRAKASLNGADIYSGCCTLKI EYAKPTRLNGSK
4394	18295	A	4423	2	257	FHHVGOAGLKLISVDPPALDSQSARIT GVSHCAQPVLCILNQLCAKAVLSPDSHP YPPKSGRHEGQVREQMSPCSYIYFKRT V
4395	18296	A	4424	106	259	CCCFKYFFSNVKICFYRDLKPENILLNE DMHIQITDFGTAKVLSPESKQGV
4396	18297	A	4425	3	364	MDEIEKYQEVEEDQDPCPRLSRELLDE KEPEVLQDSLDRCYSTPSGYLELPDLGQ PYSSAVYSLEEQLGLALDVEDSEYLTVK VISLHLVFQIGVIFLFQVPLTDFRDVIA AGRTYGRI
4397	18298	A	4426	2	241	HHVWLICFVFFVCVETGFCHVAQVGLER LGSSDLPTSVLSAGITDVNHWQSKPS PSKGTGMNRPIGLRVGGVWSRL
4398	18299	A	4427	2	438	TRLIGPNCFGVMNPGKCMGIMPGHYHK KGRIGIVSRSGTLTYEAVHQTQVGLGQ SLCVGIGGDPFNGTDFIDCLEIFLND TEGILIAEIGGNAQENAAFLKQHNSS PNSKPVESFIAALTSSSTGRKMGGHAGQLL AEEKV
4399	18300	A	4428	34	427	AGMLPAVGSADEEDPAEEDCPFLVPM TTHSEEEESGLGAKIPVTITGYLSAG KTTLLNYILTEQHSKRVAVILNEFGGS ALEKSLAVSPGGELYEERLELINACLCC SVKGNGLIAIENLMRQKE
4400	18301	A	4429	330	8	YSDRISHWIDMCPISKYIFRGVPHPPHIS TFLHTAHLNVARGNENMSPHDEEKAY QRKEKCCDDPMAGAARIHFLCFEMGFR SVSQAGVPWPHITSMQPPRIK
4401	18302	A	4430	446	222	LTSSDPPASAPQSAGITGVSHRPQPIWG VSIQLYFSGCPDTPGQGRLTREHCDGQD GEQGGPCSESVAQFCHDWS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4402	18303	A	4431	3	243	AREDSADVFVSFFPDFVWTLRDFSLDLRA DGQPLTPGTSQKDNFIFLRLCIRKFTS LIRTSRSYQSPDTSVASSRGAR
4403	18304	A	4432	433	0	PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPSPSSSSS
4404	18305	A	4433	25	185	ARWVACSELRLRCCTPAWATEPEPVFKK KKKVQQGGWPGGLTPVSYRFGRLT
4405	18306	A	4434	2	329	VRDIKEKLCYVAVDFEQEMATVEFSSSL EKSYELPDGQVITIGNERFRCPEALIQP SFLGMESCGMHETTINSIMKCDVDIRKD LYANTVLTGGTTMYPGIADRMHNEI
4406	18307	A	4435	2	374	WVTFISLLFLFSSADSRGFRDHAHTSE VAHRLKDLPEENFKALLIAPAHYHLQC PFEDHVELLNEVTEFAKTCVADESAENC DQSLHTLFGDTLCTVATLRETYGDMADC CAQQEPERNEC
4407	18308	A	4436	2	352	KVRRIDSRLAELDRIRNPQISCOLIYS PSLFLGAFLLFFFGFFPPPYLLAPKN QFNPPPLCTGGPVPRPKPIPPWEPPRP APPLESPQWDLGFQIAPFLWVINGGGS GGSRA
4408	18309	A	4437	2	369	QSCETLFHSHKDVCEVCSSALSCLSQSV HLQGLSFLFPGMEVEQRDSQMALVES LEYVRGEISKAMADFTTWKTHLLTSDSQ GGNQMLDEGFRBDFSEQMEIAIRAILCA IQNLEERKNE
4409	18310	A	4438	2	231	SDTSRPQLPCPAARERFPDGPLSLRPLP FFLSQVYNEQIHDLLEPKGPLAIREDDP KGVVQGLSFHQVWDWARVG
4410	18311	A	4439	1	365	MAHAMEEVKKCLGPDMMDDICHEQFLEL SYLNGVPEPSRGRGVPVRRRAAPPPPP VPRGRGVGPPRWALVRGTFRGAITRGA TVTRGVPPPTVRGAPAPRALTAVMQRI PLSPPPATK
4411	18312	A	4440	92	510	LAALPDGGQELHIPRSRAGPAGELSWAV VGTGALSSLSILFQMARCRPWPLRPNS PLQGWIFNVVFWLVAIPASLFGFLSDH LINQGYRAITVRKLMQGMGLGLSSVFAL CLGHTSSFCESVVFASASIGLQTFNHR
4412	18313	A	4441	2	266	FPPHLPGLKWECPWHQCDECSAAVSF CEFSPHSFCKDHBKALVPSALEGRGCC SEHDPMAVPSPEYWSKICKWESQDHGE EVKE
4413	18314	A	4442	2	279	KGAELVFLPSNTRSLMYPLDQGVVRTFK AHYAGYSMERIVSAMEENPGREKIMKKL LKLSSPKETPAGEKLCNDADHDFTELDD RVIHENHE
4414	18315	A	4443	2	371	KWVTFISLLFLFSATDSRGVSRDLAHTS EVHRFKDLGEENFKALEAIAFAQYLQP WPFHHVELGNDVTESAKTCGADESADN CDKSLHTLFGDTLCTVATLRETYGEMAD CCSQPEPCEKG
4415	18316	A	4444	2	372	WVTFISLLYLFSSGYSRGVFRDAHKSE VAHRFKDLGQENFKALVLAFAQYLQGG SFEDHVKLMNEVTEFAETCVADESSDDC DKSLHTLFGDTLCTVATLRETYGEMADC CAQQEPERNEC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4416	18317	A	4445	1	283	FRKNAEDILTMEGLRATMKHELEAAQKK HSLWELLRIENICKRIWILSFVRSAGVC WRSTPDPVCLGITSGGCRTAQIPACSF WKLHSIGAPA
4417	18318	A	4446	173	2	KKKRCVLYPEBGHGVPHALVCVCVCVCVC VCVCIQVNFNFCFISWINLSVQVSLLD Y
4418	18319	A	4447	104	221	SCHLHYSLGDKSETLSKNHHYHHHHHH HHHPAGYFKMK
4419	18320	A	4448	241	1	WVSWDKAPSWVRGLGSGSRGGVWGGGSP PHRVTDVSCSFLPDGRHVWEMEAKTRD LCKPVSAFAAGATVGPQGLGGRC
4420	18321	A	4449	229	349	WKRSHSFGLDVVAHACNPSTFGGGGGRI MRSGVQDQPGQY
4421	18322	A	4450	76	189	TESKPAATTRSSGGGGGGGKRGKKDD SHWWSRFQKV
4422	18323	A	4451	40	359	SGEPLFPFFFLARLIPGVCFVEMITRV RLLIIGLKIWEKKVPQVSTPTLVESRNL RKVGSKCKKHPEAKRMPCAEHYLSVVLN QLCVLHEKTPVSDRVTKCCTES
4423	18324	A	4452	2	371	KFQNALLVRYTKKVPQGSTPTIVKVSRL LGKVGIKCKKHSEAKGMPCAEDYLSVL NQVCVLHEKTPASDRVTKCCTESLVNRR PCFSALEDYETVVPKECNABTFTFHADI CTLYENERLFQ
4424	18325	A	4453	118	369	GRYILLLTKTKQTANNNIKTPOYLSNMS KKFRHSEFFFFYLKWSLALQRCNLGSLQ PTPPRFNQLSCLSLPNSWDYRCVPPNLV
4425	18326	A	4454	364	3	GHLSTQRLLLPFWLCPAPRGGAIRGRQ ASLSCGGLHPVRASRLCLPNQACTMAG APPPASLLPCSLISDCCASNQRDSVGVG PSEPCAGYNLLVCRFLSPSEKRSPSAGV MRFSRCRL
4426	18327	A	4455	1	379	AAFTECCQAADRAACLLPKLDELREDEGK ASSARQRLKCAQLQKFGERAFAKANAVAR LSQRFPKAEFAEVAKLVTDLTKVHTECC HGDLLCADDRSDLAICYCENQDSISSK LKECCEKPLEKSH
4427	18328	A	4456	1	362	LRPARSLVFPWFAPGGSGRLGLLLEAK CQGDGVSYEETTIPRPSAYHNLFGPLPI SRRDAEVVLTSLRLDSLALNQSTGLPTL TLPRGTTCLPPALLPYLEQFRRIVFWLG DDLRSWEA
4428	18329	A	4457	250	330	EWTHLWLNEGFASWIEYVCVDHCFPE
4429	18330	A	4459	96	319	YLTTPFSQAMENCKDARLTTSIGAYNFN HRLLEMILNKPGLTYKPCVNQVSALSLL SFLFFMPLFLSYCQVSIH
4430	18331	A	4460	50	339	NSQTLKLSNVQCLKTRALFFFPKGIYPQ IKTLPPCPTSGPDYPVRVNLPLPKGKGPC LKKISGNRKTLPKPLFDKTLKFLVPMKPV PKSPLNVVVKNI
4431	18332	A	4461	2	357	GYDGVRKWRTRDGDIFNKELLLLPIHLEV HWSLISVDVRRRTITYFDSQRTLNRRCP KHIAKYLQAEAVKDRDLDFHQGWKGYPK MYCKHLALSQPPSFTQQDMPKLRRQIYK ELCHCKF
4432	18333	A	4462	182	325	IRLSSWLCDCASCQVYEFVRKESSIAP APAEVDVTPPRKKRKHRL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4433	18334	A	4463	1	338	SRHSPGPTPQPDCLRTGQSVQVSDTS SCSQLSSSSGSSSSSVAPAGTWVLQAS QCSLTAKCRQPPIVFLPKLVYDMVESTD SSGLPKAASLLPSPSVMWASSFRPLLSK
4434	18335	A	4464	2	343	IIDFFLGAYLKDEVLKIMPVQKQTRAGQ RTRFKAFVAIGDYNHVGVLGVKCSKEVA TAIRGAILAKLSIVPVRGYYWGNKIGK PHTVPCKVTGRCGSLVRLIPAPRGGTGI VS
4435	18336	A	4465	1	371	INSTLKMSFVGENSEGVKMGSEDEWEKDEP QCCLLEIFFALASSLSASAEKGSPIILL GVSKGEFCLYCDKDKGQSHPSLQLKKEK LMKLAQKESARRPPIFYRAQVGSWNML ESAHPGWPIIC
4436	18337	A	4466	246	12	LCFTPLPSYIILFFETKSHSASPKECS GVITATSEVILGGGGCSELRSCYCTPT WVTKLDSITKKRRKRKRKDL
4437	18338	A	4467	2	355	WVTFISLLPLFSSAYSRGVFRDHTSE VAHRFKDLGEENFKALALIAFAQYLQOC PFEDHVKLANEVTEFAKTCVADESAENC DKSLHTLFGDKLCTVATLRETYGEMADC CAKQEP
4438	18339	A	4468	2	361	EDHVKLNVETFEFGKTCVADESAENC DK SLHTLFGDKLCSVATIRETYGEMADCCA KHEPERNECFQHKDDNPRLVRPEV DEMCTAFHDTDETFLKKYLYEARRHPY FYAPELLL
4439	18340	A	4469	1	373	SSQPSSPSESVSQTVSVSPSSLPSSPCL SLSVCLLVCVSLSMFSLPVCLSVPLCV SPRPHPSVSHAPHRASALVNCWGPAP TSAPVSFYKPKQSPALKTGQASPHPHPH FPTPSMQSQKK
4440	18341	A	4470	236	371	KVLGAVLKDKGGLFCFVFGDRVSLCHPG WSAVVQSQLTAAVTSQA
4441	18342	A	4471	345	201	AWMTAHLFMAWFTYFKSTAQKKKFVFK TLLLDINFDPLWDSKEGKL
4442	18343	A	4472	1	144	AGFHHVGEAGLGLLTSRDPASPCKRAG ITGLNHHTWPFVILTYTY
4443	18344	A	4473	3	333	KNHLEASIGEHFFPDHSPSCPHLLSS NYHSLSCFLGGFFSETGSAPSRLCSG VIAHCSLKLGLSTSPITSASWVAGITG MCWLYSPAVSPRPSPLTCTCTQLENI
4444	18345	A	4474	288	1	TSAVNRISIKSQADQEQKLRDYSHQ GIQILAWQKFEYKPGKVTMDPEDCILQL AKKKEEEEEEEEEEEEEEEEEEEEEED QEEEEEEGEEEE
4445	18346	A	4475	3	124	PRLECSGMIMAHCSLDLLDSSDPPTLAS QVAGTTKKISLH
4446	18347	A	4476	196	2	SCYEHPRIVYGFLFLRQDLAVTQAGVP WHDHGSLLQPLPELKRFGTSHLLSSQG YRRAQPRR
4447	18348	A	4477	3	162	LLERNKELEGSLOQMSTNEEQVQIEV RALHVLHAHTPRGPLGLCVPLCNLE
4448	18349	A	4478	167	2	ACGISPFSLSLSCFHVHRASLPAPHH DCGFPEASPAMLPVQPSQLNLFIKYFV
4449	18350	A	4479	195	26	WVSMLDIHDNGPHEVAVICFVCLFSQL ALLPRLECSGVISAHCNLQPGRQSQTPS
4450	18351	A	4480	175	1	NRSATKCDWGEKRTSQELNLFWFVCL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
						FEMESHVQAQAGVQWRNPGSLKPLPPRFKR
4451	18352	A	4481	122	357	YHAFLYQWYNLKRHKRFRCSLLIIFLG GERKLQSIQLWNISHYIQRVLEIPS GLGAVAHACNPSTLGGQGEWIT
4452	18353	A	4482	137	2	FYSYLKILEEMGPHYVFPQAGLELLGSRD PPDSAYQSTETIGMSHH
4453	18354	A	4483	347	208	GQAGLELLTSSLPASASQSAGITGAGHH TRPRIYFLKKYLAFLVLS
4454	18355	A	4484	411	268	RLNRRGGGCSEPRSCRCTPAWATEQNSI SKKNQKTKTLPLCCRLILL
4455	18356	A	4485	2	102	PCLLMQQLAGHGGMHLCSQLLRRLRCF LHSYP
4456	18357	A	4486	1	113	HSASTHAGHAGHTSLPKCWDYRSEPPR LAKFLNTRY
4457	18358	A	4487	163	353	QVAATLNNLAVLYGKRGKYKEAEPLCKR ALEIREKVQKKGAVVFFEIFVLCVCGFF FFFKRDP
4458	18359	A	4488	408	307	RGCSEPRSHDCSAAWLTERDSVSKKNKN KSPKKQ
4459	18360	A	4489	337	179	YSINFALILIFLFLGVLVWAAIINYHR LHGLNNKHLIMIMVGSPLSCG
4460	18361	A	4490	229	345	LENETLGRARWLTVPVIALWEAEASRSR GQETETILANM
4461	18362	A	4491	180	365	ENNLKTLVALDMSFYFILFLFYFILFYF ILFYFLRWSFALVAQAGVQWRYLGLSLQP LPPRFK
4462	18363	A	4492	269	385	GNLQNLKVFYKIQHFFMIKTLNKLVID RTYLNLIKAIY
4463	18364	A	4493	103	336	QLLVSLINLFLQAFKLQIDCGHTCMHFW RQNLCLLPPTLPTPRNLTLSPSLCSCG TIWAHRKRLPGSHHSPASATR
4464	18365	A	4494	305	379	YIKIENFCGLVVAHTCNPSTLGGRG
4465	18366	A	4495	47	224	ETATKTQRRWETALVPQHPRLPAEVTW VKTTGNSTIANFLILVYLSFLFLVYSC IQQ
4466	18367	A	4496	3	129	ITLNPGGRCSELRSCHCTPAWATERDS VSKKKKKFPPPPF
4467	18368	A	4497	396	112	LPELEFEAAVSHDCASELQLGHQSKTLF QKKINRIINNNSHIAISLLGIYPKEF KAGTORDICTPMITASLFTIVKQKQPK CLATNELVYRM
4468	18369	A	4498	1	152	LSLPGSQTWRRALIVPATWEAEVGGSP PRRSRLQVAMITPLHSSCGRRG
4469	18370	A	4499	92	2	KRPGVVTHACNPSTLGGRGGPITKSVVR DQ
4470	18371	A	4500	116	1	AGIAGMCLHAQLIFLYFLVETRFCHLGG AGLELLTLWS
4471	18372	A	4501	99	1	QGTVPVHRWWKCKLVQPLWRTVWSPLRKV KIDNS
4472	18373	A	4502	140	288	RQFHYVAQAGLELLGFSNLPALTSQSAG ITGASHHNQPTSRLKEKKIG
4473	18374	A	4503	330	181	FFFFFFFFFFFFFFFFXFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFF
4474	18375	A	4504	171	2	VETVSKESLRICLQDIRYFFETKPHS IAQAAVQWHYQGSQPLRLKQSSRLS
4475	18376	A	4505	345	74	SVERTCHSPKPLMLFLPLVFOARDIILN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						GSHPVSEKACEFGGFOAQIQFGPHVEH KHKPGFLEACHPYQTAEPASALTLDFFPA SRTVQK
4476	18377	A	4506	268	102	KNIRELWPGAVAHACNPSTPGGRGRWIT RSGDWLNLRTCBHVILQQKGKFRFLIS
4477	18378	A	4507	1	67	GLPKCWDYRREPPHARNCKYF
4478	18379	A	4508	339	180	ANFFVFVEEMGFHVAQTGLEVLGSSDL PILASKSAGITGISYSVRPQTNTTE
4479	18380	A	4509	174	3	NEPKVVIYIIPGDPFLFFLLFFETESH YVTQAGVQWHDLGLSLQPLPRLQRFSCV
4480	18381	A	4510	84	3	AHHIFTVGIDVDTRAYFTSATIIIAI
4481	18382	A	4511	127	2	LLIKIHCWPGVVAHACNPSTLGVGRGWI TRSGVQDQPEQYG
4482	18383	A	4512	109	345	EIFLIQHGECSCLFLGFSMCFVATGP PHVTWLILTLNLPTSSYSRAGITGVSH HARANNLFCFGSMPSHGITGLNF
4483	18384	A	4513	290	13	RDLRPTPQKGPKNHTAPNPLQRAQTHVK KGRGPTPPTPTPSKDPGPHPLRKPFW GRVWGEKKKKKNGPKDKKGGKKKKKE RKIQHSRF
4484	18385	A	4514	234	362	DGDVLSKFNFFSFKVVEGTPLIDGRR KYRLNGDFLFLRLKL
4485	18386	A	4515	190	330	CLALQSECFRRWSFALIAQAGVQRDLS SPQPLPPVFKRFSSLHPFE
4486	18387	A	4516	2	199	CVCVCVCVCVCVCIFFFLSKKNGPPPL CPPGGPKTLGPKESPPLAPKNRGNGLT PPPPPTFFF
4487	18388	A	4517	94	339	SAYLGLKFFLFFFFFFFVFPPPPF FPNKKLKPPIFFPPQKRPIFFPPPP PGGNFFFGKFFFPNPREKGPKNLG
4488	18389	A	4518	95	3	LYLPGAVAHACNPSTLGGRGQTITRSG VQ
4489	18390	A	4519	14	121	LIFGGRNRLCCPVWSQTPLKPSWL SLPKCSD
4490	18391	A	4520	207	2	ISREKLCTVRIPDMHVEDSILFYLY SLALPPRLCNGTIMAHCSLHLPSSNP PASASQVAGTTS
4491	18392	A	4521	169	1	ANLTQVGSYSLSLHTLIQVTFKNIRA VRPGTVAHACNPRTLGGPDGWITRSGDR
4492	18393	A	4522	2	82	GFILCVCVCVCVCVCVCVLYFIF
4493	18394	A	4523	300	3	LFLPPSLPSQIPGGQKPLFIYPPRVP KKFIPNFWAPPLISPRPFWVRLGPPT QGFNYPLGPPPPPPPSLGFKKSPNPF FIKKFSPPPKQK
4494	18395	A	4524	348	94	KPGEGGKGPQNPPGGLKPGNPLNPGGG GSPEPNFPWPMPRGAKKTRPQKKKK KGRKESRLNYGMEKRMKEKEKVFLSAL N
4495	18396	A	4525	313	161	RGHPKNLKSKEVNIRREAPGHPRNKKK TPNLKKKKKKKKKKKKQKQK
4496	18397	A	4526	118	3	FFFFLRGSFALVAQAVVQWRYLSSLOAL PPGFKRFSCP
4497	18398	A	4527	153	2	KDAINKMKKWPVVAHACNPSTLGGQGG WITRSGAQDQPSHYGETPSLPK
4498	18399	A	4528	258	2	GGQKRGLPGFIKKPPFRKIFLNLGEGP GKNSLSKFFFFFFETESHCLTQAEVQW LNLSSQONKPPRFKQFLCLNHPSSWDYR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predict ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						R
4499	18400	A	4529	296	39	SRIINIQTILLGFFETGCBSVAQAHLKL LGSNDPPASASESTEITEMQHCTRLSIQ IFVAPPYSNIKLSSTKKEPILIKLLLYNC K
4500	18401	A	4530	292	37	SRIINIQTILLGFCEGTCHSVAQAHLKL LGSNDPPASASESTEITEMQQCTRLSIL IFVAPPYSSNNKLSTKKESILIKLLLYNR K
4501	18402	A	4531	3	138	GLWNGSCLCVCVCVFIMGMACLVCICTC LYCCVPVNTCLCMDGR
4502	18403	A	4532	380	2	GGEPPKRRESAKAPGGRNPPQGGRREKTTP PKKKRPPQKGKKTKTTPGGGGGPPRRGGG KKKPPPKRKKECHRGGRGGGGPPVVTPK EGPPIIIIIIIIIIIIIISLPFFFFFFCFFI FILFPFNIVINGFY
4503	18404	A	4533	3	191	LKITHASIPVPSVKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKGGGFKKTLGGHN FSRGLE
4504	18405	A	4534	370	48	GPAPEVSSNGGKGGGCPKGLGKPLGSQF NGVKGYSPKSSPLFAQALPGQGPFKPQR GNGGTPTTFPPPKKKKKKCALGDGTPTS GC PRRSWNHPETOQC GGWGSRVPR
4505	18406	A	4535	147	1	KGPPLFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFSFYYIYLFLSLRL
4506	18407	A	4536	198	1	NPPYFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFLSFIFIFLYFNFI SSNIVFIGFY
4507	18408	A	4537	2	356	QNRTTGNSKTQSASP PPKECSASPATEQ SWMENDFDLRBEGFTSNYSSELREDIQ TKGKEVENFEKHLHECITTTINTTEKCLO ELTELKTTARELRDECRSLTSRRDQLAB RVSALE
4508	18409	A	4538	347	220	KCSGTIIAQCNIKLLGSSNPVVSASQSA GITGMSHHVQPKYC
4509	18410	A	4539	308	2	FSTISCPHDTAAASQSAGITGVSHCARP IFSFCIFFICIMCKIKYLLRTGDSVMYF HGLGCGFLCCYLESYIRKLSHMKKLSIL ITSREKCKCILQINIGDR
4510	18411	A	4540	2	194	IKQVVSTALS PRLECSGTTAHCSLKLP GSASASVVARVTGTCHAALIIFYSETGS HYVDVDA A
4511	18412	A	4541	101	2	MEENLGNTIQDIGRGKDFTSKTPKAMAT KAKID
4512	18413	A	4542	1	84	AEAEAEEAEAEAAAAAAAAAAAAEIKY
4513	18414	A	4543	3	183	KIQILFPVSSKTRLRPSAWHRPVFCFL RWSLALAAQAGVQWHHLSSLQP LLPGFK VDA A
4514	18415	A	4544	1	335	RKKKKKEKKKEKKKKKQGRKKRKRERKE EA AKKTKNKK
4515	18416	A	4545	104	2	QKKKKKKKKKKKKKKKKKIYDFFLQIN CMCSHK
4516	18417	A	4546	5	108	FKRLSCRSPSSWDYRREP RPANFCIL SRDGIS
4517	18418	A	4547	131	1	RPRRPQVLQDATSPIIEELITPDHAL IIFI LCFLVLYALF
4518	18419	A	4548	156	3	KGGQMGSCLSRSPSALLKFECRVISSYW AWNRAVPVPATRGAAGESLEP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4519	18420	A	4549	2	340	LNFGSAGCRELRSHHCTPAWTTTERGSVS KKKKKKKKKKKKKKKKKKTTFFGGGPLW ERFLLGNFWEKKGGGANFFPLENPNP QLKTWGKKAFFPRKGGGPLNPPQGFYQG A
4520	18421	A	4550	165	335	PHYLPRRSIIHRPFKSHSPEPGAVAHAC NPSTLGGRGGWITSQGFETSLINMEKS L
4521	18422	A	4551	123	3	GRVDRLSCLSLNWDYGHLPHLANFC IFSRDGVLSW
4522	18423	A	4552	3	131	HPEVDIPILPGLGIISDIGAYVSGISEP FGYVGMVSYDPVRL
4523	18424	A	4553	87	364	ILASQSVVFRYAASAASGGLLETESQPS AAGTASAAVPSLEAQTAAFRPTPPGLA PSSPPAPGPPAPTGVCGRHFLRSESSA SGPLRAL
4524	18425	A	4554	114	0	LTWAPHSLIETIRNQIIQALLITILLGL YFTLLQRSE
4525	18426	A	4555	91	3	TTTTYIAIATACVCVCACVCPCVCVC M
4526	18427	A	4556	239	364	CIKITFSRPGAVVHACNPSTLGQGGRI AMSRDRDHPQQGK
4527	18428	A	4557	250	1	STEHVKQLRNEFMKISVILIFLEILLYI KVHLKLCITLTDHLLLGKSLKILFRPG AVAHACNPSTLGGRGGRIPRSGDRDHS
4528	18429	A	4558	2	90	QDGLDLLTWGSACLSLPKCWDYRSEPSL F
4529	18430	A	4559	65	394	DFVSKKKKKKKIKNEKEKKFFGKKKPL KKKLADLILKPKKNFLKKREWKREK GGDPFWKNKPQVGKTGNLNLGQNGLGK GPSDLKKNTPETKLNLVQKKFOIFF
4530	18431	A	4560	93	2	GIISAHCNLCPLGSEDSPASASQVAGIT GQ
4531	18432	A	4561	125	4	GAYILYLNKKSISRPGMAHACNLSTL GGRGGRI TRSGD
4532	18433	A	4562	3	84	RSCHCTPAWATERETLSPKKKKKNF
4533	18434	A	4563	145	3	GFYHVVPGGVEQSPCLSLPKYWNHYCEP PPLASIGFFFFFFFETQSR
4534	18435	A	4564	125	388	IRKPQILYSPQSENMQHLHISVLMGVT GKRQKFMIDLDVTERCRFSLKCKTGIOE DLNKWEGIPCLWIIRLNTVKMAVFSKLI CRFS
4535	18436	A	4565	59	325	VARKNLVSLVIFYPLFDIEEVIEPLW VLISFDEGEKVELEFFFFFVKKSPF VTQAEFQWPNLSSLPQPPRLKQFFCLG LLIT
4536	18437	A	4566	326	3	PEKEFRRLVIKLIREAPEKGEAQCKEIQ KSIQEVKGEIFKEIDRIKKQLKHQETL DILLVMQNALESLSNRIEQVEERNSELE DKVFDLTQSNKDKAKRIRKYEQS
4537	18438	A	4567	333	209	EQAFDPYGTLSQGI FSPKFHEPFHKLMA RPAVALPFQVNLK
4538	18439	A	4568	125	2	HNQSMRSRSDCSDPILGHCNLCPLGSSD SPASASQVAGTTG
4539	18440	A	4569	212	2	PICLSGKKCYGQNVRVIKHMKHNRHL GVVVHACNPNSLVGGGGRFMRSGVLEQH EQHARTPSLLKTLK
4540	18441	A	4570	142	14	GRVDRSNPGRFLSTSNSSLYERPPEIRP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TSQAPSPVNHIIST
4541	18442	A	4571	2	419	ARDSFLHDSQTSFCFSDSIPTPSNMEET QKQSNLELLRISLLLLIESRLPEPVYLR MFANNLVHDTSDSDDYHLLKDLEBGIQT LMGRLEDGSRRTGQILKQTYSKCDTNSH NHDALLTNYGLLYCFRKMDKVFETFLR
4542	18443	A	4572	3	194	HEGRQLSQQLRRLRQKNCNLNTGGGGCSE PRSHHSFPWVTEHGFISQISLKLPLFIS HPEPFL
4543	18444	A	4573	2	286	CRDGLTYNDFLILPGYIDFTADHVDLTS ALTKRITLKTPLVYSPMDTVTEAVMAIA MALTGGIGFIHNCIPEFHANEVRKVNK YEQGFITDPVV
4544	18445	A	4574	44	325	RQWLQEEAYITKEQKYSFLHDSQTSLCF SDSIPTSSNMEETQKQSNLELLHISLLL IESRLPEPVRLRSTFTNNLVYDTSDD YHLLQDLEEG
4545	18446	A	4575	374	33	LRLARRSGASLCGSRSGGPPTCANICPR YAPLI PPCRTSLLEAQLVMVVGPDFRV RLVTSSERRFRYQPPPGFNRFPCLSLP SNWDYRHAPRLANFNSLFFFFFLVETG Y
4546	18447	A	4576	400	225	PIFFVVFVFLFVLFLVETRLCHVVQAGLE LLGSSNLPISASQSAKITGMSHPAPWRA EF
4547	18448	A	4577	2	372	ARETIFCFSNSIPAPWNMDTROKSNLQ LLRISLLILLYRTRLTLPCITQLHILQT YKVNARCSHFHSSSTCGPLYSCITLYVSL TGLDMKLCHSTLLKQNSALMSLLKIQVN LNQVSPVFNAH
4548	18449	A	4578	349	174	GCGEPRSHHCTPAWATRAKRLKRLKL QLKNVVKESKHQPLQNFSLTSTINTQ EN
4549	18450	A	4579	3	124	HELNPPEGEGCSEPRSCHCTLAWVTRAR LRLKKKKKKKK
4550	18451	A	4580	181	1	MSSYYFSPCSRLLMATVYNLHLPSSNS PASASQVAGNAGARHYAWLIFVLLVETG LCSC
4551	18452	A	4581	227	3	HRKRNRVSRRTALLFSLGDGVSPCLKII IIIKVLFWLGEVAHACSPPLGSRGGRI TRSGVRDQPGQHGETPSC
4552	18453	A	4582	257	2	RVRQLGAFSLSPGSGSFSKILGALKING PPRAGPVGSPRYSRPLGGPGRQIPRSGD PGPPGLPRGNPVPLKKNPKRSLLLIPAR A
4553	18454	A	4583	3	94	HEIAMAFLILTERKILGYIQLRKGPVNV GP
4554	18455	A	4584	345	50	IYIYICIFLNRNRVSLHCPGWSKTPGLK QSSHLGLPKCDYSHEPLCPAKTSHFKA QDRIPKNDPCTPSPAQMSTNLIGWASS YLQSYSPAPYNNKN
4555	18456	A	4585	338	19	FQLSRRFRPKNGGNPGSGACSEPRLGFC PSAWVTKRDSVSKKKKEYHTLSGLSTTG IYFSQFWMLGVQGASRFGVWGGAVSWSI DGAVLLRPHMAEGARQLSGLGF
4556	18457	A	4586	2	224	ARGVGRAGLELQTSQDPPASASRGAGIT GVSHRVQLLGDRAKFSLKKKRGIIILPG EFYSPLKKRFTLNTPDNP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4557	18458	A	4587	344	168	PPGTVVHTYNPSTLGGQAGRIGSLGVQD KPGQHRQGLSLGVEDKPGQHSFSPVQS NP
4558	18459	A	4588	212	328	GLAVAQAGLELLSSSNPPASASQSAGIT GVSHHTQPYF
4559	18460	A	4589	110	323	LSNQKNQLYNPNLLIYCVVRKLKSSYDK QAEVQGSKLGLSLQALPHGFTPLSGLNLP SSWEYTRPPRPPTNF
4560	18461	A	4590	2	127	ARGCSEPRSRHCTPAWATEQVSKKKKKG REKTFGQFFFVVI
4561	18462	A	4591	211	2	ARGSLEAGSSTPAWATINQSTNKKTDKT ALYWKMPSRITYKARQKSMGFKSSKDR LTLFLGAKVSLCV
4562	18463	A	4592	3	120	HEKTKTNPNFKKWKADMNRLSKEDNDN KINGWPGAVF
4563	18464	A	4593	388	227	GHVGQDGLELLTSDAPPASLASQSAGITG VSHRAQPKWLLFQHRSPCLFEAAGK
4564	18465	A	4594	1	348	PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP PLPPPPPPPPSSSPSSSPNPPATTSC
4565	18466	A	4595	2	138	ARAARGFRHVQAGLELLTSGDPPASAS RSAGITGVSHHTQPTNF
4566	18467	A	4596	315	2	ALKPNYSSTSMNIKARLPQYNINNLNLA PLYSSSTNQINIIIVILINKENHHTLFP CLVSNRLKQSSHLGLPKCWDYRRELLC LACDKFFISYSAPATQLLSC
4567	18468	A	4597	1	146	GTSVDQGSLELLTSGDPPASASQSAEIT GVSHRTQPPPLTI IQLYLYC
4568	18469	A	4598	293	3	GGTPWPRKLGQRKFPHRPPGSGGNPDF SILLFFFLRQSFALVAQAGVQWCDLGLSL QPPPPVNPFLLRKQGFSTSCFPILPAS GSFFGREASASC
4569	18470	A	4599	174	2	RSVAPFLKSARPTYRKEPTPTDTSQPQ PPPRFKRFSCLTRLSSWDYRHAPHPAS C
4570	18471	A	4600	59	252	LAPFGHELGTSESASHQTDNRHRLGYQK RLDASGLERASYPLAAEFKVGGRGCSSQ PLTLGCGYP
4571	18472	A	4601	233	366	IHYLPDAVAHACNPSTLRGQGGRITRSR DRDYPGQHGETPFLK
4572	18473	A	4602	182	325	LEVFCFLRQCKXSAQAGVQWHDHCSLY PQPPSLKQSSRLGLPSSWDY
4573	18474	A	4603	202	2	GGSSSGLLRPCAVLGLKQSSYLSLVRW DHNSWLKRSTHGLPKGWDYRREPPHLA CILKFSINLV
4574	18475	A	4604	317	2	FRLGPQVFFSPPGAGFFFCGPVWVGPGPF SRSLQLLTFGAKFFFCLSLPSFSGAPLR GPPSGFMAHCFFLVLLFFFFFRDVS LCCPGWSAVALHRRDPTTARA
4575	18476	A	4605	233	71	FFVLLVEIEDQLNEKKQEQEKIRKKRMK RNKQSLQKINDYVERPNLAGHSGSRL
4576	18477	A	4606	114	1	HPRPARVSSCCPNWSAMVWSRLAATSAS RVQAILOSRA
4577	18478	A	4607	348	3	LKFQNRGTVHGHARCPFFGGGLGRGIPF TPEVEVLVNLGPAPALFPWPPSQTLFSQ NQKNQKKKQERKKERKEERKKKKER KKKEKERKEGRKKKGQEKKIKITAKSI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
						LG
4578	18479	A	4608	174	3	TVVMVVQQCVFVCLLKQGLALSPRLECT GIIIAHCNLKLLGPSDPPTSVEKTKLV
4579	18480	A	4609	171	334	DPHSSLNIRFSRSVAQAGVQWNCNLNSLQ PPPPGFQRFLCPSLSSWDYRCAPP
4580	18481	A	4610	2	164	ARGSRGHIWSAFCHVGQAGLELLTSRPA LASQSAGITGISHRAQPPPLNTLYSMS
4581	18482	A	4611	2	164	AREPRGHIWSSFCFVGQAGLELLTSRPA LASQSAGITGISHRAQPPPLSTLDSMS
4582	18483	A	4612	180	334	CCLMGSSYLLPRKPNLRLTAGFLQQRKS LIRPGMVVHACNPSTLGGQGGWI
4583	18484	A	4613	189	1	SGFSRVVENGKCKGQKGGQSLVLLPIR VFFFFFFFEMKSHSFAQARVQWGNLGSLO PLPLGFK
4584	18485	A	4614	216	358	KSTPRLGTVAHTCNPSTLGGQGGKRITRS GDRDHSGLHKGTPLRSKNI
4585	18486	A	4615	179	393	EKQEEEGSWGAKTEDGVALMLSEAIGS CWIKAFLLTAETFTFHADICTLSEKERQ IKKQTALVELVKHP
4586	18487	A	4616	2	126	ARVQRYLFLFFTLDGPLDPSPMIRGSVP NQMPRITPQSGK
4587	18488	A	4617	338	181	RVGEAGLELLALSLPASDSQSAGITDI SHHTRPGSPFLEHLYPRYRISGK
4588	18489	A	4618	3	197	HEKRPEVQNSTVEFTASSDYMLRPLPL PFCFFLFFFKIKMGVSPCCPGSCQTPSL KQSSCLNV
4589	18490	A	4619	1	339	GTRTFGSGNGPTKPDLLQELRVATERGL VIVNCTHCLQGAVTTDYAGMAMAGAGV ISGFDMTSEALAKLSYVLGQPGLSLDV RKELLTKDLRGEMTPPSVEERRPSLQGN T
4590	18491	A	4620	3	306	LEPGDGGCSELKSCHCTPAVWTERDSIS KKKKKKKKGGPLKGTGPGPKFNGGWQRK IFSQKGGQKKPNLGLGRNLNFGGERNW NKFLT KIKVLRKKNF
4591	18492	A	4621	397	29	NTKEKILSARKNNQVFPPTQKKNFFPK KRKNFREGIPPFPKKSPQKNHPPQ KKKPPKEKCKTIARPPKKRAPPAGFKKK PPPPFFLSSLCISYSFIYFFSLINLFFF FFFFHDSVTY
4592	18493	A	4622	2	235	VSLCHPGGTISTHYNFCLPGSRDPPTSA SAYALLIFVFFVETGFPLVAQAGPKLQG TNSIPASASQSAGITGMNHCT
4593	18494	A	4623	209	324	ILRVLWSGTVAHACNPSTLGARGRQIMR SGVRDQPGQY
4594	18495	A	4624	52	287	NPFSLFFSFLSFFLFFFLFKGPRRGA RAQKGKPHPKKKKKKKRGGKKNKTQKP FSLKGPGRGPPRGKQTTPKGP
4595	18496	A	4625	102	1	THSFPVSISLSLSTHTHTHTHTHTIY RVREIR
4596	18497	A	4626	125	1	DRHVPQHTANFPVVLIEMGFLHVQAGL KLLTSGNPLVPLV
4597	18498	A	4627	3	167	ERLRQONCTNPRSEGCSEPGSPHCTPAA WATEQDSVSKKEKEKKEKKEKKIVV
4598	18499	A	4628	135	3	AATLSRGTTITAQGNLCLEPVSSNSPASA SRVAGITGARHDTWL
4599	18500	A	4629	320	210	WFLGIIFRRVENAESVNIDLTIDYQSFT

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						DTGKTPSS
4600	18501	A	4630	98	326	SSPTLAFQFYFFSCATKEAVKLSFPKSL LLGTGSRSSVAQPGQWHNHSGLQPPAQ LRLSSCLTLVSGWDHRCAPP
4601	18502	A	4631	275	2	RVKLLLFYMRQSCSVIQVSSSTVNGSL QPQPPGPRQSSHVLSLSDHDKRMPPCL ANFFLFFWRAKGLAILPVHSLNVTESPL LISIKSN
4602	18503	A	4632	180	1	KGLTLYFYFFIFKMRRLGLAMLADWSQTP ELNQFSCGLPKCWDHFRHEDPHVPKBFK PFHR
4603	18504	A	4633	234	5	KPLRDKPLRSFSLNLPKKNLNFPPFPQ KIWFFFFFETESHCVTQAGVQWLDLS SLQPPSPGLRQFLCLSLSS
4604	18505	A	4634	171	2	GRVDILTPOHFFETLFSFFSFWQGLSV TRLECSGVIMAYCSLDLLSGSNPPTSAS
4605	18506	A	4635	324	211	LRNIIFMPVTMNPNGMYTGGCMCVCCVC VCVCLCVCCVC
4606	18507	A	4636	95	1	MRQSLNLSRLECSGTIPAHCNLCPLGS SNS
4607	18508	A	4637	234	1	KKGHDTLTEKAMPVTLSSRMLSLNVCKC IYKWNKSNPNYSSLTHIINNIKPSFTRE NTLMFIHLSPILLSLNPDIT
4608	18509	A	4638	2	243	WGKVNVDVGEALGRLLVVPWTHMYF EFFGAFYISFCLFFLIFFHLLFFVSSIHI VSSPYLLFYNFPIIFFTLFCFFL
4609	18510	A	4639	118	2	GRVDLQCSGATSAHCKLHLQSRHSPAS ASQVGAHATT
4610	18511	A	4640	50	168	NKINKMHLITFLKKKKKKKKKKKKKKK KKKKKKKKKK
4611	18512	A	4641	315	87	GIFLRDRNLALLRLECSGTIIAQC�LE LLSPKDSPASPSPVARTTGVQPRPDTLT LFELIYIRYKGMIFSQDC
4612	18513	A	4642	383	2	KFKKKKFKAGGKAPARLSPLWGPKGGGP PRAGVLSPPGPPGETPFFLKNPKFPGHG GGPRKSPFFGGLKGENSLTREKGGPINP NLAPPAPFPKGQNPFPKPKKKKKKNRS SPAWNWDWIGTNAGK
4613	18514	A	4643	3	205	LKRFFCFSLGGQGCSEPRSCQCI PAWET QRDSISKKKKKKTRPGGLTLEPPFFGG VKPKGPLGAGI
4614	18515	A	4644	149	1	FFPIKADLVFFFFFLRRNLADSQGAQW HDLGSLQAPPPGFMPPLSCLSL
4615	18516	A	4645	474	344	AIHEHYLPSSASGDCDBDLQAACTILV NALMDPHQRLAHTV
4616	18517	A	4646	165	357	LCNALSHLLPQCTPTPLISILCIIDTIS LLIQPI THAVRLSANITACHLLMHLILL STLSICTL
4617	18518	A	4647	2	339	ARGENDLSPGGGGCSELRLHCTPTWAT RVNCVSQKKKNQPKPNQTKPNQTRK GSPGFPLNLKVISPEKSLNPNILKTAP KVTFRNWLTPEIPFWKMEKGSFDPRI
4618	18519	A	4648	313	187	LTSGDPPASASQSAGITGVSHALPPLV QFPHSLTPTPLFC
4619	18520	A	4649	236	324	GQVMWPGMMAHACNPSTLGGRSRWIVRS R
4620	18521	A	4650	225	313	GQVMWPGMMAHACNPSTLGGRSRWIVRS R

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4621	18522	A	4651	240	76	FCVHARTHHTPSFQASGSSEHMTYTH PSGSPETHHTYHTTFLASRSAEPQLP
4622	18523	A	4652	273	379	KQLAAQCVRPLSPSQAIASPVCTCYMPR WPEVTEE
4623	18524	A	4653	369	189	GTVKQAGACRNLGSLQTPPPGFKQPS CKSLYSIMICYSKDCMTSTLIGIRANNR LHL
4624	18525	A	4654	168	346	DRICRASSYTIHMLYFVFLIFLFYWI YFLFFVLPHFTIFIILFYFIIILLLLY FYN
4625	18526	A	4655	56	354	WKRTFPFFFFLETGSGFASRPCTLLLP YSLGNPRVLIRVFLFLSSRCYYYLFL LGLSLFLFFYIMYLLFIRLFFVLSGL LLLLSSYYRFIIFFF
4626	18527	A	4656	50	186	SACLGLPKCWDYRHEALRPAMYLLTGSS YVAQAGLNLGSDAPPE
4627	18528	A	4657	131	366	DHFVASSSVKEGLFFVFVFFFFIFIF FFILYICFFYFKFIFIILLYIIIFIFI FYFFLYYLLIFLIFIFIFIG
4628	18529	A	4658	290	155	LEYIVEKGFHQDDKASPELLTSRYLSDS ASQSAGITGHRAWPTKG
4629	18530	A	4659	163	372	LRLPALFAFLFMFFFYFLFLLYVFCVF FLFFFTFFLYFFLYFLYFLCSLVFL FFICFIFFWFFVFF
4630	18531	A	4660	227	378	FIFSNCTSTALVHPLFYLSRLVLSKNR NKFIGRARWLTPVPFALWEAEA
4631	18532	A	4661	3	141	RSRHTPAWQQSEILSQERKKERKKKK ERKKERKKERKKERKKKK
4632	18533	A	4662	346	3	TFKFLGGVCPFFSPPKKRVFSKNSPGGF FLPFLGENFFFAFPVNFPGPGGFFKGG PPPPPPPPPPPPPPPPPPPPPPPSQ DSFDNLGIFVIPYKIQDDFSSSMNATS ILIKIAL
4633	18534	A	4663	302	3	GDINRRSHSPFVWSKFPAPCFMSSLDVF YKSSDFFYFFFEFTEFHSCCPGGISAYCN LCLEPGSSNPASASQVAGITGVRHHTQL IPASVVETFKITYKN
4634	18535	A	4664	2	76	RLAFTPOLGGHWPTGITPLNPLEV
4635	18536	A	4665	1	210	SPTRSPKPTPPYYQTTLAKPFTKKKKK KKKKKKKKKKKKRGGAPLKKSPGGPKI NRGKKKKFFFLKGG
4636	18537	A	4666	2	356	GSRPGGGKRTARRWTRPWRLRGACLTG MAFAFHQVIYKIKSFLRKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKPRG GGFLKKLWGGKFFMGGGKIFFFFIRGGK KKMWGG
4637	18538	A	4667	1	323	RTRGIFCYDVCVESGCADIQLLLCLKK KKKKKKKKKKKKKKRGAFLKKNPGGAQN NPGKKKKNFSPKRGPKKTPPGNFEEKPF FGGPGNGAPPPQKNKTPKEKKKF
4638	18539	A	4668	167	446	ELNKGCLCKPKKKKKGGGRSQKPTRPK KKKKKKKKKKKKKKKKKKKKKKKKKK KS
4639	18540	A	4669	321	52	GVFSFSPKFFFSFKGLNFWGGFAPIF SPPKRRFSSKNPQGGFKYPLRGKILIW GPENWGPFGGFLKGAPLFFFFFFFFFF FFFFWG
4640	18541	A	4670	82	359	NAYGIILIKGNETKTKVKWSSCQLANT

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4656	18557	A	4687	151	2	IFFFFFDRVQWHKLGSLQPLPPRFQQFS CLSLPSSWEYRHAPPRVRPRV
4657	18558	A	4688	342	183	FFLFLRWSFALVPQAGVQWCDLGSLLQPL SPGFKRFSWAEVGLHPRSRQLQ
4658	18559	A	4689	126	404	NCQVWPLRPTGHSVFSVHPQWFLFYCF ALYFIPLFMGSYSVTQAGVQWHSIGSLQ PPQWSYVLTFLWHPSSWGYFVQNHLP FDGKVPWV
4659	18560	A	4690	2	128	GESLFYIVSPRDVVVAKERDQDDHIDWL LEKKKYEVFLILL
4660	18561	A	4691	407	2	YFFFLPRMKIFFPPHQKGFPPGCGPTI SPPNEVFFSPKEGGFFSPPKRVFFH NPPEGFFPPPPFMSPPPPPPPPPSLF FFFFFFFFFFFFFFFFFFFFFFFFSFR IILLNQKNLSACVELRSCCTFM
4661	18562	A	4692	1	176	SRRLNPGGRGCSEPRSHCTSTWSTERD SVSKKKKKRFPALKFLGEANVKPTIGGQ KN
4662	18563	A	4693	1	403	SKAEIGRRLLRQTVSQVNAKEKFLK EVKSATPMNTRMIRKRNLIADMEKVLV VWIEDQTSRNIPLSQSLIQNKALTLFNS MKAERGVEAAEEKFEASRGWFMRFKERS HFHNIKAQGEAASADVEAASY
4663	18564	A	4694	343	425	HCFLSLQLNSFEQLCINYNTEKLQQLF
4664	18565	A	4695	395	2	KNKGLFFFFFLRWSFTLVQASNVTTAV CNVTILAHCNLHLPSSNSPASASRVAG ITGSCHQG
4665	18566	A	4696	429	0	VTWKCYITKKKKKKKKKKKKKKKKKK KKARG
4666	18567	A	4697	371	217	IPVFKQSSCLSFPRSDYRHMPPCVTQK KKIEYQHISLYKKPSKRCALFLI
4667	18568	A	4698	415	59	LQQQCECFISELTKKKKKKKKKKKKKK KRGGGLKKKKKKGFAPYPPH
4668	18569	A	4699	431	0	LKKIFPPGGRVLSPPPPPPPPPPPPPP P
4669	18570	A	4700	371	245	TLGDPPASASQSAGITGVSHHAQPLFGI FIYKFTYICRKTRT
4670	18571	A	4701	410	0	KQCWFTQKKKKKKKKKKKKKKKKKK DRG
4671	18572	A	4702	340	402	PFAGGGYRLGAAPPEESAYVA
4672	18573	A	4703	188	2	TSLPKCWEYRHHPPCPAHTLLIFLFFIF VDMGSCVVAQVALELLGSSDPPTSASQS AGIIGM
4673	18574	A	4704	423	34	LKKKKKKKKKKKKKKKKKKKKKKQDL KKMVGGGNYKNVGAQILGYKKLCPSFF YRVF
4674	18575	A	4705	2	297	PRVREKEMASMKEEFTLKEALEKSE ARRKELEKMVSLLEKNDLQLQVQAEQ DNLADAEERCQLIKNKIQLEAKVKEMN ERLEDEEMNRSPL
4675	18576	A	4706	2	179	QENGMNPGGRACCEPRLRYCTSSWATER DSVSKKNEKKRSASLRFDILFGALTGR KAS
4676	18577	A	4707	432	578	PRIVCFQELRKPSYAEICQRTSKBPPSS PLQPSSSSSSS
4677	18578	A	4708	419	35	GSFFFFFLKDQPKKGRKKEGCPPPPPK IITYPPATKWGGGGGKKPPPPKRGPPK KNRGRKKKPPKKKKKFPPPPKRAPQK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKKPPPIFFYLYFFKNFIFFFFFYY FFPFFFFKFIYNLKKF
4678	18579	A	4709	147	31	NFFFFFFFFFXFXFFFXKXKFFLFF *FFFLKLKIFF
4679	18580	A	4710	3	229	HASAHASDQPERLNAGTYFLFYTLVGS LLIALIYTHNTLGLNILLTLTAQEL SKKKKGGGAVLKNPWGAQS
4680	18581	A	4711	1	158	PTRPPTRPSCSELRSHTCTPANTERL CLKKKKKKFFNLSVGFKILGILKG
4681	18582	A	4712	163	404	KKKKKKKKKKKKKKKKKKKKKKKKP KKKKKKKKKKKKKKKKKKHPSRGGAKK KKGGGAQNRRAGGKRPSRGGGEKQ
4682	18583	A	4713	3	378	FEFPVYIKSRQKRKESNPKLVSSQPHG LHDFKKKKKKKKKKKKKKKKGGGGLK KKPGGAKNKGGEKKNFPLKGGGKKNPW GFFKKKTFPGGKIGAKPKKKKSLKK KKFLRGKGKKKT
4683	18584	A	4714	2	208	VSNPAVSVPPLPFSVYKSSPMASMTFSK KKKKKTKKKKKKKKKKKKKKKKKGPQ KKKPWGAQNKPG
4684	18585	A	4715	290	56	SAPPPIFFLFFFLFLFIFIFIFFFKQI LEKKGGPPFFLFFFIFFFFFYRMGC DRWWFILIQTFFHRKQKPVLV
4685	18586	A	4716	50	424	GGFKIKFLFTQFLFLFSPSMFLISKSP AYLWQSSPRQVPMVVGKTNFLVSIKCK KEGIYFFCIPFVPGFPHPKILCSLLPF LAFLRRSLALLPRLECSGAILTHCNPC PGSSNSHAWA
4686	18587	A	4717	161	2	GRPGADFRVRPQLLQFLFYLFTEME SCSVTQAGVQWCNLGSLQPLPPGLQ
4687	18588	A	4718	2	115	VYTTAMAIIEYPEAWGSGVEVLVSVLVG LAMEVGSTRF
4688	18589	A	4719	1	416	GNQGGGYGGGYDNYGGGNYGSGNPSSSS SSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSS
4689	18590	A	4720	1	454	QPDSGISSIRSFKITLPAAQDVYRDE IGNVSTSHLLILDDSVEMEIRPFPLFG GKTHYIVGYNLPSYEYLYNLGDQYALK MRFVDHVFDEQVIDSLTVKILPEGAKN IEIDSPYBISRAPDELHYTYLDTFGRPV IVAYKKNLVEQ
4690	18591	A	4721	3	173	DAWAGFHYVQAGLELLTSSHLPASASQ SAGITDVSHRTQLDVPFSLPLPHQC
4691	18592	A	4722	2	201	LKPGGGGCSEPRSCHCSTPAWRQSETPS QKKKKGKWGLERIGWGGSTTNAGAKNR GEKFGKGGF
4692	18593	A	4723	2	183	LKPGGGGCSEPRSCHCSTPAWRQSETPS QKKKKGKWGLEIICWGGSTPNKRATNSP VERF
4693	18594	A	4724	1	395	QDATSPIIEELITFDHALIIIFLICFL DLHALSLTLPSALT
4694	18595	A	4725	388	3	SFSPLEENLGNTIQDIGRKDFTSKTPK AMATKAKID
4695	18596	A	4726	223	44	WLFFFXPLFFFWGGIIFLLKLYIF FFFSKIFFFFFFFFFFFFFFFFFFFFF FFFF
4696	18597	A	4727	41	374	KKKKKGKKKKGGGGGKNPKKKGKMEK PPGKNRGEKGKKKNFLKKGGLFKGK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KPPKKKNGGRKPKWKKKNFKKKKKKAPFF LGPKIFKKKKKRGKGLKKLGFFSQSVGP
4697	18598	A	4728	323	69	FFFLRQSLGSASQAGAQHNLGSLQPLP AGFQLFLQPPPPGSKQFGRNLNLGNKDL WGLEVLRAHPQAPPLAFIL
4698	18599	A	4729	3	197	CLALLHLRSRQRYALPLGLPGCPHIHT HSHTHAHDHHTHTSPHAHRHATHTHMH TLPYTHCI
4699	18600	A	4730	309	443	VLTLSPRLCSCSMNIAHYSKLLGSSDH PTSASQSGGIIGMSYHA
4700	18601	A	4731	3	172	DAWAFFNGPGVSLCCTGWSRTPLKRSF CLSPLKPCWDYRPEPLSPAPKTLFSYVLL
4701	18602	A	4732	98	232	QTVFLLIWLLALCSPGVLTQVKKFLEPR CIFSLGIVTFICLYRN
4702	18603	A	4733	238	1	LGPPPPSLGPPPFLLVIFRGFSFPKPTL FFSPPFFGPPPPPPPPPPPIRRSFAL VTQAGVQWRDLGSLQPLPPGFKR
4703	18604	A	4734	121	424	LIQGHVVVIFYFSQLRKVRGRQACDSTLL GHLPKVVRMFPFLSFTVAGLEPTSHYR MFVDVVLVDQHHWRYQTGKWVQCGKAEG TMPGAR
4704	18605	A	4735	319	8	NPPQKKKKKIFPPPKKKTTPKKIKKNPP PFTIFFFFFFFFFFFFFFFFFFFFFFF FFYFQHVWFCFEI IHVIFFLIEVLFLAF HVGDSIADAWSTKNSNRK
4705	18606	A	4736	297	442	TQGGFFGGGPRKIGFFFRGLKNGGGGNPK LRFKPGQLVGRGKTKKNQG
4706	18607	A	4737	430	0	CVLGSKDKKKKKKKKKKKKKKKKKKKK KAKKDS
4707	18608	A	4738	137	1	INYYFFLKQGFPLPRLECSGAI AHCS LEFFGSSDPRPSASQVA
4708	18609	A	4739	188	3	ISPALKNPRREVGPFIFFPPKKVPPQNP PGGFFTPPHKEKNFSLPPVNLGPPKDP LKRFP
4709	18610	A	4740	188	2	TSLPKCWDYRHEPPCPAHTLLIFLFFIF VDMGSCHVAQVALELLGSSDPTASQS AGIIGM
4710	18611	A	4741	410	1	RRPGGGFCPPPPPKIFFSPPPPPPFVGV LPQTPPPPKKFFFLNPPPGFFPPPKKK KIFFSPPPPPPPIFFPPPPPPPPPPF FFFFFFFFFFFFFFFFFFFFFFFFFFFFF GKDRVSLCCSDWSRTPGFKPSLL
4711	18612	A	4742	225	444	ENLKLKSFPCSHFWLRFNLTIGALSR SFDEAALLFFQNDTYWPGTVAHACNPST LGGRGGRTKSRDRNHS
4712	18613	A	4743	2	452	VSNPAVSVPHLPFSVYKSSPMASMTFSK KKKKKTKKKKKKKKKKKKKKKSGGPQ KKKNR
4713	18614	A	4744	3	144	LAAVLLKGGYGIIRLTILNPLTKHIA YPILLLSLNPDIITGFSS
4714	18615	A	4745	206	2	IQNPQTERVNSTSKLKISSKDTINRAKK QPMDEWVICKKHIFGKELISRMYKELQL NNKKQIVPPTRP
4715	18616	A	4746	523	178	RHRRFFMDIEREQVKEQORQEKQKDI KIKDKREQECYAAEQIRLMNFHEDPYS GKLSBILAQLQEQEIKGTREKQOREK YLRVVALRAQIQEKMQLYNITLPLC
4716	18617	A	4747	3	518	ENRLNLEGGGCGEPRSRHCTPTWAT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4717	18618	A	4748	491	145	LCHVGQAGLELLTSSDLPTLASRSAGIA GVSHRTRPHSHFYFYFLYSSSFFFFFLL AQRGNRAPRGKKTTPFGLATLNKSNNGV FWFLFLGFGFLKREPTFALGLKDRGGNL V
4718	18619	A	4749	6	362	NKLPNGTEFLSSLVNPTFFFSFLFPFPPF FFFFFWGKGGPPRGGGAKFYPLEFPFPPG VPPPPKGGKGGPPPTNLFLLFKKEGGS PFGPGGVKTPGPKGFPFPPSPQRGGKKGQ WAQKPP
4719	18620	A	4750	380	3	SLLLAFALLCLPWLQEAGAVQTVPLSRL FDHAMLOAHRAHHLAIDTYQEFETYIP KDQKYSFVHDSQTSFCFSDSIPTPSNME EPQHKSNLELLRISLLLIBSWLEPVRFL RSMFANNLVYDPS
4720	18621	A	4751	1	345	LFYIFKKTWSLFLCFLWMMCVFIFFFFL LFVFFLCLGGILVSPFPPGGEKREKKRR RGGEKKKKKKNVVFKKKKKNPWGGGGGL KKQRARGGKCKKKKGGGGGGGKKKQSP LRG
4721	18622	A	4752	1	407	QEFETYIPKDQKYSFLHDSQTSFCFSD SIPTPSNMEETQOKSNLELLRISLLIE SWLEPVRFLRSMFANNLVYDTSDDDYH LLKDLEEGIQTLMGVRVAPGVNPGTPL ASRAGGEKYCCPLFSNKARDQEN
4722	18623	A	4753	357	1	PLFFFKRNLFPPFFFTKKKKBKAPVFFF FPPPSREWGGFFFRVGGVNTQFLHPPFF SQNTSVFFSTLFFPPFFPPFFPPFF FFFFFFFFFFFPPFFFLFYCFIYFSR DRGLTLL
4723	18624	A	4754	1	207	LGLAGVEEVEASRLNAGGRGCSKPRSHD WTPAWAMEQDSMSKTKNEYQRRQLIHL QSSTSGFLYVHEQ
4724	18625	A	4755	2	336	HEERERERERERERERERERERERES RAQFRANKNSQAPHPRVCETLWTEEGGS FYPLTEKDFACERAHFCVLGVSHPPGW GLCKMNPCECERATHSLHGDADISGLV
4725	18626	A	4756	230	446	VGPSSLSRYCTILISASSLTKEKCEKK RSFLFCFAFWLLGFLRQSLALSPLREYN GAISAHCNLHLPSSSD
4726	18627	A	4757	3	390	QTSFCFSDSGPTPFNMEETQOKSNLELL RISLLLLIESWLEPVRFLRSMFANNLVYD TSDSDDYHLLKDLEEGIQTLMGRLDGS RRTGQILKQTYSKPDTNSHNDALLKNY GLLYCFRKDMDKVETFL
4727	18628	A	4758	234	387	LAKIFLSFSSATGWENRPQSPATGRTP VFVSEIPPLPPPPFFFAFT
4728	18629	A	4759	396	0	IYTHTHTHTHTYIYMYVFMI
4729	18630	A	4760	176	384	MVILFNKDTQHIILFWGVLIFFFLKR NFVFVAQAGGQGRYFGSLKPPPPRLKPF SCLSLGTDWYRR
4730	18631	A	4761	419	208	IYPPPPWPPEPKGGSFLKKKKKKKPGPG VPPFIPPLGGQAGGFPSNKIQIPPAQ GKPLFFQKNQNYLA
4731	18632	A	4762	158	2	GNQLNPPPPSGSAFCFLPFLRRSLALVT QARVQWHDLGSLQSPSPGKRFSC
4732	18633	A	4763	489	398	AGFELLTSSDPPASASQSVGITGMSHCT QP

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4733	18634	A	4764	420	1	FFFFFLGEI FPPGGKGGVFPFPPLKKFP FSPRGLFFLGGGGPNFPFKRVFFKPP RAGFFPPPGVLKRGPGGFLTPPQKEKN FFFFPPGVLPKGGFFKGGPPPPFFFFF FFFLGKKKKKKALFTKKGGGGTVRKA
4734	18635	A	4765	167	3	IYFFFLKKIFFYKKRINKLKKKKKKKK KKKKKKKKKKKKRAARDLELAHAS
4735	18636	A	4766	424	222	FQNIHKKNFSPPLKLTGPAPLFKPPK KKKKYFFPPPEKLGPPREFLKGPPPPFF FFFFFFFFF
4736	18637	A	4767	254	423	VIKSWARRNKNKWDWFGAVALSCNPSTL GGPGQANPLRSGVDHPGQHGETLSLLK
4737	18638	A	4768	363	0	KTTSQARGPTSVIPAAQETEAGDSSNP SGYSYSSSSSSSP
4738	18639	A	4769	51	169	YYTHTPRTGFVKKKKKKKKKKKKKK KKKKKKRGGGF
4739	18640	A	4770	188	3	ISPKALNPREVGPFPFPKPKVPPQNP EGGFFTPPQKKNFTLPPVNLGPPRDP LKRPP
4740	18641	A	4771	1	131	KLDKENALDRAEQAEADKAAARGKQLE DELGSLQKKKKGGPF
4741	18642	A	4772	363	452	RLECSGMIIXHCSLNLPGSSDPTSASQ LA
4742	18643	A	4773	121	1	RPRRPVAQAGVQWHLNSSLQPLPPGFKQ FFHLSLLSSWDY
4743	18644	A	4774	31	226	MISSQLSIPTPTQEOGLKKKKKKKKKK KKKKKKKKKKKKKKKKGGGLLKKILG GAKFLGGEKKNFFFF
4744	18645	A	4775	161	1	KPPPPFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFLFFFLKKSRRP WGLKSAPAL
4745	18646	A	4776	394	67	SPPRGEGGVAPPPPKNFFPRAVFFLG GGGGPMPPQKRGFPKTPGGVFKPPPK GGKFFPPPPGEGGPPPEFFKGPDPFF FFFFFFFFFFFFFFFFCFFFFFFFFF
4746	18647	A	4777	2	409	GVCIFSGHKHNKAPLFPVLYSIQYINS LEKKKKKKKKKKKKKKKKKKKKKKKK KKT
4747	18648	A	4778	456	0	FFYKKKKKKKKKKKKKKKKKKSSS
4748	18649	A	4779	438	0	LLKIDKKKKKKKKKKKKKKKKRTSKR GG
4749	18650	A	4780	58	330	SPFYQLKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK GKKNCGGGGVLVGKPHKEKKRGGGKKKN FSG
4750	18651	A	4781	435	73	FFPPPPRGKFFFKPPGGKLFSPPELGV FFPPFLKIFFFPSTPFFFWGGFPFSP PPKKVFFPKFPFGFFFPPLKKKFFFS PPFFLPDPGFFFSPPPPPPPPPPPPFF FFFFFFFFFSP
4751	18652	A	4782	420	109	LFKFFFSPTEREGVFPFPQPPNFFFSN PLFEGGGGAQNFPPQKNFFPKNPPGFF FSPPKKKKKFFSPPGKILAPPGYFFKGP PPPPPPPPPPPPPPPPPPPPPPPPPP
4752	18653	A	4783	230	2	LGLVVGALYSPFLGGLGRKFLLPWRPR VPLTPISPPPSRLGGPPKKKSQAWWA PVVPTTREAEGGSLEPRRL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4753	18654	A	4784	271	440	VLYSKRDNNKSFKNNTYTGIGPGAVAHA CGPSTLGGRRGGQIMRSGVRDCKPYRHGET
4754	18655	A	4785	2	266	KKYGIIFCSFFLSLFLKDGGLAPLPR ECSVFAAHRGLGLLGWSDPPKSAFLVA GITGMHHHAWLIFKVQPSNLMGPWSYTW SAVD
4755	18656	A	4786	216	435	HRSGDSSLKKKKKKKKKKKKKKKKKK KKKKKIWEFWKGPFLWGGKKRKGSGG
4756	18657	A	4787	249	437	MNNEVVPLKTETSRPDVVAHACNPSTLG GRGGQITRLGVQDQPCQHGEPSPLENR KYLAWSV
4757	18658	A	4788	107	368	AHGSLDFLPGGPKKSHQWFPKPKDGKPP PFSKKPLKKKTPGKKGGHPTPGARSKK GGYPRGGDPGGPFFFKKPGQKKKTPFL RRD
4758	18659	A	4789	1	225	PTRFITNNIFPASPFQTITPLYLKLT LAVTFLGLLTLDLNLTKLKIKSPLC AKKKKKKKIKKKKKKNEG
4759	18660	A	4790	2	216	SGRNSRVDGRQEAACRDYQSSLEDLTFN SKPHINMLTILAEENLPFAKEIVSLIEA QTAKVFIHPAASYE
4760	18661	A	4791	389	30	EKKSPQPKKKKKFFPPPPQKKFFSPPNQ KTCGGGGPKKPPPKKGGSPQKNPKGVKK PPPKKKKKIFPPPPQKKGGPPKILKKPPP PPPPPPPPPPPPPPPPPPPPPPPPPP FSYKIFL
4761	18662	A	4792	164	3	LFPGFFNPGVKGEKGISPPPPFFETES HSVIOARGQWRRLGSLHPLPPGPKR
4762	18663	A	4793	550	413	AEMGFHHVQGAGLELLTSSDPPALASQS AGITGISHRAQPHRPIC
4763	18664	A	4794	456	352	RSQDGLYLLTSSFACLGLPKCWDYRRBP PCLAVFF
4764	18665	A	4795	242	3	KPFSGGGGAFQTAFITFGKKFVVSRLG LLKKKVFLKFLPQAFPPPPFFETESHVA QAGVQWRLGSMQPSPPGFKRLS
4765	18666	A	4796	218	346	GFSCFVFETVSLCRPGWAVVRSRLTAT SASRVQAIIILQPPE
4766	18667	A	4797	383	80	KFFFNQGGIGGFFPPPPPPPPPPPPPP FLGGFSPFFPPPKIFFSKIPPFFFFSP PLKKKIFFPPRLILAPPPFFKAPPPF PPPPPPPPPPPPPPRPI
4767	18668	A	4798	1	126	ILIKLSSTWEGIQAGKELEBQHGHCNM TLLFSFAQAVACAE
4768	18669	A	4799	81	356	ILFFFFFFPGGCTPKKSQVFFKPNQNP GKPTRMGKEKPPPPRGKKKKGGPPTL GKNKNPVPGWPGAFLPPLBKKKPPFGP PPLKKKK
4769	18670	A	4800	1	99	GCSEPRSRHCTLSWATRKLHLIKKKKK KKKGA
4770	18671	A	4801	238	5	NHONSQNYFKNLRIQOLIYSLSMNLPR SSFKLKSMTSISFSPLSFPIQSHSV AQDRIKWHDLGSLQPQPPGLK
4771	18672	A	4802	166	62	IFLFSFFLELRDRVLLCYVGWSVMVQST QTPGLK
4772	18673	A	4803	102	6	AASTTESPSVAHAGVQWCDLGSLLKPGSR RFQ
4773	18674	A	4804	17	374	FGSRAATLFFFFFFLGRGGFFLGRPGPK KKTGPGEGFTRFDPGNGKGPEKKTPPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WGGKGGPKKMNWAGAGKIKFLEIRGKSF PRGTTNFFGPPLFFSPPKIQGPGNFLD FSFKLN
4774	18675	A	4805	59	175	SFYFFLMMKKKKKKKKKKKKRGGAL LKKKTGGPN
4775	18676	A	4806	406	300	SSGVLYSRAPTYFCGQTLTFRQVDIKTS HLPQAE
4776	18677	A	4807	123	1	KSIAWLGTMAHSCNPSTLGGQDGTTRS GVRDQPGKHGETP
4777	18678	A	4808	319	406	LYKSYSSWPNVVAHTCNPNLGGQGGQI I
4778	18679	A	4809	236	351	GFWPAPGVHACNPSILGGQGGRVTPK GNLLGQHGEI
4779	18680	A	4810	173	2	EVLFLGFRSTLISLLQMNVLVLIKFA FVAQAGVQWNLSSLLPPPPFRFKFSCL R
4780	18681	A	4811	2	94	TRILKVWQKRKCSVKNGFLTISHGTVSI LF
4781	18682	A	4812	358	2	FFFFFSETESCSVAQAGVQRDLGSL
4782	18683	A	4813	362	3	YSEVCTIISLQQAHDLSVINFHLECVI QLPVLNRELPGAVAHSPGLSELCFSDSG SVPSHTRSFPKAAIRLTANHRRGCTESG WPFSLVFLPERCMWPGTVAHTCNPNSTLG AQGGQIT
4783	18684	A	4814	341	1	WNQKRAHITKSILSQKNKAGGIMLPDFK LYYKATVTKTAWYQNRDIDQWNRTPE SEIMPHIYNLIFDKPKDNKKWKGDSL NKKWCWENWLATCRKLELDPFLTPYTKIN S
4784	18685	A	4815	2	283	VYTGBEILQKKEITIRDQEAPLYLRNLS DHTVAISSSTLTDCHANGVPEPQITWFK NNHKIQEPELYTSTSPSSSSSSPLSSS SSSSSSSSS
4785	18686	A	4816	266	3	AASTLQAHRAHQLAIDTVQEFEEITYPK DQKYSFLHDSQSLRQPLHTHTGSGVTRT LAASLSSGRTAHTRTHMTQHTKRTAH TNA
4786	18687	A	4817	365	1	SFFFFFSETESRSIGRLEFSGTISAHCN LRLPDSSNSPASA
4787	18688	A	4818	87	372	ASYKDKYCMIPLRVIRKPPQTERKKWL SGLGGBGNKELLPNGCNMAVFLVLGGGF ETEPPSVTQAGEQWCDLSSLKPLPHRLB RVSCSLSPSGW
4788	18689	A	4819	5	175	FAPLTIPLSRLEFDNAMLRRRLVQLAYD TYQEFEEAYILKEQQDSFLQNPQTSCLF S
4789	18690	A	4820	235	351	FFKFFFXFFXFFXFFXFFXFFXFFXFF XFFXFFXFFX
4790	18691	A	4821	2	155	IFLLLTIESWLEPVRFLKSMFANNLVYDT SDSDDYHLLKDLEBGIQITLMGRL
4791	18692	A	4822	90	2	LFFFFFETESPSVTQAGVQWHDLSLQ P
4792	18693	A	4823	247	3	KVKGSPSHRRAMVAKGNLSLHERMKSPG ISNYMGNSKILFSYFKNCWPGTVAQAYN PSTLGRGGWITRSGVRDQPGQYSET
4793	18694	A	4824	93	407	QHPKKKKKWGGGRGPLKNKEKVPKHKT FFSRQKKKKKKKKKKKKKKKKKKGGG GLLKKFWGGPKFPGGKKKFFFPFGGKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						NPPGVFLKKNFVWGGEKKKKK
4794	18695	A	4826	2	129	TTAHCSLNLPGSSDPPTSRLVAGTTHV CHNAWVNFVFCRRG
4795	18696	A	4827	342	140	GGFFFFPPPPFFFKFLFLPPPPFPGPS CVGGVQKFTFPFPPQLSRLFFLFFFP PPETDNPPFFS
4796	18697	A	4828	1	259	GGGCSEPRSCHCTPAWVTEYDKKKKKKG RGKGGKKIGKGGFQRKFGPNPHGRFLR ESHNSPKKGFPPKFGNPPPGTSKKVPL PH
4797	18698	A	4830	125	1	KGTRTFETESRSVAQAGVQWHDLSLQ LPPGFRRLTCLSL
4798	18699	A	4831	1	323	ARGREREREREREREREREREPPL SRGGSESYLKSARERLLERDPLFFFG GKMGNLFPPPPPPVGRGYTGGLITGGP FWWGEVSHTHHTHTHTHTYMSV
4799	18700	A	4832	3	297	TRRERERERERERERERTL
4800	18701	A	4833	1	150	AREREREREREREREREREREKKKN HSRGGGPGPQFPLGGGVKKFPGGV
4801	18702	A	4834	1	98	ARGRERERERERERERERERERE RERGAGGGPT
4802	18703	A	4835	2	66	HEEREREREREREREREREAR
4803	18704	A	4836	2	73	PEERERERERERERERERETAR
4804	18705	A	4837	146	2	FGLVYSISQFCLFVRSLALVTQVGQ WRNLGSLQALPPGFTAFSCL
4805	18706	A	4838	354	0	PPPPPPSPPPPPPPPPSPPPSP SSSP
4806	18707	A	4839	62	358	GLVHDKHSPHGGCGSHHVLPSLNPSFPT FSTKSPSVPPARALWPPDSRWALQVGH GLTPTTROESAQAPRRKALLEGSGFQG AOWLTPVIPALWEAE
4807	18708	A	4840	121	13	RPGRPPPEFTPFSCLSLPGSWDCRRPP RPANLLYF
4808	18709	A	4841	3	221	LVMGFVGFSSKPSPIYGGALIVSGVVG CVIILNFGGGMGLIVFLIYLGMMVGF GCILDFSLNPNVGLNF
4809	18710	A	4842	3	84	CHCTPAWTANLDSIKKKKKKKKKFKN
4810	18711	A	4843	33	230	LTVTISKAAEVLKHKKKKKKKKKKKP KKKTFKKNPNPPQKGGELGKKIFFFFWE RFLPQKKRP
4811	18712	A	4844	3	368	HELNPRGRSCGEPBCHCTPAWATRAKV HITKKKKKKKGNLFPKPGGSLSNFFPKK KETPWSQNFEEKGPRRFSRGNPPLA LRGKKKGKSLSGKIFPPFPRGKTPPWA FMGTQKGEYS
4812	18713	A	4845	163	2	HHGHSISKFLTVSSPKSFNQLRPDAVA HACNASTLGRGGWITRSGVDQLV
4813	18714	A	4846	387	234	KGCGEPRSCHCPPAWATIAKLLFKKKKT KPKKNPKKQEKTFPYNLNRVCY
4814	18715	A	4847	189	349	KFSRFSGQKALLKDLRLGTAHTCNP STLGGQGRWIMRCQVFKTSLAKMVK
4815	18716	A	4848	3	95	HENFYCPGSALGRNEGNIFFNPEATFVK EM
4816	18717	A	4849	2	325	DSHTIIMGDFNTPLAILDRSTRQKVNED IQDLNSALHQADLIDYKILHPKSTEYT FFSAPHRTYSKIDHKIYSQGNHETDCRY GKKGGGWKDERFPDVEDCEKFKSQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: In USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
4817	18718	A	4850	241	348	SFFSQTQASEQLTKSQGLALRTLPPVQ FPPPPRP
4818	18719	A	4851	2	176	LVETGFCHVGQAGLELLTSGECDYRCE PPSPAYCFLHTIVTIYPLLCIAFFSYLC DC
4819	18720	A	4852	2	191	VGRVGLELLASSDLPTSGSFSAGITGMS HCPWPNFLLIFIGYFFTTLTPCEYSSGG MTVPLWL
4820	18721	A	4853	67	376	IKCTTFNIIKKKKKKKKKKKKKKKKGG ALKKKPWGGQKKTGEKKKFFSKRGKK KRGPGRVLKKGEREKIFFWNFLKNFFW GGGNLQPPFKKLRLGKK
4821	18722	A	4854	278	363	IWPDVVAHTCNPSTLGGQGRNTRSGVR
4822	18723	A	4855	3	282	RGCSEPLRYCTPAWATEQDSASKKKK KKTQIFWEGPGGGVSPFKPHFFKGPQK KPWGQKPKNPPQWEKPLFFPKKKTKF SPGGGGPP
4823	18724	A	4857	382	224	PVIQLIGGVRQEKNFNLGVKGFNEPKSP PCPPTWVAKQNSLSKKKKKIGKK
4824	18725	A	4858	392	102	FFFFFLLRQGLSVVQARVQWCFCSNLGL LGSSNPPTSASLSCFLNKKYRWENVTN KV
4825	18726	A	4859	3	111	PHRISQEGLLILLTGSALHGLPECDYR REPPRA
4826	18727	A	4860	282	83	AQIYKVQNWSSGNKICVCVCVCVCVC VCIYIYMLCMSRPFYKCIVGCNIDSIV VYIPNIQCYI
4827	18728	A	4861	3	417	NHSNLGGRGCSDDPSRHCTPAWVTERDS ISKKKKKKKKKKIFPGLREKLTLPFFLG KKNENSGFPLNPNFFFGKGGKATLGPL GLVLRGVPPFRGGETQNGENQKPGTTLE KFEKHFVWGPPELKI SPHKGKQTK
4828	18729	A	4862	1	88	MEEMYKKAHAAILNPVYEKKPKKKKK K
4829	18730	A	4863	274	369	VSLCCAGWRAAVRSQITAALISRAQAIL PPQP
4830	18731	A	4864	37	444	DPRVRSEKKIPFKILLIDNAPSHPKAL MEIYEEINVIFMPANTTSILQPMQGV STFKSYLRLNTFHKALAAMSDVSDGSG QSKLKTFWKGFTILDAIKNIRDSWEVK LSTLTGVVKKLIPTLIDDEYEGFT
4831	18732	A	4865	341	210	VYMCHVGLLYHQPVYIIRNRIEASEITP HIYNYLIFDKPSHQF
4832	18733	A	4866	206	412	QLCLSQACTLARGNAKGFYIHRNNS MPSVAGHTWGPDLVKGGQGETCPATIEF SDSPSLKYTMYPM
4833	18734	A	4867	248	78	SHFEAGLAAQLTVSWFPQGTVPVHVAGP FANIAHGNSIIADRIALKLVGPEGFVG
4834	18735	A	4868	637	2	EFDRWPRQIVSSIGLCRYGGRIDCCWG WARQSWGQCQPVCPCKHGEICGPNKC KCHFGYAGKTCNQDEHI PAPLDQSEBP LFQPLDHQATSLPSRDLNECGLKPRPCK HRCMNTYGSYKCYCLNGYMLMPDGSCSS ALTCSMANCQYGCDDVKGQIRCQCPSPG LQLAPDGRTCVDVDECATGRASCPFRQ CVNTFGSYICKCHKG
4835	18736	A	4869	276	426	VSFFLFFFWGANPPFVQAGGQGGFLG SLNPLPGLKHFFCLTPPSSGN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4836	18737	A	4870	100	485	EERNREMTERTCSVTQAGVQWHDLSLQPSPPGPKRFSCLSLPSSWDYRLCDGMNL AHGKLR L P G S S E S P A S A S R V A G I T G M C H H A P L A R L V S N T L P Q V I L P L G L Q Q A E L P R R Q E V E H N T P S L V P I
4837	18738	A	4871	718	408	EVLTQLAHFPGFLGAHWNQQAALGR ATDSKEPPEELCPDVLYRTARTLHGQET YTPRLILMDLHYDVSGLGLVLTAAGYRA SSCSQSVAVCTGSSVLEARA
4838	18739	A	4872	392	246	RGGCSELRSCHCTPAWATRVKHLKKKE KKKCKIRPEGNEILVNNAKG
4839	18740	A	4873	1	156	GGGGYSEPRSCHSTPAWTTRAKLRLLKK KKKKKGGVCPGVGFLGPRPKGGFF
4840	18741	A	4874	246	2	AHGSIYASMLAMSIISRNVSFRRAGQ VKAVFPVSUVFGPLHRHHLGEHFLFFLR QSFTLVAQAGVQWCHLGSPPQLPPA
4841	18742	A	4875	72	2	CFPAAPDEDSTTNTTKKQKWTVE
4842	18743	A	4876	375	221	GRLRQENRLNPAGGGCGEPRSHYCTPAW VTEQDSISNICIYINIFSVVHQ
4843	18744	A	4877	151	2	RAPFFFFFFFFFFVAQAGVQWRVLGSLQAP PPGFTPFSCSLSPSSWDYRRP
4844	18745	A	4878	401	70	PHRREGGCVPPPPPKNFFSPGGYFFWG GGGQNP PPPKGGFFPKTPPGFFSPPPQK KKIFFFFPPPERGPPPGFFLRPPPPFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFF
4845	18746	A	4879	4	152	LPYSTPSTPFRAKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKRGNFK KR
4846	18747	A	4880	267	1	TPPKKKKKKIIPPKNGFPPIFKKTPP PLFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFTRGRTRGRTRGRTRGR
4847	18748	A	4881	2	408	LQDATSPIIEELITFDHALIIFLICF LVLVALFLTLTKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKGGGPKKNRGG PKKLGGEKKIFFFFKGGKKTRGGVGKK KI FLGGGNFGPPPKKKKPRGKI
4848	18749	A	4882	413	69	LP PPPPGFKHFWAPPPGPGVPGPPPP RVNFVFLGKKGVSPFGGGRPLFPNPG GVGAGDPLDPRGQGFHGPFPMPCPPARG TKREPPFPKKKKKEKEKKBPKEKEKK EI
4849	18750	A	4883	46	394	KQYQVSVKLLFVTQNLGTKKKKKKKKK KKKKKGGALKKKPGGQKKPGGKKKNFF LKRGKKKKPPGIFEKTLFGGGENWGT PQRKKPPGKKKKILKGGGKKTLYFGRG KNFS
4850	18751	A	4884	399	3	FFPKKFFSPNEFWFFPPPLKIFFPPP RLFFFWGGLAQFSPPPKVFFSKFPRGF FFFPPLGKNFFPPPGYFWPPPGFFLRA PPLEFFFFFFFFFFFFFSVSIRNAIAI RMGTMRSRRLAMGMLLRG
4851	18752	A	4885	391	47	PHFFWGGVFPFPFKKKFFFLPQKGGG GGAPKKKKKKKFLPPNFSGGFFFFSPP GGPRRFFFFIFFFFFFFFFFFFFFFFFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFFFFFFFFFFLSKMFIFILKYTLKQNEFY
4852	18753	A	4886	32	379	LLPVKKKKKKKGEKKKKKKKKKKKKKKKKKKKKQKQKGGGPSIKIIGGGHLSGGGRKNN SFSHRGGLKKPLFLGRTYFLGGGLWP HPPPKLAGGAKNIILRGWGEQKPLLP PGEK
4853	18754	A	4887	178	33	IFKRKVVFRRFFFFFFFFLYFFFKFFFF FFFFFFFFFFFNICHHPKLY
4854	18755	A	4888	238	3	KPFNFKKKKKIGPQKKKKKFPPLKINP PKYKTQININIKYIKIFFFFFVRGSDS VAEAEVQWHHLGSLKPASPGFK
4855	18756	A	4889	93	1	DGILLSPRLKCSGTISAHCNLCPPGSS NSR
4856	18757	A	4890	6	219	IEKAHKALGTVPGSTFVRVHHYHHHHNY HHHCHHHHPQDNSEWEKAQSLEPDKLF LNPGFATSQRLGLR
4857	18758	A	4891	1	364	TSSRSRAGRPMDFGFFFKKKGHREPPGG VEKKKKNWGSRKTPPSGVKNFPGFDPK MWNKGGPPTPPVNFPGFKKRGFHKGLK PPPEIAPLNPQKGGKKGGPPPPPTPF LGGKFQGGK
4858	18759	A	4892	387	81	GVFSPPRGPPPGGKTPPPFPRGGPPCG PGGRGPIFPPLSHKFFFPFPPLGGG GGPKSAPPKGVFKFPENFFWGAFIKK SFFLKGGFFGPPRGFF
4859	18760	A	4893	213	14	KTPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP PPPPMLEVMFLVNRGKICRVPTFFNL SL
4860	18761	A	4894	384	10	PLPPFIPPPPPPPPLFGGGVCPYFSPPP HLGSPSPPPGGRSPPPPPRSTPPPP PPPPPPPPFVSGAPPPPRSCLAPPP PPPPPPPPPPPPPPPPPLPPFLKKSD FIFSLQMKYFMI
4861	18762	A	4895	240	355	LIITPALEFKIFVLWLGAHAACNPSTL GGQGQIMRS
4862	18763	A	4896	339	3	GVGWHLFFPPQKKFFFFQVTGASCAK SSKESHKGLHLNIYLPKIFFYRPPPPF PPPPPPPPPPPPPPPPPPPPPPPPPP PPFLVVRGYNQHFRMGPIGRVGGRV
4863	18764	A	4897	56	335	TCFLYKLKKKKKKKKKKKKKKKKKKKK KKRGGPLKKNLGGPKKNRGKKKIFPFK GGEKKNLWGFEEKPPFGGKICPTPPQ KKKPPGEKK
4864	18765	A	4898	7	206	LCLQPDNRWDDQSKSFLIEKKKKKKKK KKKKKKKKKKKKGGGPKKNPGGAPNN PGGEKKNSP
4865	18766	A	4899	74	250	INICSEKLPKKKKKKKKKKKKKKKKKK KKKKKKIKRGLNSQTSLLKKREKKKRG KI
4866	18767	A	4900	151	312	KYHFHKNYFFSLLYFSQNVSQLSPDGPL PQLPLPYINSSATRVFFGHDRPADG
4867	18768	A	4901	1	364	LNLGGRGCSEPRLYCTPAWATEQDSAS QKKKKKKPNF
4868	18769	A	4902	1	96	GGGGCGELKSCHCTPANVAEQDSVSKKK KRG
4869	18770	A	4903	3	225	GFHRVGQDGFDLPTSWTARLGLPRGWDW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RREPPRPVWAGLQLLTSSDPPASDSQR AGITHLSHLTLFCHLRF
4870	18771	A	4904	384	194	HWVGRPFNNLWGQKNPPPPPKRLBYQG WGPPPPPPPPFFFKKTPIFSQVFNPPPPF FFFFFG
4871	18772	A	4905	3	387	TTITPILLTLFLITQLKILNTNYHLPLP AQYPLPQKKKKKKKKKKKK
4872	18773	A	4906	1	327	PTRTPIEPENPKFSVPPITPHPKKKKK KKKKKKKKKKKKKKKKKKKKKKGGALKK KTWGGPKKRGKKKIFFFLRGKKKKPRG EFLKKTFSWGGENLATTPKKKKKARKKK KNF
4873	18774	A	4907	134	2	ALYSLKVKWFGAVAHACNPNTLGGQGEW IRRGVDRDQPGHSET
4874	18775	A	4908	59	449	ATRYTITMLAYTSVGIPITAVVLGKQAT KGARFQVRRITENYDKQQLIHKGGRRPP GCHSTHTVLLPPVTWVKTGNSIVANFV LILVCLSFLLLVYRCIQQLQRDSNOREG AMMMVVVLSKRKGGYAGK
4875	18776	A	4909	337	3	LKTAWATRGNNPLYKNTQISGARGEGP PIPLIGGGLSQKNFTPGGENSINPDPP PSPPPGAKKETPPPGKKKKKPTTKELG KDWLELWSDSQRAGKLAEPVGESSP
4876	18777	A	4910	14	162	AESGAKRETAFFPAPQGGATDKRLNIYY AAKHKMTCLPSLAIREMQIK
4877	18778	A	4911	331	2	LPLAPKEGQKILGYKKPPPPGLPPFF GSTPPRNKEGGPPPPRGNFVFKKNGG FPRLGGRGPPPGPQKPPRPPQKGGKQG GNPAAGPPPPFFTEFHSCCPGWSA
4878	18779	A	4912	116	316	ACAAHTLFFFFFLKKKPPFVPLGGKG GNLYLKLWLPGLKKVCLTPPRTGNYGG APPHRIIFCFL
4879	18780	A	4913	93	16	SPPGWPGTVAHACHPSTLGGRGGRIT
4880	18781	A	4914	316	2	KPRPGNPLRARVFNPPGPPGETPFFPKN PKFTRGGRGGPIYNPFGRVRPKNFLYP RGSRFHWPNISPCPFAWGTPNFFSKKK KKRKKKEKLCFSASVPDAQ
4881	18782	A	4915	3	289	TSCNPSTLGGRGGRITRVGVRGQPDQHG ETPSLLKNYIYIYICVDVLYVCMYVGA YIYICIGYIYIWRYLSLTSEHTHTRAP GQYRVYFFCG
4882	18783	A	4916	1	222	ARGERERERERERERERESRHQGGAGP PHTLWGEVGVLLSSPQTGVREKNAPIWG CAAPVLAPRVGRTPFGVD
4883	18784	A	4918	1	281	ARGERERERERERERERERERERERE RERERERERGAPPPPPRGGVRERGTPCP SARGARALSPTISCGDFHRGPKIYRGVG VHTORYFSVGSSLCINTHT
4884	18785	A	4919	1	259	ARGERERERERERERERERERERERER MVTLPAGIYHRFGGGEKKYTKAVRVCVR KPGWRAHNRPADHFGARGPHVKFLAQTV YE
4885	18786	A	4920	797	910	NTMQPGVVHTCNPSTLGGQGGRTGSG VQDQPGQHGE
4886	18787	A	4921	2	67	LEBRERERERERERERERERERSS
4887	18788	A	4922	1	698	TLLLAELGTICDPYRSCSISDSGLSTA FTIAHELGHVFNMPHDDNNKKKRGGPF KGNFNSPPVRASKNFFFGPPNLNSWARF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						LTPGEGKTPGVPPFPNPFATKAEL
4888	18789	A	4923	323	2	LVCRTIHKFRCVPHLTGRRFEHGVTDCTYLFRDAYHLAGIEMDPFHREDDWRRNGQNLVDNLEATGLYQVPLSAAQPGDVLLCCFGSSVPNHAAIYCGDGBLLHH
4889	18790	A	4924	3	225	HEEALHLPQTLMECMKRKELITVFHIGSDEHQDIDVAILTALLKGGKPLRTFLFVRPFILCMYMCVVICVCI
4890	18791	A	4925	371	169	HTQTSISVVLVERRFFHSGQENPLNPGGRGCGELRLCHCTPAWATRKSRLKTKQTKKDAIKCSLCN
4891	18792	A	4926	2	352	ARAARAGRIIKELFFFFFPGNLKKKGLFWWPGGVKNPDLGNPPFPKGGITGLTPRPGMGVIFKKFGKKGSPSTGPKSLGPREFFLALQRCGDLGLNHRGPPFFFGVLETM
4892	18793	A	4927	2	379	ARANMEETQKSNLELVRISSLLIKTGLBPVRIILRSMTNNLVYDTSDDYHLLKDLQEGIQTLMGRLNGRRRTGQILTQTSKFDTSNDNDALLKNYRLLYCFTKDMDKVETFLRMEQCRSV
4893	18794	A	4928	175	31	ILGDLFPAPWLHPFLFLLPFSRPSLAVTEVAVQWRNLGLKQPLPPGF
4894	18795	A	4929	368	247	VDRLFPCCPGWSPSLNQSACLSPKLCWDYRCEPLCSVS
4895	18796	A	4930	2	110	ARGEPRSHCTPAWAMSETVSKKKSGGLFFLPRLV
4896	18797	A	4931	150	1	KYVAPCRPLFLVLSPCRRSCFPFPFCHDKFPESFSEATMFFLQPAEPRA
4897	18798	A	4932	2	155	ARDDLNPGGCGSELRSRHCTPAWATERDSISKKKKNPQNIWGNLKKKWNLK
4898	18799	A	4933	144	249	ETLYPQPPQSLNASCVVCVCVCVCVCVCLCVCV
4899	18800	A	4934	2	153	ARESFEKGFHVGQVGLKLLASGNPPNLATQSAGIISISHCTOPWRQGL
4900	18801	A	4935	1	355	GTSQEFEGRKDRLASPLETGNAGAGRRLAEVSTCPGSKPLQTPRPGGQEGTPGLGRRMRHSAGSPNPAPWSIRDPSLTSALLVACSIHIEDPILHDVLISRCMSIKTSHR
4901	18802	A	4936	112	358	NIKFSKAFFSFYIFILINSVGLASTFMWGGELKFSFTSGILIIQFPFKIKGHPQRGILRTGTFKEDPDDPEGNKVSSLLQ
4902	18803	A	4937	1	258	GTSPYVTQOFFSGWGRQGLTSPKLEESELRLCHCTPSWVTERDSISKKKKKLFYLAGPTFFPFGGNGFNALGRLLKRGGGEKK
4903	18804	A	4938	380	1	FFFFFSETEPYSVAQAGVQWC
4904	18805	A	4940	255	1	LGNLAGYKIRGLYSISLRNRRHSPVILSCGNLFYVIRFFDMESCSVTQAGVLWCNIGSSQALTGPIAPFSFISLPSTRQNSRP
4905	18806	A	4941	10	173	KYIEYDTNKWKHNSCSQIGRINFVKMSLPPKAIYTFSVFPIKIPSVYLPVHLSI
4906	18807	A	4942	144	3	DKCIRRPGTVTHTCNSSTLGDQGRVMRSGVRDQGGQHSPTPSVRV
4907	18808	A	4944	484	274	PSSQSRPRTARMIALSTRPTTRSMKFCHVAQAGLKLGGSDLPASASQNVGISGVS

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						HHTWERFYLS
4908	18809	A	4945	103	412	KKKKKKKKKKKKKKKKKKGGGGLKKN PGGAKKKRGRKKKIFFFKRGEKKNPGGI FEKKPPFFGGGKNWAPPPKKNKPPGEKKK FLRGKGGKNPPIPPGKKKL
4909	18810	A	4946	309	81	KFFFFLKLGLIFLGGFCPIPPPPKKIFFF KIPPGVFFSPPFKKKNFFPPPLIFGPP RVFFKGPPPPPPPPPPPPPP
4910	18811	A	4947	18	264	NYTORFKVEYLNNIINQDLDTDIYRILY PTVEYTFKKNPHGTLCRTDHMLGHNTGL NKKFKRTECTQSMSSDHNGIKYHSAP
4911	18812	A	4948	418	293	QLLRVRQENCNPPGGGCGSEPRSPPCP PTWVTKQVFFSKP
4912	18813	A	4949	3	252	DSAKHLGLKHVVYCGLENVKRLTDGKLE VPHFDSKGEVEEYFWSIGIPMTSVRVAA YFENFLAAWRPVKASDGDYITLTKTK
4913	18814	A	4950	434	270	KRGFPKPTPPGFKKPPPKKKKKIFFFFP KIGPPQKILKKPPPPPPPPPPPPPPPP
4914	18815	A	4951	399	1	VGFSLFPPPPQKKGFSKPPRGFLFPPPK GKKKIFPPPPGKIGPPQGFKRPPPLFFF FFFFFFFFFFFFFFFFFGPPSVTLFLVTIL LQIQTTALGRKSWGKGRIPKPVCPVPA QQTQGAHLLGQVVEINSCA
4915	18816	A	4952	235	56	FTVPPPKKKKKKNPPGGGGVPVPPWGGK NKKIFLPPKFKGPPSFGAPLFPFGQKK KPL
4916	18817	A	4953	13	194	SILISLQISLIITFTATELIIFYIFFET TLIPTLAIITKKKKKKKKKKKKKKKG GGAF
4917	18818	A	4954	177	1	PPQKKKKNIFSPPGKIGPPQGFKRGP LFFFFFFFFFFFFFFFFFRFEGCSDLDG RV
4918	18819	A	4955	450	0	LPNKADKKKKKKKKKKKKKKKKKKAR
4919	18820	A	4956	29	158	AMIVPLYSSLGDFKKKKKKKKKKKKKK KKKKKKKKKKGGGF
4920	18821	A	4957	397	0	PSSPPPPSPPPSPPPPPPPPPPPPPPS SPPAPPPPPPPSPPP
4921	18822	A	4958	257	397	FFFLSFTFVAQAGXQGXGSLDPPPPG FNLFSCLPRIWNYTAPP
4922	18823	A	4959	419	266	RFHHDGQDGLLELTSSDLPASASQSAGI IGVSHRAQSISLAPQYWFPSF
4923	18824	A	4960	300	190	FFFFFFFFFIVAFFFFLFCFLFFFFFFF FFXIFNNIF
4924	18825	A	4961	3	179	DAWVLPFIIAALAHLLFLHETGSNNP LGITSHSDKITFHPYTTIKDALGLLLPL LS
4925	18826	A	4962	2	182	RVNAKDSKWLTPHRAVASCSEAVQVL LKHSADVNRDKNWQTPHIAAANKAVK CAKL
4926	18827	A	4963	273	440	KIHIOHCWWEYKLLQSLWKAAWHFLKEL KAELPFNPAIPLLDIYPEYKSVYLKDT
4927	18828	A	4964	179	3	SLPFCCLNTPKKKLFKFCRKNGFFFFK MESHSVTQAGVQWCNLSLQPCPHGLKQ FS
4928	18829	A	4965	268	364	TVCVIELLTSGDRPASASQSARITGLSH HAQP
4929	18830	A	4966	374	2	QNFFLKKKKKKRVGPGVPPFNPPFPWGQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GGGFPRSLGNPIKPLFFLNPKISPPL WGPFFPLPWGVWAGKNPLPRGGGFLT KFPPLPSSLGKKKKFRPKKKKKKGQAR WLTPAIPTPREA
4930	18831	A	4967	79	346	DKIFSNISCGIVIDLLAIYNWDAYATRL GIYKHWFIIIDKDTSSCRLSPSSYPRF LESLLDDFYILSSGLILLQTTSVFNKTL LKQVI
4931	18832	A	4968	3	93	FLHVGQAGLGLPTSGDPPASASQSVGLQ A
4932	18833	A	4969	158	1	SKSNFAYIFPIKDNGLTGKKTINRVVTK NWARDLNRHFSKVNIQMAKRYMKK
4933	18834	A	4970	2	266	VGQAGVELLSDDPPASAYEGAGIPGVS HHTWPKHFFPALFVACISSLVNCLFQLF ACTISIGLSFFFFFRGDLGNLLKIAGL TFLG
4934	18835	A	4971	3	96	GVRHHAHLIFVFLVETGFHHVQDGLNF L
4935	18836	A	4972	253	348	NFIFLLFIYFEMESHVARAGLQWHCLS SLQP
4936	18837	A	4973	326	2	PMEIPQHKLSLWPGEAISVSYPFERKLLF SADVSYKVLNRNETVLEFMTALCQRTGLS CFTQTCEKQLIGLIVLTRYNNRTYSIDD IDWSVKPTHTFLKRDGTEITYVDY
4937	18838	A	4974	3	244	DASLVFKVAETANEEVKKMCMYKYPGN KCGREGGREKKREERREGRKEGREGLR EGETDEEREEGEGLSYSPFKNSI
4938	18839	A	4975	6	79	THFSLTITSLQPEDIGTYTCQOYD
4939	18840	A	4976	15	339	PGEAGNCLNPGGSCSEPRSRHCTPAWA TERNVSXKKKKKKKKKKI PRGRGLPPV SHPPFWKAGGADWFDLGTLEPPWPTGETP VFKKKKKLTGGGAPLVAPTWGGG
4940	18841	A	4977	204	275	IIIEVDPDTKEMLKLLDFGSLSLNLQ
4941	18842	A	4978	3	352	RRPSPHGLVGAVSVGGAGVMAVETLSPD WEFDRVDDGSQKIHAEVQLKNYGFLEE YTSQLRRIEDALDDSIGDAWDSNLEPMA WRRLPYEQSSVLELIKTKENKVLNRVVTG YAGL
4942	18843	A	4979	219	3	AASTMAMSFEPWQYRFPFPFTLQPNVD TRQKQLAAWCSLVLSFSRLHKQSSMTLM KSRLTSLSITVMLDC
4943	18844	A	4980	142	3	FQGFFFLRDKVLLCCPGWSRTPELKRSS CLGLPKCWDYRRELPRLA
4944	18845	A	4981	351	2	FFFFFSETESRSVAQAGVQWRDL
4945	18846	A	4982	133	3	SFFFFLFETECCSVQAGVQWCDLHPLQ PLPPGFRFRSCLSLP
4946	18847	A	4983	3	161	LGSLHDTANTLWPRLESRTIMAHYSLD LPGSSDPPTSASHVRGTTGMRSTRP
4947	18848	A	4984	363	3	GPSNKKRGRSKKAHVLAASVEQATENFL EKGDKIAKESQFLKEELVAAVEDVRKQG DLMKAAAGEFADDDPCSSVKRGNMVRAR ALLSAVTRLLILADMADVYKLLVQLKVV EDGILKL
4948	18849	A	4985	101	1	LQVCYGRRVVMNSREYGANKQQVESKNM PFQDA
4949	18850	A	4986	341	1	PPPMSPFDVLKTSPPVADAAGWVDVDKET LOHQRYPNVFGIGDCTNLHTSKTAAAVA AQSGILDRPISVIMKNQTPSKKYDGYTS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predict ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						CPLVTGYNRVILAEFDYKARPLETFFPDQ
4950	18851	A	4987	86	1	KCSGTISAHCNVRLGSSNSGPSASRAI
4951	18852	A	4988	124	3	LPWLCSKFETKTFFQFIYYAKGVKTWV YSHKDRNIDOWN
4952	18853	A	4989	305	150	WLLNYRYSHSAEVQCFOFLTWFSTLIG SPDHFSKFFNQYFFKICFDYWKN
4953	18854	A	4990	64	340	KKKKKKMILLKFPQGOREKLSPNFLGLGLG GGKNGPPGGKPSRDPPPGIKPGEKKK NPLKKKKKKKKPLSKGGGGKKTPLKKK KKPPPKGF
4954	18855	A	4991	3	158	PSLVQTRLRHAGQAGLKLLTSTDSPASA SQSAGTTGVSHHAMPKDSCSLNSN
4955	18856	A	4992	116	66	FFFFFFFFFFFFFFFKE
4956	18857	A	4993	3	107	GQAQWLTPVIAALWEAKVGGSFEVRSLR PAWPTQ
4957	18858	A	4994	1	105	KLDRLARHGLYEKKKTSRKQRKERKNRM KKVRGTW
4958	18859	A	4995	110	3	RRIGRYKTVFLCTQLEILMARYPLPFSP KPIKIKN
4959	18860	A	4996	109	3	DEVSIILCPRLCNGTILAHCNRRLPGSS DSPALAP
4960	18861	A	4997	1	148	ACCFECTIYLLPMFMIIKAPLMGTSKKK KKKKKKKKKKKKKKKKKKKKKKKKKKX
4961	18862	A	4998	3	110	VILQGSNDVELVAEGNSRFTYTVLVDGC SKKTSTRP
4962	18863	A	4999	3	330	PIADRGAEYVSAREWMTCIFELLQLLKA HKAIIRATVNTFGYIAQAIGPHDVLAT LLNNLKGHERRONRVCTTVAIGAETCS PFTALPALMNEYRVPELNQNGVLK
4963	18864	A	5000	3	110	VILQGSNDVELVAEGNSRFTYTVLVDGC SKKTSTRP
4964	18865	A	5001	25	329	NSRRRRNDQGSFNLCQTTFMTLPYLPE HRSLLLKIRSCABRETKKKDDIPEDKG NIKQCEINYVKFKQSPODHKLKISKES KILKKAQKGDLFHETLLN
4965	18866	A	5002	278	345	EDEEYNDGVEVDDEEBEELGG
4966	18867	A	5003	101	3	VRIISGTGKKKKRKGKLPKNYDPKVTP DPER
4967	18868	A	5004	18	350	VSHECLIFHIQNVLTLGLVISLSCPSPVP HTKHHTHIHTHTHTHTHTHTFS
4968	18869	A	5005	26	147	KEEVRNALFANDMIVYLENPFVSAPYVL KLISCCKGRLG
4969	18870	A	5006	85	1	SASRVAGIIGKHHTRLIHFVFLVETGQS
4970	18871	A	5007	370	3	RARKPLLWVLKKIWSPWYKKKTRINPQ KEKKSPPFSRPFFLFKKGGLPPGVVFS RGFLKKIPPPFFFFFETESRSVTQFGW SVQWCNLGLLQPEPPGSKQLLCRGLPSS WDYRCLSTRP
4971	18872	A	5008	1	85	IRILSKIKNALTHFLPQGTPTPLIPILF
4972	18873	A	5009	218	93	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFF
4973	18874	A	5010	3	250	RPRRRRLRQENHLNLGGEGCESERSRHC TLTWATEQDSVSKKKKRVPFPHPGRGK FWAGGETFFPPLKTVPPFGGGKPNF
4974	18875	A	5011	336	0	SSSSPPSSSSPPPPPPPPPPPPPPPPPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4975	18876	A	5012	2	80	SNQNGTGGESTYGEKFEDEPHYKVK
4976	18877	A	5013	53	324	FLVFFVPENSEKISLQLHLALTSNSSWV QSPSHELMNLCRHINIRVDPTGLREGM HYTEVCGYDIASPNARSLFRGPITAVIA AQVNES
4977	18878	A	5014	329	1	FFFFFSETESRSVAQAGVQWRYLGSLOA PPPGFM
4978	18879	A	5015	193	32	PLILCSERLCHCTPAWAIERDSVSKTN KTKQQQQQQNQGTKCMFLALLGQI
4979	18880	A	5016	354	235	CGEIGMLLHCWWECKLVRPLWTNLFLRD GSTLTGSKSSF
4980	18881	A	5017	348	2	RLLVGKLMELHGESSSGKATGDE
4981	18882	A	5018	76	1	IFFLSQVSPLSKEDAGEYECHASNS
4982	18883	A	5019	68	356	YFGVGVGFFFFFFFFFFFWGSPSGVFPVG VQAIFFFFFFFLGGFFFLVRDYFFVAVF WWGLLFFFFFVFVFCVFFFFFGWKRK NIFYGWVFLFCW
4983	18884	A	5020	1	288	FFLNLEKNIKMLSSYTDNGIVVATAEDF MQNFKNLVGYHNSITEENLPQLGANBNL ESQSGNFSVVFIFFNADRKRGVLLLPN NEMTILKPRTSV
4984	18885	A	5021	133	1	VVATETMWSTKPKMWPGTGAHTCNPSTL GGQGGQITSPQKFKTS
4985	18886	A	5022	2	337	RRSDPNFKNRLRERRKKQKLAKERAGLS KLPLDKDAEAAQKFLEKIQLGEKLLAQ GEYEKGVDHLTNAIAVCGQPQILHLVQ QTLPPPVFQMLLTKLPTISQRIVSAHSL
4986	18887	A	5023	1	325	VDGCPANLLSSHSRLVLRATISLGEHP CDRGEQVTLFLFNDCLEIARKRRKVIQT FRSPHGQTRPPASLKHILMPLSQIKKA LDI IETEDCHNAFALLVRPPTQA
4987	18888	A	5024	135	2	ATMFLNSKVSYSYLLGFHECREKGWM TWDGERDPSPGILQLQ
4988	18889	A	5025	2	94	KTATKLIGGXHYDSXNIKAIIRDGLLARR HAL
4989	18890	A	5026	2	362	QELERSMAQRVCVLAVALMLLVFPTV SRSMGPRSGEHQASRIPSQFSKEERVA MKEALKVFPTVVSTSFQHEVVEEYSHL FTIQGSDPSLQPYLLMAHFDVVPAPBEG WEVPPFSG
4990	18891	A	5027	222	84	AASTFCHVSQAGLELLTSDPPASASQS AGITGMSHRTQPMVHLY
4991	18892	A	5028	366	0	SGRSKKKKKKKKKKKKKKKKKKKKKK KKKKKKRGR
4992	18893	A	5029	231	68	AGMGSRALPKPLLSHSSSLKAVELPDSF SPELRSLLLEGLLQRDVNRRLGCLGRG
4993	18894	A	5030	2	366	LNLGGRGCSELRSCHCTPAWVTETPFKK KKKVPHGGYFVAQLLPPRKMTRHRPQA QGERTGPGWGAPVHTGLLPRRQQAFTQP PSAFKGFPHPTNKSSSEAKKKKKPRVG RKNVGYIL
4994	18895	A	5031	241	368	QVERNFKSQSGAEAHICDLSTLGGCGGQ ITRSGVHDQPCQHG
4995	18896	A	5032	279	396	DGGMWPGTVAHACNPGTLGGQGRWITRS GVRDQPGQHG
4996	18897	A	5033	173	398	SNESSLRVNPPFFFFFLKTNFSFCPPGG RQGFNFSLLDPPPKVKEIFCLTPPKRW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EYRPAPPPPRNFGFLIKTG
4997	18898	A	5034	2	143	SNFPALTSQSMGITSMTTRHALPIACFLV FVFLFFEMESHSLAQAEVQ
4998	18899	A	5035	350	2	QEISSVQTSQTLFNGMTVKARATTREVM ATYTTIEDIVIELIIQLPSNYPLGSIIVE SGKRVGVAVRLFIFITQKSFIFLFSFLT LCLCLQHFHNDFLLLIVPILIAMAFML TERK
4999	18900	A	5036	1	100	HECGSSSQRTLSVQEAAYLKVSNEIRI LIAIF
5000	18901	A	5037	247	334	LQIDISAVVAYTTIAVKEDGBLNLKKAAS
5001	18902	A	5038	2	296	DKAPMLKVIIVNSLKNMINTFVPSGKVMQ VVDEKLPGLLGNFPGPFEEEMKGIAAVT DIPLGKXVHLEALKKKVKKFYKFLRCD IHTAKCTGLRYTAQ
5002	18903	A	5039	152	335	RPIWSYLLFFFLFWGLYLDVNKRIFTF ILSEKYFDMKKNQCKEGLDIYKKFLTRM TRISE
5003	18904	A	5040	336	1	GGLTISLLKEKEGSEVAKFTLEQLCLI CNIMSTAECVAATQOLEEKLKEKVDVS LFDRINLSGDMGTFSPISSSIHLLVQD VDAACDPAMVAMSKMQCONVQHVGVKSS
5004	18905	A	5041	3	204	LNLGGGGCSEPRSCHCTPSWVTARHLK KKKKKKRGKNPLKNGGKENFKFLQILVN PKNSLENLAV
5005	18906	A	5042	382	148	WCNHRGPRSRKKRSEGSTKSRRLGATIR MVTPHTRTRCARDPELTSRKCVCYIEEH THTHTHIYIHTHTTTCIYVKTTH
5006	18907	A	5043	137	1	RPRRRYMKKFSTSLIIRKMKIKITMKYH LSHLIPVKMAITKTKD
5007	18908	A	5044	198	34	KPASRFCHVGQADLELLTSSDLPPASASQ SAGITGVSHCSQPNFITLCLVVDHFF
5008	18909	A	5045	11	357	LLTVFIIMFKILEIYEKEQLIIRKQISE GQEKVKELRQFKEHRKAKDSALQSIESK MLELTNRLRESQBEIQIMRKKKKRKNAR GPYWKFKYSQRWKSPPGPFQWGWGPRKN FFV
5009	18910	A	5046	2	193	GLQLLTSSDPPASASQSAGIAGMSHCTQ PQVHLMPSLYHFRFLQVDTKOLLRASAD LIHRGIT
5010	18911	A	5047	1	196	KLCLVMNSPMKAAPRNFSCAPSLSLLPF SFRKTTTTLTSNTADDFAYFDLCKMEPC SMVLEFFVC
5011	18912	A	5048	386	276	AQAVLELLDSSDLPPASQSAGISGVSH CTQPDSTF
5012	18913	A	5049	1	324	VDAAEKLEASTGWLMPFKERSCLHNK MHGEATVADTEAAAGYPEDLAKITDKGV YTQQIILNGDEIAFCWQKIPCRIFLARE QAVPGCNASKARLTVLLWANAAGD
5013	18914	A	5050	1	129	PRSCHCFPAWVTEQDSVSQKKKKKKKE KEKKNPVEKSAKVI
5014	18915	A	5051	193	356	RSFIPASASASTLCLKCSQNGQPGAVA HACNPSTLGGQSRQLTRSGVQDQSGQY
5015	18916	A	5052	192	341	AKRVKRNFFFLKQFCVPPQAGGRGP DPGSLKPLPPGLKGFSCPTPLN
5016	18917	A	5053	340	1	KRIPDKPQKELRRLATKLIREAPEKGQA QGKEIHKSIQEAKGEIFKAIDRIKKSQF

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						DRQRAIDILLVMQNALESLSNRTEQVBE RNSELEDKVFDLTRSSKAKGKRIRNYDH S
5017	18918	A	5054	2	383	VVKVATQPADNPLDVLRSKLHLGPNVGR DVPRLSLPGKLVFPSSSTGSHFPMIGID IVMPGLLLCFVLRDNYKKQASGDSGA PGPANISGRMQKVSYPHCTLIGYFVGLL TATVASRIHRAAQC
5018	18919	A	5055	2	383	GSVLSKKGDYLLKYHYNASLLDGTLLDST WNLGKTYNIVLGGQVVLGMDMLKEMC VGEKRTVIIPPHLGYGEAGVDGEVPGSA VLMFDIELLELVAGLPEGYMFVWNGEVS PNLFEEIDKOGNEV
5019	18920	A	5056	2	383	AVIDEVRTGTYRQLFHPEQLITGKEDAA NNYARGHYTIGKENIDLVLDRIRKLADQ CTGLQGFLVFHSGGGTSGFTSLMER LSVDYGKKSLEFSIYPAPQVFTAVVEP YNFILTTHTTLEHSD
5020	18921	A	5057	26	452	KLMSLRRLQAWHEAAIDFRTGTYRQLF HPEQLITGQEDAANNYARGHYTIGKENI DLGVDRIKRLADQSTGLQGFLVFHSGGG GTGSGFTSLLMERLSVDYGKKSLEFFI YPAPHVFTAVVEPYNFILTTHTTLEHSD CA
5021	18922	A	5058	2	385	AVIDEVRTGTYRQLFHPEQLITGKEDAA NNYARGHYTIGKEIDLVLDRIPKLADQ CTGLQGFLVFHSGGGTSGFTSLLMER LSVDYGKKSLEFYIYPEPHVCTAVVEP YNFILTTHTNLEHSDC
5022	18923	A	5059	3	390	GDAANNYARGHYTIGKEIDLVLDRIRK LADQCTGLQGFLVFHSGGGTSGFTSL LMERLSVDYGKKSLEFSIYPAPQVSTA VVEPYNSILTTHTTLEHSDCAFMVDNEA IYDICRRNLDIERPTYT
5023	18924	A	5060	103	3	KIFFFLRWSFALITOAGVQWRGLGSLQP LPRAT
5024	18925	A	5061	262	412	KASEFRTGTAFNGKTS DYLLLGNGFGYT FGGITGCLKAGLETSYWTWPTH
5025	18926	A	5062	293	406	VIIGSIFEVIWAVIKPGTSPGISVLRLAL RLLRIFKVTK
5026	18927	A	5063	419	15	WEEEGPLPKKKKGFSNKRGNIMGPFL KRPEKKPPPPPRKINPFFFFFKRKGPP PPRVKGKGAIGSRNPPLFGSRDFFSPA PQKSGAPGPPPPPVNKNQFFFFFLVE TGFHHVTQAGPELLSSSPPTI
5027	18928	A	5064	2	216	GLTNLFIFCRDRILLCCPGWSQTPSLKQ SSHLSLPKPVDYNYEPLCLYFLYPWFCL SLSLSFPLSHTYFFG
5028	18929	A	5065	259	36	SQPHWDYRASRAEEIATFLEVLQAI CCLFLRQSPPIAQAGVQWHYLSLQPPP PGLKQFSCFSLLLVPRLA
5029	18930	A	5066	2	404	GKGAPTTSLISAVTKIAKVLEDNKL GAICSLTCGGANIGTAMAKDERVNL TGSTQVGKQVGLMVQERFGRSLLLELGGN NAI IAFEDADLSLIVPSALFAAVGTAGQ RCTTARRLF IHESI HDEVVNL
5030	18931	A	5067	1	400	GENMITGTSQADCAVLNVAAGVGEFEAG ISKNGRTREHALLAYTLGVKQLIDGVNK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						MDSTPEPPYSQKRYEIVKEVSTYIKKIG YDPDTIAPVPISGWNGDNMLEPRANIPL VTGWKATPIDCDASGTTLLDA
5031	18932	A	5068	41	392	GSPPHPCAHERKKKPYNSNIGFYTKRN ALRVAEVMDDYKSHVYIAWNLPLENPG IDIGDVSERRALRRLKCKNFQWYLDHV YPEMRRYNNTVAYGELRNKAKOVCLDQ GPLEN
5032	18933	A	5069	3	395	GTPTREPHILLQALFIRAMLPDPTD KTGLDQALKICQAMLEAANQGWLVTVL NNTNLIQMAIQGRWVKDSSILLTPYIEN HHLHLFKRRKPKIMKGPBARSRTSIECLP ELIHACGGKDHVFRSLVQQ
5033	18934	A	5070	3	405	PRASEVCGFSCHITCVNKAPTTCFVPPE QTKGPLGIDPQKGIATAYEGHVRIKPA GVKKGWQRALAIVCDFKLFLYDIAEGKA SQPSVVISQVIDMRDEEFSVSSVLASDV IHASRKDIPCFRVTASQLSAS
5034	18935	A	5071	3	393	ITRQEFIDGILASNFPTTITMTVGADI FDREGDGYIDYEFGAALHPNKDAYRPT SDAPKTFHQGTRQVAQCICAKRFLVEHI GENKYRFFLCNHFQDGHQMLRVLRLST VMVLDGGGWMALDQFLTT
5035	18936	A	5072	3	394	ITRHEFIDGILASKEFTTKIKMTVGADI FDRDGDGYIDYEFVAALHPNKDAYRPT SDAYKIEDEVTRQVAQCKCAKRLLAHI GENKYRFFLCNHFQDGHQMLRVLRLST VMVPGGGWMALDEFLVND
5036	18937	A	5073	1	393	GEDAANNYSRGHYTIGKEIIDLGLDRIC KLADQCTGLQGFLVFHFRGGGTGSGVTS LLMEHLSPDYGPCKLEFSIYPAPQVFT AVHEPYNMMLTHTTLEHSDCAFMGDNE AIYDICTNLDIERTTYTN
5037	18938	A	5074	39	482	LGLHSAWRDDKIGYNPDTVSFVPISGWN GDNMLEPSANMPWFKGWKTRNDGNASG TTLEALDCILPPTRATDKPLRLPLQDV YKIGGIGTVPVGRVETGVLKPGMVATFA PVNDTTEVKSVMHHEALSEALPGDNVG FNVKNVSV
5038	18939	A	5075	1	390	GVSMASLVIIYQYVVRNMPDPHNLPIV AGWKYPLFFGTAVFAFEGIRVVLPLEN QMKESKRFPQALNIGMGIGTTLVTLAT LGYMCFHDEIKGSITLNLPOQVWVYQSV KILYSFGIFVTYSIQFYV
5039	18940	A	5076	330	462	VNFFREGGTSPSIAQARVPWCSLNSL QPLPPGFKRFSCLSLP
5040	18941	A	5077	1	403	GGWGVAEDEFYAPDVEPLEPTLSNIIE QRSLKWIIFLGKGGVGKTTCSCLAVQL SKGRESVLIIFTDPAHNISHAFDQKVK VPTKVGYDNLFAMEIDPSLGVAELPDK FFEDNMLSMGKMMQREMSAF
5041	18942	A	5078	348	1	RPQGNNIERWQGGVLIILQLRIAKSVK NVQLLWKTQFLIKLHILLFYDPRIPFVS NYPKEKKTIVHKKTYAQIFISLPRTFLF LRQSLNMLPRQDLSS
5042	18943	A	5079	248	3	PGQVLEREHTCRRPWAVVNVICLAGPA KPNREDVSSQEESSLQNSIPPTTLTS TAVKSRQPLWGLKEMEEDGSELDF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5043	18944	A	5080	3	192	GDGSELRSCHCTPAWLTERDTSSQKKKK KERTNWPAPLFFFLLEKKGQNGKP NMKKVL
5044	18945	A	5081	10	171	CFCLGPVGVCRLKPKQLCFLGFWLQD ARQKFRSVLVEATVKLDLVTSTRP
5045	18946	A	5082	94	1	DFWPGKVAHACNPSTLGGRGGWITRSGV QDT
5046	18947	A	5083	142	3	AASTGSHSVAQAGVQWHDLSLQPLPPG FKRFSFLSLPSSWGRKIA
5047	18948	A	5084	257	177	ISLGEVAHACNPSTLGGRGQGITRPG
5048	18949	A	5085	143	1	GGESHSDTQAGVQVCLGSTOPPLTLTF KQFSCNLPSWNYRCVPP
5049	18950	A	5086	3	87	HVGQAGLVLLASCDPPSLASQSDGIV
5050	18951	A	5087	375	220	LESLSQHIATRSKKPAFNLFAFGTLSPV STNWVGFNPISPEGLMLIIFFFFF
5051	18952	A	5088	40	203	IFLPLLLVSFFFYILTGWGTFWGLTLI NDLLNFFFGNSGISFSWFGSRAGELG
5052	18953	A	5089	1	145	MDMRVPAQLGLLLWLSGARCDIQMTQ SPSSLSASVGDRDGDVDA
5053	18954	A	5090	146	328	FMFFPLLESLEIFSSKLFNPPNLFPPFE TESCSVAQDGVQWYDLGSLQPPSPGFKR LSCLS
5054	18955	A	5091	338	1	PNLPSVOLPPTTSCPTLIGDLLVARAHF AGWKHQGINSPLPMAPREGMEAPRNP HPHIFLCCLINGFHLAVSKLYSLFYYYY YFSRWSFTLVAQAGVWRDLGSLQPLPP
5055	18956	A	5092	2	327	PPLTPPIFPSSPKKNPPPPHYNPPPP FRTPPPPPYPLSPPKSPPPPPRVDPL PYSIFPRPNLISPPYSFFYLLPQLQAF P
5056	18957	A	5093	133	3	AQTCTPSTQINSKWITDLNVKGKTIKLL KDNIREKLDLGCGE
5057	18958	A	5094	170	350	AGGQGGNFYSLQPNFPWIRESSHSTLPK FWNYRHTPTGPPNFGFFFLKMGFLVAQ TIFN
5058	18959	A	5095	133	274	RDIIIFLESGIKGYFLFFSDKITSSELVS KIGDKNWKIRKEGLDEVAG
5059	18960	A	5096	2	188	REMQIKTTVRYHLTTARMVLIKKSEKNR CWHGCSEKGTLLHCWCECKLLQPLWKIG WRVDAA
5060	18961	A	5097	235	81	FPKKKKAQIKKPOAAQSLNLSLYIYA FTYTHTRHTHTQTHHTYIHIS
5061	18962	A	5098	355	169	KILLITDSCAHTSCRFSECMKYFNFFF HPHSVYVTDKIRLLEBQLPHVPSNKM PFKVCN
5062	18963	A	5099	160	1	FSASYFNSKKKLI FLLKL RWNFFVCFF GMESHVAQAGVQWCHLGLSLQPLPS
5063	18964	A	5100	364	151	QMGFCHIGQADLELLTSSDPSASASQSA GITGVSHYASQEFLLKKEPHSAHLIPLQ TCVQGKTAQPYSEAL
5064	18965	A	5101	205	3	AASPGVQWPDRLQPRPFGVKQFFPLS FPSSWGYRGAAPPFGHFFFFPSRDEIS VCLPGWSPTE
5065	18966	A	5102	349	207	DGASLCCPDWGLELLSSSGLPALALQNP EITGVGHHTQPWTLSLLIY
5066	18967	A	5103	425	0	CEFFKXKDFCFLSKKKKKKKKKKKKK KKKQSSSQTYS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5067	18968	A	5104	437	184	LFLFFPPPPKKVFSQKTPRSVYSPPPKK KKKNSPPPLKLGPPQEIPTPPPIFFF FFFFFFFFFFFKGHRPRFISLWSPPL
5068	18969	A	5105	401	10	MPSPPFGGPRGGVPLRPGFKNPPGPKGK TPFFLKNQNYLGPPLYSPFLERLNKKKA FTLEAKGPNPNSSRSPPGAQKKNPPF KKKKKKKKRIIFMPQAHPAVYVCSGNQ LPITFPYSIISGPLSSFT
5069	18970	A	5106	413	2	PNKKPSPPPPSPPHKTPSSSPPPPPNK PTPTPPPNKKNFPPQPPKKKNPPQT PPPQKKTTPPPKKKKHPPPHKKTTPPP HTKNPPPPPLPPSLIPPLFPLYINSP FFIPFFFFFFFKIFPYLGRVGGRV
5070	18971	A	5107	269	115	GFFFFFFFSFFFFFFFIFKYIGSTN
5071	18972	A	5108	238	4	QWLPLVDRIWVILFFDLSNLKMPQYQ IGLQKIKVKNNTTFYFLFSFFLRWSFTL VTQAGVQWCDLGPLQPPPPRFK
5072	18973	A	5109	496	0	STPSRASPKKKKKKKKKKKKKKKKK KKKKKKKKSSK
5073	18974	A	5110	1	243	DHLSLGGRCSEQRSCHCTPAWVTERDS VSKKKKSFRLDIFFFNGKKILGTLRGK NQKPPREVSSGNYFHFGLFGPCYK
5074	18975	A	5111	78	4	LGMVAHACNPSTLGGRGGRITREGV
5075	18976	A	5112	2	96	AGVQWRDLGSLQPPPPGFEQFSCSTMP NFL
5076	18977	A	5113	128	6	IYKDVLPEGVRLRLDNDNRVLPTEAPT RIIIPSQDVLHS
5077	18978	A	5114	132	2	DDLSSLQPLPPRFKRFCCLSLDSDWYR RPPLRPAIQEAEEAE
5078	18979	A	5115	1	146	AVETGFCHVAKAALELLHSNDPLASASQ SAGITGMSHRAWPSLFSILS
5079	18980	A	5116	213	3	GAVGFSSGCFLLYLYALGFPPLPLLQ LKFCIWPGAVAHVCNPSTLGGRGGRITR SGVRDQPDQDET
5080	18981	A	5117	407	0	LGWAWFTPVIPTLREVKAGGSPEVRS
5081	18982	A	5118	215	414	KIRPKEIRNNGGSQQRKAQLGKLEQTN PVLNFKAPFFGBQGDYYSFFKTCLDNL PRRGKGVFFF
5082	18983	A	5119	40	326	KKKKKKKKKKKKFKKTGGAKWAPFLNLK KKGIKPQKKKGFPQKKKRGKKKPKI LIQGFQKKKNFSKKKISQKKKNGFWP LGKGFCKPKKT
5083	18984	A	5120	99	2	GRSTRHSPAHTHTTLRHTGTLHHTSH RHSP
5084	18985	A	5121	3	219	ELRLCHCTPTWATRVLRSQKKKREKKKK NFVGKKKGGKKKPPNPKKKGSLGFRG FLFSKFFKTRGTTII
5085	18986	A	5122	262	351	TRPGTLAHACNPSTLGGRGGWIMRSGVQ DQ
5086	18987	A	5123	340	0	KKKKISQAWWWVPVVPATWEAEVG
5087	18988	A	5124	94	2	LMPIIPALWEAEVGGAPQBFQTSANM VK
5088	18989	A	5125	310	68	LSPPYKLGFWGRVIYPPPPPKVSPVFG APPPPEKKKKPPPPPKSSIKKPTCKKI CLAASGKLEVCCKKPLIQSYFL
5089	18990	A	5126	343	131	SRPRRPGLELLTSDDLPAATQASAGITG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						VSNHTQIWPISVGLMNTGVVIPENRIV SELLREIHFLRICL
5090	18991	A	5127	2	145	FSLLGSSVGRLEGTTISTHCTLPASRD SPASNYRLTPPCPADFLYF
5091	18992	A	5128	1	130	SRSVTRLECSGTISAHCNLPSSDSPAS DYRLTPPCPADFLYF
5092	18993	A	5129	1	338	VVRKEGIRFEKEKSKDFKNHVIKYLETL LYSQQVCKLWVTFI
5093	18994	A	5130	346	3	DFFFFHPILFFFFFKKTLFFSPPEGNGG HTLFLKNTPPRGRIFFFLPPLLWGGWA PPPPPKKNFFFFFFFFFFFFFFFFFFFF FFFFFFFFMPPTQSLFKDQGPVQGGEEA PV
5094	18995	A	5131	3	114	FLHIGQAGLELLTSDDPPASASQSAGIT GMSHHAQP
5095	18996	A	5132	292	180	AASTDSIEGHGASLPSKKTPEEDFETI KLISNGAYG
5096	18997	A	5133	338	216	RGENRLPPGGRGFSGPKSHFCPPAWATE RDSLSKKKKNPV
5097	18998	A	5134	337	3	IVVLGNGKGIIRNNQIFSNKEAGIYILY HGNPVVSGNHIFKGRAAGLAVNENGKGL ITENVIRENQWGGVDIRGGIPVLRSTL ICFGYSDGVVVGDEGKGLIEGNPISAN
5098	18999	A	5135	227	343	NYVKEKLIPTWNWVMSIMDSTEAQLPYG SALTSVVDPGQ
5099	19000	A	5136	166	375	ATFVSLGVFCSAVILLYFKNMMKLDLSL TPHTTINSKWIKRLHTRPEAIKFLEVNI GKKFFDIGHEIIL
5100	19001	A	5137	90	2	KTTLWPGAVAHACNPISILGGRGGRITRS G
5101	19002	A	5138	213	379	PTFQSVGETGSLKMHILGPGAVAHACN PSTLGGRGGRITRSGVQDQPGQYGETP
5102	19003	A	5139	384	2	FFFFFLLVMESCSATQAGVQWCDLSS
5103	19004	A	5140	41	317	TMSRDRPSDKITWTYNRSNVMPDGAFF RYSFSALKDRHNAVEVNWIDPNNGWETA TELVEDTQAIARYGRNVTKMDAPGCTSR QAHRAGL
5104	19005	A	5141	29	523	VKAEAAKKADDIWNLRKDDYFVNDEAR ARYWDDREKARLALEAARKAEQQTQOD KNAQQQSDTEASRLKYTEEAQKAYERLQ TPLEKYTARQEEELNKALKDGKILQADYN TLMAAAXKDYEATLKKPKQSSVKVSAGD ROEDSAHAALLTLQAELETLKHAHAG
5105	19006	A	5142	432	144	GGFLPKAFLPPKKKKGAFFPPPGKGATP PLFWGGWTVFLIPEKNPPRGFPFPPKRGB KPVGGPFFRIFAPPPQKKIGGGGFFLER FFFDWKGITGP
5106	19007	A	5143	403	6	FFFFFKQIGPRGGGPPQKSPPLGGGGRG GSPRPGVLTPLPGQGNLFFLKKKKKLG GGGGPRNPFLGGGPGKSLYPGGQRFQ PKILPFFPPRGKKKKI FPKKKKKKSHR KLIQTLLIQTGKLMKMLWRT
5107	19008	A	5144	115	427	KKKKKKKKKKKKKKGGGPKKKKNFSPG GGKKKFFFGAKKKKPRAPVKKTGEKKK GGKKKKCFEKNPFFGGGKKKKKCSSS YPCPKKQ
5108	19009	A	5145	2	79	GCSEPRSCHCTPAWVTEGDSISKKK
5109	19010	A	5146	317	444	IHQPVCAHAYNPSTLGGRGGHITRSGD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino-acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RDHPGQHGETPYPL
5110	19011	A	5147	3	413	SFYRGFIPVLQTVTVLIIGDPSLHGDAW SWMEFFLTIVIFIALWMLPLIGLTIVVNA IWFQDIADLAFVSWTKPHPPSPVSI ADMLFPPLLQALFLIQGIASVLPPIHLV GQLDSLHMTLLYSLYCSEYRLVIN
5111	19012	A	5148	409	247	QTKFRHVAQAGPHFLGSSDVPPTSASQSV GITGMSLHAQHQQHFTASMGRAFGN
5112	19013	A	5149	284	1	AEASRAHMEAHARTQGTGSKAEGVGPV EEYRIWRRPGPDRAHASDSESGEPGGP PPHPANFVFLVETGFFRVGOAGLEFPTS GDPAASAPV
5113	19014	A	5150	439	120	FGSPRLCEGVSIAHCNLRLLGSSDSFA SASHVAGITARPNAIIRKAFGAPSTCTV VWERHEQQTICIQSDLPAGRQKKTGPKN RPGLVAFPFPNASPLGGPGGRIA
5114	19015	A	5151	415	0	FFFFFFFFFFFFLFPVQSFYIYIYMI
5115	19016	A	5152	67	179	ICLSLFLTVHVCVCVCVCVCVCVCCEM VFGVSI PCN
5116	19017	A	5153	280	2	KTPFFLNLEKTRAPFFLKKTFFKKKPF KIFFSKRNFFFFPPGKRPTLFKKKF FFFFQKKNFFSPKKKKKKKKGRRS RSRTSPRV
5117	19018	A	5154	296	406	DRVLLCHSSCSEVAESRLTAASTSWAQA ILLPQPPW
5118	19019	A	5155	114	402	VWRIKASVEKKKKKKKKKKKKKKKKR
5119	19020	A	5156	110	1	QRFLLTLKSLILRLGAVAHACNPSTLGG QGGRIMRS
5120	19021	A	5157	382	95	SSSSPHFLTSPQLRLFFPPFPLKIFPP KAFNFCGGVFPIFSPPKKFFQNSQVG FKNPPQKEKNFSPPPVKFGPPKGFPR PPPPPPPPPP
5121	19022	A	5158	2	350	TLQPGRQSETPPFQKKKKKKKKKKKK KKKKKKRGGGFLKNLGGGPKINGVEKPF FFFGGGYKKPLGFFLEKIFFLGGGIWA PPPPKKISFWGKKKFWGGGKTPLPFC GKK
5122	19023	A	5159	1	208	PTRTLYLVLGLMGPAEIFLSSFQEI RL IDYDKMVDHRGVRVVAFGQWAGVAGKYA RAYITHFLNWLGE
5123	19024	A	5160	1	208	PTRBLYLLKLSLMGPVEIFLSSFQEI RL IDYEKMVDHRGVRVVAFGQWAGVAGKYA RAYITHFLNWLGE
5124	19025	A	5161	419	25	AQKKKKKKKKKKKKGGGPKKNFGGK NKRGGKKKNFFLKRGGKKKTGGILEKN FFGGGKGEKPPQKKKALKEKKFLRK GGKKPLNWGGKKK
5125	19026	A	5162	475	150	KPRTSGTARVPGDPPRCLDDKRLPSRP VIFVFLAETECDRVGQDLQLLTSGDHP HLTFPNCYNRRBPPRPTSSGFQHDIE LHYRRGKADRFKAHLPK
5126	19027	A	5163	237	409	FHNQKTYLDSALCTLVYFVFLRDGIF LLPQLECSGTVMACNLKLLGSRSPPAL A
5127	19028	A	5164	373	476	LGFILLSFLETRSHSVAQAEVQWCDHGL LQPQTP
5128	19029	A	5165	374	132	IFYSPFLYYHMLGKYHKIKNLKIKHML DAVAHACNPSTLGGRRGRTIRLGD RDHP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GQHDETPSLFLWTFASSLSGFPL
5129	19030	A	5166	332	2	RPQGLANCFPGALPPTKSEGFPGQSPGF QIWGCKAFFLRGFPFPQVESKGAVSPP CKVPPGLRFPSPAPTPPKNGDKRGFPFG RATGFFFFFVFLVETGFHHVSNGLY
5130	19031	A	5167	238	1	GGFTGTGGKYEPAGIVHRGEFVFTKEAT SRIGVGNLYRLMRGYATGGYVGTGPGSMA DSRSQASGTFEQNNHGSAGESRG
5131	19032	A	5168	1	89	FFFFKTESRVAQAGVQWCTLGSLQPPL P
5132	19033	A	5169	3	127	DEDFSDFDEKADDEDFVPSDASPPKTKT SPKQVSYLIWVLS
5133	19034	A	5170	20	254	IAPPARIHEERERERERERERERERER ERERERERDTRAERARLFFFFFFFLPA DQCFFIKPSGQRFLPPGGGGVP
5134	19035	A	5171	36	479	TXGDKNKKDLLISVGDLVDRGAENAECL ELITFPWFRAVRGNHEQMIDGLSERGN VNHVLLNGGWFNLDYDKELAKALAH TADBLPLIIELVSGDKKYVICHADYPPD EYEFKGPVDHQQVWNRERISNSQDGIV KEIKGADT
5135	19036	A	5172	278	448	RFLCPLLHPFSSSETKSLTLLPRLGCSG VIIAHCSLKLGGSSNPPTSASRVAGMTG S
5136	19037	A	5173	205	1	HARLIFVFLVETGFHCVGQAGLELLTSG DPPSASQSETPSPKLKLSAGCGGANST ALASGLLFSLGP
5137	19038	A	5174	409	194	FFFLRWSLALSARLVQWRDLGSRQAPPP GFTPPSCLSLLSISFPQSATYMRFLNTI TIVEYSFAYFPISQP
5138	19039	A	5176	339	472	AKFTCISSNIKLSNTRPGTVAHACGPST LGGRGGQITGSGDGDH
5139	19040	A	5177	426	148	GGRGPPPLSHPPGGGGGGGGLRAGGQKN PGPKGETPFFGQTQKKNRGATPPFSQK LGGEKHKNSFTPGKENSIFDPPAPPT WGEKKNFFF
5140	19041	A	5178	328	474	NNTEYNKRLGAVAHACNPSTLGGRGRW ITRSRDRISP
5141	19042	A	5179	448	330	ETGFCHVGQAGLELLGSSDLPASASQSA GIIGVSPHAWQ
5142	19043	A	5180	259	14	LRYKAILCSWIRTNTIVKMAELPKVIYI FNAIPIFKIPDMFCRIARFILKCMWNVK VSTIDKTIKKENRVGIPPRVLMVV
5143	19044	A	5181	2	423	KFYATLVRYVGDRKNLVCREMSMALLSN LAQGDALAAALAVQKSGIGNLISFLED GVTMAQYQSQHNLMMQPPPLEPPSVD MMCRAAKALLAMARVDENRSEFLLHEGR LLDISISAVLNSLVASVICDVLFIQIGQL
5144	19045	A	5182	182	312	FFIQVGFHHVAQAGLKLPSSSSPHLS QSAGITGVSHCAQPG
5145	19046	A	5183	301	472	GIPFFFFLRRSFALVAQDGVQWRDLGS PQPPPPGLKQFFRNSTAWTKGLQFPRL
5146	19047	A	5184	216	413	KPXXXXXKKKKKKKKKKKKKKXGGAVK KKGPQKTPVPPGGGFFAPPLGVSPPPG VFFAGGGAPP
5147	19048	A	5185	357	465	IKPTKILAPGPGAVAHACNPSTLGGQGG WITRSGD
5148	19049	A	5186	467	0	FFFFFFFFFRFLFPFFPSEKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
5149	19050	A	5187	346	3	RFLPLGQGGVEILTPTSTCLGPPKWDY KGEPLRPAQKCFKKRRRKKVQNSVA VYVYHSMCGENKLRRWWGIFTHHTH THTTQKKQNILSRTHKKLVITTSSEB TL
5150	19051	A	5188	11	109	GETPSLLKVQNIKXAWWHMPVIPAMWEA EARES
5151	19052	A	5189	3	151	QLLRPRQENHLNPGSRGCSEPRLHCT PAWATVQDSISNTNNNNKCP
5152	19053	A	5190	2	373	AVAADKGVPLRYRIANLAGNPDLILPVP AFSVINGGSHAGNKLAMQEFMILFVGAS SPKEAMRIGAENVYHHLRGVIAKAYGKDA TNVGDEGGGPIILDNDALVELVKTAIQ AAGYPDKGAIGR
5153	19054	A	5191	55	421	ARVADVCESMKEHLLVLVERAKYIPGFC ELPLDDQCALVTAHAGEHLLLGATKRSM VFKDVLILLGNDYIVPSHCPELAEMSRVS IRILDELVLFFQELHIDNEYAYLKAI FFDPDKETEA
5154	19055	A	5192	163	466	TCFLGSQSAGITSVSHCPSEVFFLKLY HWRQGGQVALLVATPHSPCCPQYRLAPI PRARHDFACASLIIFACILLVHVLMPRV SAGRGVGVPRPAGIQAGR
5155	19056	A	5193	470	0	ECLWPGTVAHASNPITLGGRGGRIMK
5156	19057	A	5194	491	281	RGLALLPMQCCSGMMLAHGSLDLLDSSD PPASASQSVGIMGVSHHAWPSLVNISFV CLIHRSPTKKEGR
5157	19058	A	5195	3	222	LSFHSLSHRCLYMLGTTSENVSPFSLLEL LSRLATLLGDYCGSLSEGTISRNVLVY ELLDEVLRLESRCVAQA
5158	19059	A	5196	20	191	STWNSSRGGGCSEPRSHCTPAWVTER DSVSKTKKKINNKPALALPAVHPTSHDGS
5159	19060	A	5197	460	350	RRLRRENHLNPGGGCCSELRSSHCTPAW VTERGPSD
5160	19061	A	5198	174	41	SLGELLTECLFETKSHSVTQAGVQWRHP GSLQPPPPQGFKRIPPH
5161	19062	A	5199	131	454	FEYFKNRKPPFFFFFGKGVSPCAPGGK AGDPFKLREPPPPRVKGGFPFPPPSGN NGPPPPPRVFFFWFKKGGSPFWPGGVL TPGGGPPPPAPQRRGGINGLDPPAR
5162	19063	A	5200	168	51	TVKTPIRPGAVAHACNLSTLGGRGMWIT RSGARAQPNR
5163	19064	A	5201	414	497	LLFXXXDNGSIYNPEVLDITEETLSHR
5164	19065	A	5202	381	614	VQPGAPPEWVALSTCPGAAPGSGQQPYI PPTFCFFPVKLLSVTWLYLFIYFLSWI SVAQAGVQVCNHGSLQPRPSRL
5165	19066	A	5203	377	485	PKEPGPQPCAPQPPHAPQPPRAPQPQ PCAPQPQ
5166	19067	A	5204	54	434	MRTPENLELTNPQFEGSSWAAVECPDTL DPRDMCVLNPLREPPFAKKECSILLSEVF EICHPPVDVTFYNSCLTDTGCSQGGD CECFCASVSAYAHQCCQHGVAVDWRTPR LCRECPQRSPEGTE
5167	19068	A	5205	201	418	GDAGAHAVLRLLPGHPGTSHLPFSSLT SPLGLKRVTTGGFNSKNRCDARTCYLLP TFAFAHKDRDVQDETY
5168	19069	A	5206	27	177	NSFHHAGQSGLELLTSSDPPASASQSAG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ITGVSHRAQPKAGTFLSPFHR
5169	19070	A	5207	6	1175	DLGPHTPAWTRPKREDLVQSTVRLPEV RISDNGPYECHVGIYDRATREKVVLASG NIFLNVMAPPTSIEVVAADTPAPFSRYQ AQNFTLVCI VSGGKPAPMVYFKRDGEPI DAVPLSEPPAASSGPLQDSRPFRSLHR DLDDTKMQKSLSLDAENRGRPYTERP SRGLTPDPNILLQPTTENIPETVVSREF PRWVHSAEPTYFLRHSRTPSSDGTVEVR ALLTWTLNPDIDNEALFSCVKEHPALSM PMQAEVTLVAPKGPKIVMTPSRARVGD VRILVHGFQNEVFPPEMFTWTRVGSRL DGSAEFDGKELVLERVPAELNGSMYRCT AQNPLGSTDTHTRLIVFENPNI PRGTED SNGSIGPTGARLTIVLALTVILELT
5170	19071	A	5208	401	3	FFFFFSETESHVQAQAGVQWHHLGSLQG PPPGF
5171	19072	A	5209	402	229	GFFKKGPPPPPPPPPPPPPPPPPPPPPP RLSGSKVEWVWGSQKLYMNFCCCRGRSW FT
5172	19073	A	5210	198	2	PPQAKILSSSSPPPIRPPPKGFFPKNPQ VGFYSAPHKEKTFTLPAPVKFGPPKDP KRPPP
5173	19074	A	5211	516	222	GSTLRLTQSRMPASSSTMAPSSKRLLLP RPERSVPAAGTAGHHEASRNCGRGGAG ADEGPATKGDSPKPGYCAAHPAAPW PPGPEKNFMRVG
5174	19075	A	5212	103	203	DKVSLRCPGWPQTPLGLKQSSCLSLPKCW DYKCE
5175	19076	A	5213	409	249	RRNQVGGPRLNPGKRIKSPGIDPYIYG QLIFDKAVRAIWRKSSFLQKALE
5176	19077	A	5214	2	170	ERKILGYIQLRKGNVVGPGYGLLPFAD AIKLFTEPLKPATSPYPLQSPAPPLKP
5177	19078	A	5215	270	464	GQLNKNVWGWDPGKVTFRDGVSLYCLHW NAVAIHGHRHSVPQPQTGFKQSCRLRP SSWDYMPLY
5178	19079	A	5216	156	248	PKDSYIICVVCVCVCVCVCVCVCVCVC CP
5179	19080	A	5217	412	2	PPPQIFFSPPHFFSPPPKGGFFPPPPPP KIFFPPPLFFFWGFFPPSPPPKFFFP PKSPPPPPPPPPKPKKFFPPPLFFFP PGFPLTPPPPPPPPPPPPPPPPPPPPP FRMGCDRWHEGFWILRDGFD
5180	19081	A	5218	165	1	QVKYHNKKTNPPIKIGKRSEQTFHEKDT QMANKYMKRSPTSLRIKGIQIKTIMRY
5181	19082	A	5219	408	88	PSSSPHFFSPPLGGVFPFFPKIFFFP PGLFFFWGVPLFSPPPKRVFFPNSPPG FFFPPLFGKKFFSPPPFFWPPPGFFLS PPPLFFPPPPPPPPPPPPPPPPPPPP
5182	19083	A	5220	3	259	NLLLLIVPILIAMAFMLTERKILGYIQ LKKKKKKKKKKKKKKKKKKRGGAFKKK PRGGQNFPGEKKKKFFFLREVKKKPRGN F
5183	19084	A	5221	10	479	KLMPAESDGRHREERERERERERERER ESSSARARCVSLSDRYKNRVYMKVAEA LCECRLLAYISQAPTQMFLLRLINI IH AHTLTQENDMCLHTTLEILTARQRRV PLYLRVLQRMHEKKKHGPFVLLNNSHNLV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						RLWQQLYLHRDRDSIC
5184	19085	A	5222	142	56	KFQPGAVAHTCNPSALGGWGGQIKRSGV
5185	19086	A	5223	14	471	LEMRS EIDSONYCNCDAGRNEWTSDTIV LSQKEHLPVTQIVMTDAGRPHSEAYTL GPLLCRGDQSFWSASFNTETSYLHPPA FHGELTADVCFFFKTTVSSGVFMENLGI TDFIRIELRGKLATLDKSGQTHYLAIKA LTQKKKKKKTRG
5186	19087	A	5224	480	0	FFFFFFFFFLIVAQFYFL
5187	19088	A	5225	16	422	VRRTARIRHEGKPYECNACGKAFNRS LTHEQRTHTGEKPYVCKECCGTFSRSTH LTHELKIHSCKVPYQCNECQKLF CYRTS LIRHQRTHTEKPYQCNECGKSFSLSSA LTKHKRIHTRERPYQCKKKKKKK
5188	19089	A	5226	99	436	GHPSFEIPATMTAAPAGFPFPQVWEDVR YLFDBIMYGGHITDDGDCCLCRVYLEEF MNP SLAALSGTHACGEKPRLPANSHVS BPSWKWILQPQSSLOMTAALANILTATS
5189	19090	A	5227	473	9	FQITATPHLAVYDPTVQPFWFSEKQIA DIRQVEASTRYLGTALYWIAASINIKPG HDYFYFIRSVNTVGKSAFVEAVGRASDD AEGYLDFFKGKIAESHLGKELLEKVELT EDIASRLEEFSEKWDASDKWNAMWAVK IEQTKVGERDVTSG
5190	19091	A	5228	1	473	PPPIDRLPNTACTACNSARVMTDAGQPHS EADYTLGPLLCCGDKSFWNSASFNTETS YLHPPAFHGELTADVCFFFKTTVSSGVF MENLGITDFIRIELRGRLATLDKSGQTH YLAIKALTQKKKKKTRGGAGPPFFLIGS RITIHGPPFNNAAMREK
5191	19092	A	5229	170	25	KTPLLPGPTVAHACNLSTLGDQSGCIMR SGVRDQLRQHDETPSLLKRI
5192	19093	A	5230	465	0	VVLYPPQKAQKKKKKKKKKKKKKKTK ARG
5193	19094	A	5231	419	56	CVLLRSTKKKKKKKKKKKKKK
5194	19095	A	5232	79	451	AGSNLQEHRLRPESPFNPGGGCREPR RRHCPFAWAKRAKRLKKKHGRNQEVA QGRHGPFPPGLGPEGFLPRRPGSRKRRK GRNVPGPELKGPAVLFSRHRGGADLR PPRGPRGGGGG
5195	19096	A	5233	39	467	VQQQRAQEQQQHPVLHLQPPQIMQLQ QQQQRQISQPPYPQPPHPPSQQQQQQQ QAHPHQFSQQQLQFPQQQLHPPQQLHRP QQQLQPFQQQHALQQQFHLQQHQLQQQ QLAQLQQQHSLLQQQQQQQIQQQQLQRM HQQ
5196	19097	A	5234	194	45	MILKFFNFKIHFFFFLRLQSLALVAQAG VKWCNVGSQQPPPPGFKRNT
5197	19098	A	5235	204	475	ASITVHLWYVEKCYQSSTKVTMPSSS WFGPQPDALQKHGLRPGAVAHACNPSTM GGRGRIITSSGDRAHP
5198	19099	A	5236	59	357	NHWRKIYCKVYNRKKIKHNTTNTKNYQ NFQRNRTKSSFTIFRIQSHYNKHKKHI QRKRQSIETDLEMTQMLELVWIFKVIV ILT KIKTPKTLKING
5199	19100	A	5237	447	166	ELLAFWQTQYNNMNAVNLFFFWIKAPGI PTPSFASRRTHSPFFSPLFFLFFLGKK GFPLCGPGGPKSLNLKTPPLGPPKGGK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5200	19101	A	5238	34	296	LSVAEFLAFWQTQYNNMNAVNLFPAWIK VPGIPTPSFASRRTHSPFFSFLFFLFFF LGKNGFSPCGPEGPKFLNLITPPLGPPK GWE
5201	19102	A	5239	340	472	SLNETHVRSPAHRPGATAHACNPITLG GRDGLIMRSGDQDHPG
5202	19103	A	5240	460	0	PKKKIFTIYFFYFFFFFFFFFFF
5203	19104	A	5241	161	46	SPYSTHRKPCHWPGSVAHACNPSTLGG GGRITRSRDR
5204	19105	A	5242	175	36	LKYYLIFTIYLLSFFFLRQSRVQAGVQ WRDLSSLQPPNSTALQYR
5205	19106	A	5243	11	442	DTIRWGLPTLGSKSTTNEKKREKRRKK EQQSEANELRNLAFFKIPQKSSHAVCN AQHDLPLSNPVQKDSREENWQWRQDE QLTSEMFEADLEKALLSKLEYEEHKE YEDAENTSTQSKVMKKDKRKNHKGKDR PLTV
5206	19107	A	5244	459	333	FLRVTQAGLKLSSSDPPTLASPKCWDY RHEPLCPAQWSVS
5207	19108	A	5245	229	436	FNSTVVRKRGLGGFIHLNLIQTSTFAHL VVSLLTYVLCVSFFVCLFLRQSHFVTQAG VQWHNLGSLQPLP
5208	19109	A	5246	227	30	VFFARWVFLRQDLDSLRLSCSDVILVH CNVRLAGSRGTPSSSVKVGATTGMLYHT WVFFYEFHR
5209	19110	A	5247	173	442	FLGSSSKAATLYYCQYMEFFFFFFFFFF KNFFFSPPGGGEGPNFILLEFPFPLKK ISCPTPRGWDYGVAPPLVNFVFFFKKN GVPPPW
5210	19111	A	5248	255	358	TGPGTVAHTCDPSTSGGRGGQITMSGDR DHPQGH
5211	19112	A	5249	3	130	QPQLAAPSISWAPTSASQVAGTTGVCHH AWLIFLFWVESRRG
5212	19113	A	5250	90	1	STRLENNGTMSAQCNLRLTGSSNSPN SA SR
5213	19114	A	5251	358	447	SFISYRRRSPSPYYSRYRSRSRSRYTP
5214	19115	A	5252	55	202	CWNTSMRGPIWEAEAGESLEPGRRSCG EARTCHCIPAWVVRKLVDA
5215	19116	A	5253	330	3	EEMGFSHVGGGFKILASGDTPAWAFQK GGISGVSPRAWAGFIIFIWNFGGPGQTG FPFYPPRGIFFPRAKINYIRVLNPKGLC QKGVFFFFFSGFPHYRCRLCQISV
5216	19117	A	5255	175	3	MYLRFPLGLSLSERPGMVAHACNPCTYW ESKAGGSLSLGVQDQPREHGGTLCLOKS K
5217	19118	A	5256	263	1	RPRRRFNDRKTALLQEMPFTFTALGKL ISDFKDSKDGTLTYFVETASRSVVLGL ELLTSSDPPTSASQSTGITGVSHFSQPG LAF
5218	19119	A	5257	1	103	CHVSQAGLELLASSDPASASQSVGITG VSHRTW
5219	19120	A	5258	128	2	THKWRDCKMVQPLWKRAWQFLMNLNTHL SCDPTVLLLDILTQ
5220	19121	A	5259	381	2	FFFFFFSEMESPVAQAGVQWCGLSLQA PSPGFT
5221	19122	A	5260	2	173	ENYLNMGGGGCSBPSLHCSPALAIED SVSTTTTTTKQQQNNQLGLFSYFPNPL I

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5222	19123	A	5261	1	175	IKGNQIGKKEVKLFLEFDDNMLYMENPK DSAKNYVQSKTFCLPVVLGRSCKRTCP LA
5223	19124	A	5262	2	145	QVSLKLLGSSDPPALTSQAGIMGVSHR TRPRNTDFKNNTQKSKNTQ
5224	19125	A	5263	182	3	STTSFLNFFLTENVSHVVSQAGLKVLS SDPPSSASHSAGITGMSHTRPQQPLN LKV
5225	19126	A	5264	183	369	WNSLDFFFFPSPFRGYSSMGKVQDAFI FYRRFIDKSKPRANTWGSIGGLYQQQIH PMDALR
5226	19127	A	5265	329	207	RGCSELRSHRCTPVWVTEQDSVSQKRKK KSPCHLQLGTSQ
5227	19128	A	5266	177	13	TLTILLNFFFLRQSYSAQAGVQWHNLN SLKPPPPGFKRPSCLSLPEFQGGHNR
5228	19129	A	5267	474	122	FICSPHPPGGFLTLPKLNILGPSQPLFP LRGSKKQGIFFYSYKIKGPPGAGPPGS ARYSNPFGYGGRVLPPEFPDPPGEHK PRFFLKKKKKGHVPTSKYLPEYLFAYY NASLE
5229	19130	A	5268	55	311	GIQTFGNVAVAGRSKNVGMPIAMLLHT DGEHERPGDATVTIAHRYTPKEQLKIH TQLADIIIVAGSLSSISHAGVQRNHS L
5230	19131	A	5269	238	133	NKNIWVQKKCVFYIYLPICVCVCVCVC VCVCVCV
5231	19132	A	5270	336	517	PVLYILEHSPYNASTYQALKKYQSRPG AVAHACDPNTLGGGRGGRITRSGDRDHPG QRGE
5232	19133	A	5271	262	467	VLSMRPRTHGSAAREEDEHPVELLLTAE TKKVVLVDGKTGTFPTTPGRNTSKGIF KVCDEWKGKMS
5233	19134	A	5272	213	2	MKIYINVYILLFSLKKRQGPPLSPRLEC SGMIIVHRSKLKVGSSDPPALTSRIAWL IGARHTPDCSVCKF
5234	19135	A	5273	284	105	YSCSYSPDEPVELRNSFFRWNHSSDS YWKKKSSKTRPVLPKPPGYSARYECKTV GSS
5235	19136	A	5274	290	449	IFYPSGRVRAKLSAPLAGMGNAKADSRG RSRTKMVSQSRMYCLSALLYLSLC
5236	19137	A	5275	248	423	NKVNITLMTKLEKDTTKENYRPISSLN IDMKILSKILQNIQQYIQSIIHDDQVK LL
5237	19138	A	5276	425	30	TRRGMPHRQGSPRKAPVSVRRQVRREEC GREPLLWFLQSLLGLRQETHLNWGR GCSEPRSCHCIPAWATRANSIFCNFOAS SVEVRRSARKLFSIDLKRHNITITWRVS GLLLVDSYFGRLATPVRTQ
5238	19139	A	5277	25	185	SLFSVAEFAFNAYKVQTEKEEKEEARSK YKEAKESFORFLENHEKMTSTTRYK
5239	19140	A	5278	263	483	VFTVVFQFLFCVYKLIFFSLTECRSVAQ AAHAGARWHNLGSLQPLSGFKQFSCLS LPEFPRMYSVLSPSP
5240	19141	A	5279	25	252	LETGLMTLVQCGGIPGFCHVGQAGLKL LTSGDLPASASQAGIAGMSHTRPILL HFIYFILLYHPPCLAYPIIF
5241	19142	A	5280	326	203	IETESCVAQDGLLELLGSSNPPTSASQS AGITGVSHHTWT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5242	19143	A	5281	210	459	NKNNKKFNEKKKKYKKWARELYRHFSK DDIHVANRYMKRYPTSLIIRKIQIKTSM RYHLTPIRIATIPR
5243	19144	A	5282	262	454	LLFTDYHEGMLHSVKLLFCFLGWSFTLA IQAGGHWRLDGLSLCPLLPRLKQSSCLNL LSSWDYKR
5244	19145	A	5283	451	303	GTEFHHVAGLELLGSSDLPVLASKSAG IIGMGHHAQPKQYSEVILTQV
5245	19146	A	5284	217	489	PVSIITILRCLSLPTPGSRVLCMLEGMD GISLGWVPLPSLPVPLHPLDLSLPVCRQ VGGTKTGVRVYVGETDFAGGEWCGVELD KPLGKND
5246	19147	A	5285	247	99	FFFFFFFFFLYGFFFCFFFFFFFFFFFFFFF FFFLKNKTQPYFIYKRNILSM
5247	19148	A	5286	2	117	PRVRPRVRPRVRPRVRPRVRPRVRKKKK KKKKKKKKKGGGF
5248	19149	A	5287	121	3	KFWPGAVAHACNPSPLGGRGGWITRSGD RDHPGQHSETP
5249	19150	A	5288	416	48	IGKPGSFFFPSPRGAPPPPKIFFLP PPPPFFRAGFPLFPFPQIFFPKIPPP FFFTPLKKKFFFPPIFESPLGLFFP PPPSLFSFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFLGVR
5250	19151	A	5289	503	0	FFFFFFFFSPFFFFSSSSFFFFFFFFFFFFF
5251	19152	A	5290	70	236	IFCNSQLTSPHKHQKKKKKKKKKKKKK KKKKKKKKKKKKKGGGDPKKKIGGAK
5252	19153	A	5291	443	287	QFTKKKKKKKKKKKKKKKKTKQKRTI IPKPPLF
5253	19154	A	5292	334	115	KNPNALFFFFFFFVDRISLPRQWHNLGS LQPLPPGFTQFSCLSLPNSWDYRCEPLR PALFFSSKSKIHKPL
5254	19155	A	5293	413	3	SSSPPIFFPPQKKKIFSPPPPKPPFP KTFFFLRGFFQIFPPPKNFFPKKPQNF FFYPKKKKKIFPPPPKIFPPPKIFLKT PPPPFFFFFFFFFFFFFFFFFFFFFVS LEKGFPDAWADAWADAW
5255	19156	A	5294	291	11	IQPYIKRLMOHDRVGLSSEKQSWFRIYI YINVPGFQNKGFIIIGSSQKAQKMIFF LDRVLLCHPGRSTVVQSQPTAALKNWAQ KTLPPQPS
5256	19157	A	5295	2	401	NPRSTEAAIKYFLTOATASIILLIAILF NNILSGQKKKKKKKKKKKKKKGGGPK KKKIGGGKKKPGGKKKIFFFIRGEKKNP RGEFEKKTFFWGGEKRANPPPKKTLGE KKKILGGGGKKKFFVVGKKK
5257	19158	A	5296	49	363	RLQKKNKKKKKKKKKKKKKKKKKR KKKKKKRRNGGGKLLWKGQGILTK KILILVAVSYTCNINNLRQKWIIGG KSEPNYEFKRNIGAGRGSL
5258	19159	A	5297	100	323	EYLNTCVRICHSHAHFLPPSYVSFALLP RFLFKVLLYMQVFGEATEAVKKSLEGI FDDIVPDGKVKINVCFLF
5259	19160	A	5298	595	0	VCVCMCMCACICIC
5260	19161	A	5299	412	141	TVDSYSEKKILFQILLIDNGPGHLRA LMEYKEINVSMANTTSIMQLMNQGV ISIFKSSYLRFNAFCKAIAAHSDFDES GQSNLL
5261	19162	A	5300	216	2	SQDWLRKFCYHPRVFQRQPIQKLMGLFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						FCLPNMVKNVGVFFFFEMEGRSVVQAEVQ WHDNSPLQPKPPGLK
5262	19163	A	5301	368	3	IFFFPQKGGGLFYIFFPPKKKGFFFK KKIFFFYPPPKKKKKIIRAERKGPPLF FLKKTRPNFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFLVREK VENSTISTQ
5263	19164	A	5302	389	2	AMAQASGSCSLCSRLLDGFIWGVFRYF IVEAGSCYVDQGGAILASSYPTTLVSQ SAGMTGLSHRARPPPLNGPPGLTPSLSM VPKANVFSLLEKPTGLTQALRITLANVS NAPGQTRSGLEGGWGCFF
5264	19165	A	5303	84	333	FHDCCRPERSRILRNFLSSAGIQSIAD AYRLALPQGLLYGPTNFAPINHWARFA AHAHQGTASVRVVGSGSGGNQGLP
5265	19166	A	5304	485	93	PPLFRFRSPPPPPKFFFSPPRAFFPGGF FSFFSPPKSFFFKNPPGFFFPPLKKK KIFFLPPLFLAPPKDSFLAPPPPPFFFF FFFFFFFFFFFFFFFFFFFFSRENIFFI IIFIYLFDRDRFLFCCLG
5266	19167	A	5305	157	2	PPPPPPPPPPPPVWVITLNVELEPSF SPNTESQIGPBEAMERLQENRVE
5267	19168	A	5306	1	133	TQESIMDLENDKQQLDERLKKKKRPAV LKNPWGGQSLPGMARE
5268	19169	A	5307	239	2	PPRNWGFSSPLSPLKSSSPKAFNFWGG VGNFPNPPKKRFFSKNPPGFFFPPLKE KNIFSLPPVNLGPPRVFFKGGPPP
5269	19170	A	5308	454	116	FRLPSSNSPAPASRVAGTSGFRVCVGR GLQLLTASDPPASASQAGIADGVSTQ CSMVPRLECSGMISACYNLHLPACLGP PKCRDCSLCLATPSGK
5270	19171	A	5309	123	1	CSVSKWYPTAFLEKNIIMLWEAEAGGSRG QEIKTILANTVKP
5271	19172	A	5310	153	33	WPGVVAHTCNPPPLGGRSLITRSGVQP QPGQHSSEPSI
5272	19173	A	5311	350	3	NSRNLILTQEHSPPEKNEPLFSLPLQSV SMNTTHSPLLSNSLPHFIIISFLPTRFLV GPSPTRSFPPAQSPDRISFSSRLCSGT ITAHRSNLNLEGSSDPLISVSQVAGTTCM CHH
5273	19174	A	5312	1	392	RTRGRTRGICKSITIIHHINRTNEKKNH MIISVDAESAPLQIHSAKLKK
5274	19175	A	5313	1	239	LKTSFHHVGVAVLEFLASSDLPALASQS AGITCMHCAQPYISINFIPAETQOSS PELVPLPASQKTPSFSTPLFSLP
5275	19176	A	5314	345	237	LYFYIYFLKSACVILSTLCVCVCVCVC VCVCLCM
5276	19177	A	5315	268	412	GMISSNNSSDSFGNCLNPGGKGCCEPGS YHYPPAWATDTFSKKKKKL
5277	19178	A	5316	112	224	PWMLLENELGLHASYLAMSTPLSPVEIEC ASKKIFTFC
5278	19179	A	5317	377	139	KPPRIFYLGPQKKKKLFYPPPFKNCF LGPPPPPLFMIFFFFFFFFFFFFFFFFFF PQWVMFLFFLLSASNQNSPSWSP
5279	19180	A	5318	216	385	RGVLLCCPAWSQTPGLKGSSCLSLPKCW DYKHELPRPATSCNSILFNLQGAIFYH
5280	19181	A	5319	376	3	RIDFGGPKKILLPPPPAVKIVSLKGGP LFFFLNSFFAPAGQWGVFLISSGDP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
						PPAPESVRI PGVSFCAGVPQGFFFFFL NSSVAQAGVQWRDLGSLQPLPPRSKRVS CLSHPSWDYSH
5281	19182	A	5320	377	287	ELLTSSDLPALASQSAGITSMSSHHTQPG SF
5282	19183	A	5321	381	65	SSSPSSRTSGPFFFFSPPKKKKNFQKKK NFLYPFFFFPPPFYKNPPKKLKGPKKK KKISPPPPKKNLSLKNPPPPPPPPPPF FFFFF
5283	19184	A	5322	132	396	EGGFVLKIIREGIGPHFLGLEEEGSKFH EHIFWEKHRESFPGQPIPHFMELGTWG LSKNPYFRVKQRVEHIEGFKNFNEKKD FLKE
5284	19185	A	5323	366	1	GFLKKGVPPPPPGKRGGNQTPPKPFVL GGKQPPPPPLKKKNPKGPPQKKIFF FLTRGGVSLFGPGGGPFFFPKKKPP GGFPFFFLKKPPPLPLFFFFFETGF CSCRPGRTG
5285	19186	A	5324	131	1	DGALSPRLWCSTILAHCSLRLPGSSA SCVSASRVAGITGVC
5286	19187	A	5325	112	1	DGILLLLPRLESNGAISAHCNLHLPSTS ESTASAFLS
5287	19188	A	5326	404	18	PVSPHGKNHEKHTVTCVGSTSGAFLHGE EHCHGNTHHPPEPSNPQTACQSQANRIR HCNSFKNLWRSWAWRTPVVSATQDAEM GRPLEPRGLSLAWATQDPSLKQKQKQK KPTHLWSYILGHHQLP
5288	19189	A	5327	109	3	KCVLTPVIRALWEAETGSGRGQDIETIL SDTVKPR
5289	19190	A	5328	1	117	ETGFCCVAQSGQLQLDSSNLLALVSQSA GVTGMSHRSP
5290	19191	A	5329	3	120	DAWAAEAEQNDTIEEPNKVQKRKRG NDNVFAGQAH
5291	19192	A	5330	105	2	RSGVVAHICNPSTLGGQGRWITRSGVQD QSVQDG
5292	19193	A	5331	204	411	SKKKQKKKKKKKKKKKKKKQDKKG
5293	19194	A	5332	185	2	FFPETESHSTQAGVQWRDLSSLQPLPP GFKSLPSSWDYRCLPPCPANFCIFSRDR VSLCW
5294	19195	A	5333	561	325	WSTLHSFPIWLLNTGYFKELTGFFFFL TVALSPRLCSDTI IAHYSRLRLGSRDP PTLVQSTKITSVSHCTQPSVRF
5295	19196	A	5334	3	96	EGKAAPSQEKSRVRVKEENPEIAVSASTI PE
5296	19197	A	5335	375	228	LSPWLECSGTILAHCNLRPLGSSNSPGV FGFYFFLTLLGSGVHVQLC
5297	19198	A	5336	403	0	NISVPASKHISPPPKKKKKKKKKKKKK KKSQKKKSRG
5298	19199	A	5337	397	80	IIITSKKKKKKKKKKKKKKKK
5299	19200	A	5338	406	34	KRTLKDSKKRKEKKKKKKKKKKKKNR EKKKKPKKKKKKKRGGAQKKNNHPAG GKAYFFFLGGTKKRGGGDTKPLGEKNS PAQTKKLGNNPPFVERGKKKTPGI
5300	19201	A	5339	410	0	KKQKKKKKDAAPGGGGGGRKKKGGPQKK KKGSHLKTpkKEKTGGA
5301	19202	A	5340	306	392	IQYKILPQKENDWDKIQQQLAIPVSSLN F

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5302	19203	A	5341	3	173	TFTATELIIFYIFFETTLIPTLAITTRG GNQPERLNAGTYFLFYTLVGEGLLARS R
5303	19204	A	5342	247	426	GRAWWFTPVITPLWEAEAGVQWRDLSSL QPLLPGFKRFSCRLRLPNNWDYRHPVPPRP ANFL
5304	19205	A	5343	3	149	SWFLHFGAGLELLTSGDPPALALPKCW DYRLVSNWSWPEVILQPQPPK
5305	19206	A	5344	464	147	LRRLRWENRLRPGGGGCSEPRSHRCTLA RVTESLSRVQCQDRRLAQTSSRRPGAS SFFPAGPAFSAVNSTYQALPPAQGAPW TPRLPLGPHGTTSTSSYLPV
5306	19207	A	5345	228	1	VIRLEETVFLFFVFLFLFFRQTRSGS FAQAGVQSSHLSLPSSWDHRYTPHLANP CIFLQKQSLAMLRLVSNITK
5307	19208	A	5346	2	106	FVLELLGSNNSPSSASESAGITGVSHCG QPLENF
5308	19209	A	5347	140	436	FLCDMRVLYVTFFFFGKGVSFPPGWR GGEFLIENPPPGFNPFLLNLPPKKGEL RAPPPAPIFFFFFEKRGFTRLTQEGLN FWTWEPPPLTLPRGG
5309	19210	A	5348	1	465	LESRRFEDGTRVPGSTISWDPPPEAVCP FSDLQLRAGRTTLFKAVRQGHSSLORI LLPFVWQCPAPRGGVYRGRQASLSCSGL HPVRASWLLCFPSEAWMSGTPPPASLP PCNLISDCCASNEQGSVGIGPSEPGVEY NLLLRHLKPEEKRS
5310	19211	A	5349	183	58	ERDYERGPGAVACACIPSTLGGRGGWIT RSGDRDHPDEIVDP
5311	19212	A	5350	288	404	IEXNGMILAHCNFQPLPGSSNSPASASPV AVITGMNHYAR
5312	19213	A	5351	413	305	AEAGLKPLSSTYLRSASQSAGITGVSH HTQPLLLF
5313	19214	A	5352	91	356	TVPKRNTFSPKMVAITTAGTVSTSVLAL GNRESALPTRLGWALCCFIWGGRGHRV PLCHPGWSTVARSLTATSTSQVQAILL PQPP
5314	19215	A	5353	2	410	FVQWQFLKTGSDRSHKAVESLGYEKVEK AMTVNYSFRSLNTKGKLELLGKISVNL AKWKHFREKGRYNTLTGPTATAAFYST EKTEFLPVVEQTCKPFIDSFNKYLLPGA ADHACNPSTLGGRGGKITRSGDRD
5315	19216	A	5354	3	288	SLDDLLKLLPLMLQYSDEFVQSAYLS RRLAYFCARRLSLLSDSPNLLAAHSPH MMIGPNSSIGAPSPGPPGPMSPVQLA FSDFLSCAQH
5316	19217	A	5355	187	3	KKILWQTPGVNLFSEFKGAPLFFFFLRRV LLCCPGWSAVARSPLTATSASRVQAILL PQPPK
5317	19218	A	5356	383	261	GKINGQKSQAFLYTNNRQTESRLWYCY DSPORLIHLSIK
5318	19219	A	5357	367	241	FFFRHVAQAGLQLGSGNNPPASPSQSVR VTGVSHCTOPLCFV
5319	19220	A	5358	217	1	SCDRENTGLKLLSILLIHCE TDTRISL LCISLSIKREIWLGAVARACNPSTLGG GGRITRSEDRDPGETP
5320	19221	A	5359	255	412	TQLCRKRNAFFFLATNHSQKQSRWGT AHACNPSTLGGRGGRITRSGDGDH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5321	19222	A	5360	391	271	RSCHIAQAGLKLASSNPASASQNAEI TGVSHHLPIC
5322	19223	A	5361	232	397	EGLKEPAGLFTMEYYTARKRNKIMPFVV TWMQLEAILLGESTQEQTFCMFSPV
5323	19224	A	5362	213	392	LFIKVEGKFFLRSINILNESLLFLSSNG PGLLKKLGWPGVVAHACNPSTLRGGG RTA
5324	19225	A	5363	306	418	SDGITGTLPASQESAVVEDLLYVLGV DGRYVSAQP
5325	19226	A	5364	347	48	KKRWLKPGGKKNPPKGGKGGTTPFFQ KKGFFPPFFFLKRDLSFQAGGKGEK KKPPQPKAEGKKNPWGNPQRRGGYKGN PTRPPPGGFFFFFL
5326	19227	A	5365	412	172	PDSNLSFGAHYQASLLGSFSLMPLLLYS KCSGQWDVARSAECTSKSSQNKERKKER KKERKKERKKERKKTRKQKNPLT
5327	19228	A	5366	400	296	LVEGGFHHVGRAGLELPTSSDPPTSASQ NLGLQA
5328	19229	A	5367	162	1	APSSLDETPTLLKKTLPGLVAGICNP STLRGRGGRITRSGVRDQPDQHGTEP
5329	19230	A	5368	152	403	TTVLCKLVQPLWKTVMRFLKELEVDLFF NPAVPLLGITYPTEKKSYEKGCTCHVFLA AQFQIARIWNQSKCPPINEQKKKGAPV
5330	19231	A	5369	170	367	IVFEILVISYFKSFQKTTEWNTFFHFP FKVENWPSTVAHACNPSTLGGRGRQITR SGDRDHPAR
5331	19232	A	5370	396	1	QMCVRAHTFAGGRARTHHTHTHTHTHS VVATPRVSHNHCVCVCVCVCVC
5332	19233	A	5371	139	3	PKLECGASIIAHCSLELGLSKDPPPSAF QVAETTGCAPPCLAFFF
5333	19234	A	5372	1	341	PLINILSHLILLCRNYFSFVKFCIRHTS LLYVVISLFHVLCCVVSFLTDRRAHNAS VTYGFVLPVTFKNSPLPGAVAHACNPST LGGRGGQIMRSGVQDQPGQARSSRPALP T
5334	19235	A	5373	280	449	ICHNLQLCPSKDTIEKVKRQPIEWERIF ANHISHKGLSS
5335	19236	A	5374	170	1	QKRGFSMGTMPVSI FRPQDLTLPFGPKA WDPRVNPWGPWCPLFFKGNPQLFQAPG
5336	19237	A	5375	462	165	PPTRFLHVQTGLELPTSGDLPASASQG AGITGVSHHAQPRGHVFDVLLLEYSQQGV FTLLSFLGFSVFFEPLFC
5337	19238	A	5376	3	451	PRAKLGTTRGLRLNLDITGVAVDLILLFR ELRVEQESLLTAPPQGLQFLRNIA SRHE DSQSIGWVHAFFPPVWPCLSLPPHTGS SSSITLPPLLPHRPHPPHSHPPMATLS RPPYPHPPHPPHPLPPLSLPPALSPPP PPPPPPPSL
5338	19239	A	5377	460	300	KVLLCCPRLECRGAIMAHSLELLGSSN PPTSASQAGVTGVSHCRSPVVEFL
5339	19240	A	5378	452	191	DSRFHHVQADLEHPTSSDLHASASQSA VITGVSHRTRPDIAFAPSISFYSCVAE ISLLHLSSEFPKQFL
5340	19241	A	5379	240	395	LATSSVANLRNTFYLLKSSVLGVRAHS CNPSTLGGQGVRI TKSGVRDQPGQ
5341	19242	A	5380	210	411	TSVNSAPNSGQKASVEECFGQVTKVKIQ NVFLGWAQWLTPVI PALWEAGAGGSRDQ EIDTILANTVR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5342	19243	A	5381	406	300	FHYVGPGLLELLTLGSTCLGLSKCWDYR REPPHQA
5343	19244	A	5382	364	479	INDGISKISLFLSHLKDQAGQVWMLTPV IPALWEAEG
5344	19245	A	5383	182	395	HHLRGSAAFLKSAQEPTDFRHTGFKRF SCLSLPSSWDYRCPPRRGGVLCPLPGW RTVVQSWLTTSISQ
5345	19246	A	5384	37	478	GGIHSYPVICFILMGSSVSLPFSSVAC LLAWLLPSFLPSLLPSFLPSFLPSLTGR AFL
5346	19247	A	5385	201	458	WNPPFLSPRKWAARADTEWVGKTAQEP GLSSRLQAYEERQRHWQREREALREDCA AYAQAQRAQQLLQLQVFLQOEKRLQ DD
5347	19248	A	5386	206	407	FFSPGGRAGEKFGFMEPPPPGFKTLWL NPPGKWKQRAPPPIPVYFLEFKKGGWP NMVQVGLNRP
5348	19249	A	5387	468	0	NFFPPRPAPPPPPPPFVAQAGVQWRVL GSLQAPPPGFTPFSCSLPSSWDYRRPA RVSPHC
5349	19250	A	5388	136	2	LLLLFLFETGFCSEVRLECSGTIIAHCS LKLPGSCNSPTSVSQV
5350	19251	A	5389	397	0	ILYPSQKKKKKKKKKKKKKKKKKKQ
5351	19252	A	5390	299	3	AQPLAPPPGFSFILMYFFMLLLFGIPLLY MEVINGQWLHVDNIRVWQQLVPWLCSMS YAHSLVNEGSPSPSPISLCGLQVSAHR VHPQVCASVSLYNS
5352	19253	A	5391	264	202	FFFFFFFFFFFFFFFFSENKI
5353	19254	A	5392	2	150	PRVRFLIETEFCHVGQAGLKLTSVDPP TSASQSAGITGVCHLVRPEKS
5354	19255	A	5393	382	0	NSRAQAWWLMPVISPHWEAEVGSLEPT S
5355	19256	A	5394	395	239	SLPSSWDYRHAPQCWANFIFLVETGFSS VILCSFRLGGFGLSLNILCSLKS
5356	19257	A	5395	24	265	LLPHRKSRNVRTPTPSLRQKNGMNLGG GACSESRSRHCTPVWATERDSVSKKLF TIELVYVFLKNSKGEPLPKVLGL
5357	19258	A	5396	174	118	FFFFFFFFFFFFFFFFFRSS
5358	19259	A	5397	406	134	PSAPSSPPPPPLIWGPPGFPPLFKNP PPKFFFGAPKKIYLPPPRALNFVLLKG PPPPPPPPPPFFSF
5359	19260	A	5398	294	64	IIIIIIIIIIIIIIIIIIIIWELHILWGALF LLKSRIPGKKKNTCKIFLCTPLTGYIP LLKCFQKQNKKSQSQNTLKS
5360	19261	A	5399	1	211	LLLPPTYHHINQDSSNKYHETKKKKKKK KKKKKKKKKKKKKKKKKKKKRGEKKK KKKKGGGGYKKR
5361	19262	A	5400	305	1	SPPRPFLFLFLFLPSFFFKAPTINH FFSPPLFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFLKLFLYKMHRIINTSNI LKINIFVSSPGSGRR
5362	19263	A	5401	416	3	ENTERDRGRQRREDRSRAETQETNRAGQ QESTPPQKKNNTYISSSSSSPTPQK GKKGGPPGPPPPPAGEKGGKPKKRGQ KKKIRPPPGKKKPPKTPPLFFFFFFFF FFFFFHKQTFIVGVNTYILLRSVS
5363	19264	A	5402	154	416	KKKKKKKKKKKKKKKKKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKKKKKKKDSGGGAF
5364	19265	A	5403	327	2	PPPQKFFLGGVFFPPFFYNPPPPFFFF SPKKKKYFSPERGKIFPPPPPPPPPPFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF LRWSLALVAQAGVWVWLNHGSLSQL
5365	19266	A	5404	372	181	YKGLAHTRCISIRNLFNFIYEMGSRFV AQAGLEPLGSSDPPTSASQSDGITGVSR RTRPINIC
5366	19267	A	5405	110	1	PVPVSSTEVKKLVLWPGTVVHACNPPTS GGQGGRT
5367	19268	A	5406	2	401	GFHLTTYGNRKQMRHVREASARPLQGT PPPGHALEWTLENVLLAAPRPRKQVLF AIVASETSSWDREKLWTLSEAKCKGIT LFVLALGPGVGTHELAELVLSAPSEQ HLLRLQGVSKPEVNYAQQGFR
5368	19269	A	5407	3	181	QLILFHDKLSFKLLSWGNVDILINFFLS HCSPERARRLQAKMMINLVMAKDRIQLL GIN
5369	19270	A	5408	371	222	SVEMGFHHVAQPSLEPLGSSDPPASASQ SAEITGVCHCARPNHDSYRRS
5370	19271	A	5409	204	416	NQVGEWVLRKGTGLDLMSMLPHFLVVR SKDEKNTKIWPGAVAHTCNPSTLGGRG QITRSGVRDQGRHG
5371	19272	A	5410	236	308	AGRPGTVTHTCNPSTLGGQGGRT
5372	19273	A	5411	375	216	GCSEPRWCHCTTPAWVTVDSPPKKBBK RKEKKKLLTENSCKALKRNGYL
5373	19274	A	5412	1	381	RFHHVAQAGLNLGSDNLSASASQAGI TGMSPTQP
5374	19275	A	5413	144	3	RPPPIFFFLAKKLALFFFFHSVIQAGV QWRNLGSLQPLPPGFKQF
5375	19276	A	5414	412	32	LFSSKKKKKKKKKKKKKKKKKK
5376	19277	A	5415	414	2	NNNSFVFFSKPIFLKTVGGAPPPSPIYN PIPIFLYIYPPHKWGGVYIPTHMYGGGD IWGYMTTPPPPLFIYFFPPPPFYIEKK KKTIVCFFAQGGVRLCLKKKKNKDRGWG DTMTMGHGGRLMVAHVCGGLKRYV
5377	19278	A	5416	1	240	GGEGCSEPRSCHCTPAWATERDSISKKK KKKGPFKRTHFSSPGLPFFFFFGAPK FNSRARFLTPREGKNPGLPPFYPA
5378	19279	A	5417	2	63	LCLKNNNNNNNNNNNNNND
5379	19280	A	5418	322	1	WPLCFSRCSKKRGSPLGPFPSPLGQSK KFVRFACKTPSAFKPFPSLSFFQRWAGP PPFLQGLGELPKGLFFQCCFFFFFLRW SLTLVAQAGVQWHDGSLQPPPL
5380	19281	A	5419	1	392	FRMAGSYPEGAPAILADKROQFGSRFLS DPAVFHHNAWDNVWSEEQAAAERKV QENSIQRVCEKQVDYEINAHKYWDFY KIHENGPFKDRHWLTFEPPELAPSQNQN HLKDWFLNKSEAPSQKK
5381	19282	A	5420	273	91	RWYIVLDNLIIFILENICCETSLKIYIGP GVVARACNLSTLGGGGQITRSGVRDQ GQHGE
5382	19283	A	5421	1	149	GGGCGSEPRLRCTPAWATERDSVSKK NLKFFCPGLGLYQKQNTWL
5383	19284	A	5422	381	179	SSCLGLPKSWDYRCEPLCPARTALNLT IKKSKDNRNRWRCGCEKMLMHCWNECDM VWLCVPTQISC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5384	19285	A	5423	195	369	CSLSFIKECKLHISGLQDSSISLVNIGL AIRNIRNKPGVVAHSCNPSTLGGQAGWI T
5385	19286	A	5424	253	414	KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKXXRGAACKKPHSPAPAEKDL
5386	19287	A	5425	160	2	NLKGSAFSSKSTSPFFLVKENPLFFFF EMESLSVAQAGVQWRDLGSLQPLP
5387	19288	A	5426	53	426	ASSSFFFFFLGKGGSIFFPKGGGEGKN FFLWKPGAPGGGGPPPTPRGGGKGGPP PPGQKIFLGMFFEKRRFHGGGGGFKLR GKKKPPPLAPKRVKNKGGNPGGGQPLKF KKTLEPKMGLKK
5388	19289	A	5427	60	1	KWPGTVAHACNPSTLGGRRG
5389	19290	A	5428	87	247	KKKNPQKKKKKKKKKKKKKKKKKKKA PAGAGDLSLYPRAGRNNLFFNYLP
5390	19291	A	5429	209	405	KLNLVNFSSLSLKAMISAILLKLSVPI FPMKIVILSTLNSGSGWPGAVAHACDPSA LGGGGGRIT
5391	19292	A	5430	324	237	VMNAFVCVCVCVCSCICVCVCVCYFLF
5392	19293	A	5431	409	3	FFFFFSETESRSVTQAGVQWRDLGS
5393	19294	A	5432	270	402	MKIIFHLIRITGWAQWLTPVTPALWEAE TGGSRGQEFETTVKPC
5394	19295	A	5433	107	277	YNFNNHRYREAIQKWDEALQLTNPDATL YEMKSOVIIMKNFTFLMKLCYVCSVSEQ
5395	19296	A	5434	95	1	RNRKNNGQSGTVAHACNPSTLGGRDGWI TRS
5396	19297	A	5435	412	105	GGEGCSELRSCHCPCPAWATRRLHLKIK KKERWDLAMLLRVGYSGHRQVHCTDHGT LQPQFF
5397	19298	A	5436	276	488	PLPQPNKDSRLPLLVCLGFLFAPLLML GHGPKRARLPIFFPQEAYFITFRLVFAB KKGVRGPLTMCCLAPR
5398	19299	A	5437	179	2	GISPLKGGTPSLKKKKKAKDFNRRVSKE DIQFTNKHMKRCITLLIKQMQIKITMR YLP
5399	19300	A	5438	3	156	TPLYSQILISLRQEHYFKAEGRGCNELT SYHCTPAWAKDGDVSKNKQNT
5400	19301	A	5439	47	173	SLQLFLQTEERKDSDEKSDRNPWWRK RFVSAMPKGNFIKY
5401	19302	A	5440	3	122	TTTLTSLIPILTTLVNPNKNPPKLI RILVLFQTEK
5402	19303	A	5441	390	489	KYKSYSLQPPPPPKFHFSCVTLPKHWDY RREPP
5403	19304	A	5442	86	275	RQEFETSQQGETPCLLKIQKLAGRAHLN PGGRGCSEPRLCDCTAAWVTRAGLSQIK KIKKKKK
5404	19305	A	5443	424	166	CFFVSPKAKSQGVVLGSPPPPPGLKHF SAPTFRGLFLFFFFPRGVPLGKGGSKS PPPGVFPWPPQKGGDSGGYPPPRAKIF LF
5405	19306	A	5444	356	3	AFFWFTNFPFPGKGFPCPHPLSGISKG GPPPRGNFFFGKAHFFSPFFKFLPPIF LPFLAPQKVGFPFGPPPKPSQGVFLFF FFFFFSFLFFFFFETESSVAQAGVQWR DPDAW
5406	19307	A	5445	198	86	PWPLGAQAILLPQSSCLNLPKCWDYRRE PPHTALLNS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5407	19308	A	5446	198	86	PWPLGAQAILLEQSSCLNLPKCWDYRRP PPHTALLNS
5408	19309	A	5447	143	3	TMIFYFYFFFLSQSLALLPSLEGNGTIS AHCNLRLPQGSSDSSADAW
5409	19310	A	5448	324	1	KKNSATSFVSFVEFPFSTGGVLANKGALTQ EKILPCFKIKKIRKRVGAVAPARNHFLF FSPFFKEGLQGIYVFFFFFELESRSVT QAGVQWRNLCSPQPLPPGPKRTRG
5410	19311	A	5449	403	0	LPFFFFFFFFFPKKNH
5411	19312	A	5450	114	409	LNWTLKYLISKHLLIVLPDTILSSLC LKIYIGLQGVLIFFPKQPSAIDKLGQN IAVVGKFGFAHYSLLTKKKWLFQGNITQE QNMIVTGGLSWWND
5412	19313	A	5451	192	406	RNFFLGHLYKVRFEQIGWGRDFMFKTP KARATKNKMDKGDLIKLKSPCAKETTF RGTHPTKGEKIFAT
5413	19314	A	5452	254	48	NAFGWLCVHYALQFIDKSVKNSVCWLG VAHACNPSTLGGQGGWITRSGVRHQPGQ YGETLRTASTR
5414	19315	A	5453	1	288	PLLFIILPSPFSFPHFCGPIKFIILPRE KKKKKKKKKKKKKKKKGGGPFKKKKI FPRGGKKIFFFFWAQKKKIRGGVLKTGG RKKPGGKKNKSG
5415	19316	A	5454	285	415	TSGCCFVFLVLKLSIFCKGKVLNAIEDN GLKNSTFTYFTSDHG
5416	19317	A	5455	372	125	ITPAFSFSPMGKKGVFPPPKFFGFPFPGF PPPPFPKPPPGIIFLGPKKKFFSPPPR VYFFFFKRPPFFFFFFFFFFF
5417	19318	A	5456	3	159	AHASAHYDITTKDALGLLLFILSLMTLT LFSDDLGDQKKKKKKKKRGGP
5418	19319	A	5457	109	392	NIILIKRSTSLFLRPIFPPHLPFFILYL FISLRTLFFFFFKREFCFLPQVGGQGP FLNSLKPLPRGLMQFSCLTLRSGNYGP PPPPPINF
5419	19320	A	5458	243	402	FLKIGFIHKYLRFPVWGILNIVFNRFNS HERAPHAIVFNGTTIEGHVEKCYW
5420	19321	A	5459	394	105	IPPPSPRPGGGAAPPGGGGSTTPPPK KPPPPFNKNQPGGGGAPPSPPPRGL GPKIPLTPGTVKPKETKPPPPPPRGAP PKFLSKKKKKT
5421	19322	A	5460	56	379	VCFSPSTYGAUVLNKSPLRSHGSSSTSG WGGLPSFFPAQRLPLASQVQEHNGHVFA SYQVSIQSCQCLSYIWLMDKALLCSG EWLPHQAPKPSMSPPTPHCSRGLQ
5422	19323	A	5461	184	420	FFFFFLNNLFFFFFFF
5423	19324	A	5462	295	384	LGAVAQARNPITLGGRGWITRSGVQDQ PG
5424	19325	A	5463	413	257	FLNPGGRGCSEPKSHKSTLAWVTERDLI SKKKKEKCNIPQRMPERGQWSPD
5425	19326	A	5464	2	181	SLYCSGWSQTPGLKQSSCLSPKCDYR CELPRPVYVLLYKTSFPKRYVFGIHLCP MSQ
5426	19327	A	5465	1	229	TGSCYVAQANLELLSSSDASTSVSQNAG TTGVSHHVQPYTSSFSQVFPFLRAQSAAT ETTSILWVQLRLQVVRCSV
5427	19328	A	5466	1	368	KERETKKEREERMRMRREGRKEKGRK ERKKEREKERKKREKKRNLGQSAGIT

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						GMSHHTRPKSHNVLSKFTNLCWAAFKAI LGHMWGRDLKLNVEQCSTELSALFSII ATSHMRLWVI
5428	19329	A	5467	183	3	VSLCYGEKFSQPMNESQLYFRPGAVAHA CNPSTLGGGRQITRSGDRNHGQHG GRV
5429	19330	A	5468	1	128	GGAGYSELRLCHCTRAWATRAKHLKKK KKKGPLRALKKIGG
5430	19331	A	5469	1	155	NKFPVLISNVINTIGMCHCTPAWATERD SVSKRKKKEKKRSLARHSVLCL
5431	19332	A	5470	113	1	FFFFFQKTSRLGTVAHACNPSTLGG GGRITRSGD
5432	19333	A	5471	407	281	NGMIPGGACSELRSRHCTPAWATEQDS ISKQNKSKNPGLK
5433	19334	A	5472	1	177	GGGCSEPRSRHCPAWATERDSYLHKMK QSKTKGERMEVACYCIIILFMLTDALEV LMA
5434	19335	A	5473	76	267	KERREEKEKEKRSEKGRKKEGRDR EKEKEERKDERREGEGBEGRKEKED IKRRGVVP
5435	19336	A	5474	133	2	LCRMVVLFCFEAGSHSVTOAGVQWCGLN SLQPLPPGFKQFSL
5436	19337	A	5475	5	394	YGVGTRGFRAGVKEFQALFLITVHSQ LCHIEGTRHHSRIIVVDFINQIENGTF PPLVLSNGCIWLLIVLFWNIFTRQEGQ FFYGLSHYSVFVFCFLRRSFALAQGV RWCDLGLSLQPLPPGFKRF
5437	19338	A	5476	163	2	SEKPVVVALTMTFSHYFFIYFYIYFI FQMESCITQAGVQWRDLNSLQPLP
5438	19339	A	5477	111	2	FLFLKQDLPGAVAHACNPSTLGGGRQI TRSGDRDH
5439	19340	A	5478	232	0	HLVWRMESGSVAHAHVQWCDLSSLP PRFKPFPS
5440	19341	A	5479	388	225	ALFSSKKKKKKRKRKKKKKKKKESM QRKGGHLPRVCCGASMVSPGHKLSL
5441	19342	A	5480	150	2	HRVAVIYEVFVCLFFYFLRQSLTLV TQPGVQWRNLSKLQPPHGF
5442	19343	A	5481	156	395	DSVCTCVLHTCHSSGLSQGRSLHCSLG LPSNCPVCVCVCVCVCVCVCVFC PLHQGVVCVCVCVCVFLSAHFTKGC VCVCVCVCVCVCPPI
5443	19344	A	5482	391	115	RACPDRCVRFPHTSPCLPCGPEAEFGP GPALRELVPPLPGQLQPPFGMPPSGLGA APSPAPPACAWTRPPLHPSFSSSVPO ISSLFLCF
5444	19345	A	5483	392	2	FFFFFSETQFRSCCPRLCNGAISVHCN LRLPGSNNSP
5445	19346	A	5484	381	282	PVPWQAIFLPPPPYLGIPGPPPPGL FLFP
5446	19347	A	5485	407	3	FFFFFLRRSLTVAQAGVRWCDLGLQA PPPGFT
5447	19348	A	5486	2	417	QENHLNPGGVGCSEPRSCHCTPAWVTBY DKKKK
5448	19349	A	5487	3	413	VYLHPSLQPSLSSLPDQALSHDIWLKK KKKKKKKKKKRGGISPPSPVGGVGP TWGVWPGANLFRGGVRELFSQKKKG EKGQRNPEKPPHKKRPGGPKKEFIFFE KKKKGGKPFKKTKPPPPRVNPDG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
5449	19350	A	5488	229	411	IHGPGFKNGGRGKTGLPLMALKKIPFSPGGYKPKNP
5450	19351	A	5489	190	50	YHHHHHCHHHHHQCHRRHHHDHYYHGDNDYSSHSRSTCHVAVTV
5451	19352	A	5490	615	402	RWCLTSPRLSCSGMISAHYNLHLPQSKQLSCLSLPSSWDYRCPPPGKTTFSRGIRDALKPRKPKRINLI
5452	19353	A	5491	338	53	KGPPFFFFCKGGLFCSNWFLTPGGKWFSPPTPPRSQGRVPPPEGGGKGFSLFFVVEGGSCHIAQAGLKLGGSSDLVTSASQSA GIMGKSPHAWP
5453	19354	A	5492	266	412	NPNFFERKSCSVSQAGVHRRELNSLKAA PSGYTPASCVSLPSSWDYRRP
5454	19355	A	5493	285	412	RDGVSALSPGLECGGMIIAHCNLELLGSSDPSALASQSTWNY
5455	19356	A	5494	1	1350	MGFMTGICIEDNVVGPSPESGSLTVGGVRIQMLDRCHTAHCPVPGLLRGQLWTE NLAERNSHDRPPPTVVCSEHAQDLWPE QSIKDSYQKVI LRKFEKCGHNLHFKKG CESVDECKLHKGYNGLNQCLTTTQSKI FQCGKYVKVFHQFNSKRHRKRRTTEKKP LKYIEGDKAFNQSSHTTHKKIDTGEKP YKCEECGKAFNRSSHLTTHKITHTREKP YKCEECGKVPKYPSFTTHKKIHSGEKP YICEECGKAFMYPYTLTTHKIHTGEQPYKCKECKAFNHPATLSSHKKIHTGEKPYTCDKCGKAFISSSILSKHEKIHTGEKPYKCEECGKAFTRSSHLTMHKIHTGEKPYKCEECGKAFTWSAGLHKHRRTHTGEKPYKCEECGKAYTTSSNLTEHKTTHTGEKPYKCKECKAFNWSSDLNKKHRIHIGQKPART
5456	19357	A	5495	4	146	PPTRPTCYLSFYVSYPYTKYEDTRMVN KHMRCSTSLVYLLWINFY
5457	19358	A	5496	5	388	CGCFFFSPPPKKKVFPPPPFFAPGFFFPPLFFTPPPQFFFWAPKKKQNSPPPPGKKIFFLKGPFFF
5458	19359	A	5497	231	163	FFFFFFFFFFFFFFFFFXXTNKNF
5459	19360	A	5498	163	2	SVKFTLGKVSQFLKHTPAGWAHTVIPALWEAEAGSGRGQIEITILTNTVKPH
5460	19361	A	5499	229	388	RTHLQASSDLFCLYSLRTGSCCVAYAGVQRHDLSSLQPPPPFRKRSSCLRPE
5461	19362	A	5500	405	289	HVAQAGLKLASSDPPTPASQSAGVTSVSHCTHPRCLFV
5462	19363	A	5501	286	375	GDFVRFSFWPGGAHSCNPSTLGGRGQVVT
5463	19364	A	5502	20	374	ILQFQNFVIVLFKNFYHFGKFLIYILNWFSGLFWYFSELSCFSLSSKINILNLLSGILNVFFSISGVRKKIFLIKRYCWLGTVTHACEPSTLGGQGRQITRSGDRDHGQQRVVKIQN
5464	19365	A	5503	1	185	FHHIQAGLILLTSSNLPASASQKAGITGMSHCTQPIIFLYSLFLQLSFSWQDFVMRKKF
5465	19366	A	5504	202	402	NSFSSTAKLREKYRQFLYTPIPTGTQPLPLLTFCRTPDTVAHACNHSTLGGGGQITRSGACNQPGQ
5466	19367	A	5505	118	7	IKKENNWPGAVAHACNP SILGGRDGRIT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						RSGDRDHPG
5467	19368	A	5506	205	422	ANHPTSTIRMAIINNKKQTENNKCWQQQG EVGTLVHCWWECKMVWMLRQIVNSFLKK LNIQLSRDPATLLLA
5468	19369	A	5507	3	425	RSCHCTPAWATERDSVSQKKKKKKKK
5469	19370	A	5508	3	86	EKKLQVLLNCMTETIYYQPKDKAERSK
5470	19371	A	5509	395	108	GVLECNDDTITAHCSLDLVGSSDPPTSAS QVTGTGTGTHHAQLGLPKCWDRHEPRL PAWNKTLRRKNWHSLLPVVPAIQELEVG GSLRPRSLRL
5471	19372	A	5510	421	59	FFFFFLLRRSLAVSQAGVQWDLGSLQA LQA
5472	19373	A	5511	168	3	EICKMCPVFFGVFFLWIVFVFVFFVL RWRMESLSVSQAGVQWCLSSLOPPP
5473	19374	A	5512	446	149	FFFFFFFFCFETESCSVARLESSGMISA HSSHNLCI
5474	19375	A	5513	74	398	DRITDAGPKGNVAREFMNHCCQPCETQK WSVNGDTRVGLFALSDIKAGKNHFRILQ LTSEFQGFCLQTASSDYNFKHFYMYRS LELSSTFLCNHHHHPSPFLFSSS
5475	19376	A	5514	73	335	EGGSLFCFGWSAGALFWLTAPSASRGWG GAPGVVVGEVGVQKNCWNPGGGCGNELG LHHCIPPWGTGKTLSPKKKKKGATDMG GAS
5476	19377	A	5515	416	0	WLGPGAVAHTCNPTTLGGRGRWITRSRD
5477	19378	A	5516	242	423	AGSPLIHQQGQAIILTQNPFGWGTVMF QPVLRPVKGLYNANHVTSFPVASQPIIF TTAG
5478	19379	A	5517	2	151	GRVGFVGMGSHCVQAAGLELLGSGGPPT SASQSAILIAGVSHRAWPYFPPS
5479	19380	A	5518	312	405	GQVRPGAVAHACSPNTLGGGRGRITRSGV PDQ
5480	19381	A	5519	3	387	ACSGPRSCHCTPAWATHQDSVSKKKRKK KREKPFLEKKRGPTLTWGEPPKGIPLG ERNGPSPSHFKKGPPLAPKPPGGLHPEI AQGPSPPTDGNKKGDLNPTPVFYKFKTP EQAINWAAPFFPSEK
5481	19382	A	5520	292	140	KKGPPTARPGGGSPPLFFFFFFFFFFFF FFFFFFWESTLKKRELHRSDLVCV
5482	19383	A	5521	1	399	KKWLFSSAQIFTKLSRRRRNRRETWPKE RSKINLHKPILKKQRHELDPDKEFKIALI KMLYELKVTMHEQNENINKETENTKKKK KKKENPPLFGTGKNQSPPEKFMGGQPP PPPPQKKKPPPPNRRFFVFPSP
5483	19384	A	5523	316	399	MLLYWPGTVAYACNPSTLGGRGGRITRL
5484	19385	A	5524	400	0	FFFFFFFFCFFFFFFLFFFS
5485	19386	A	5525	3	429	TTNIGRAMGATTSIVGSDTSQAERPQGT TVVSPGASSTSQSSRPQTSVTPDSSASE SETVITKEFSGTTAISRTSHTGTTPAASG GQATGSLTATTGVAPGTTVAPGSSNTEA TTSVGEKKKQKKKASSP
5486	19387	A	5526	135	3	GGKICTLIKQSVIQESWPGTVAHACNTS TLGGRGGWIMKSGDR
5487	19388	A	5527	105	5	KKKKKKSGRWPGAVADACNPNILGGQG GQITI
5488	19389	A	5528	411	31	GQRVPLSRGVAKKKFLWNPGGGAGKNG GKNFLKKKPPGAPPSSGGPKKGGPPPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKPLILVSPPPRKGGAHNMHFROKKSGN KGGEGSTKGGKKEI FLGKVFQKNFFFFF DPEPHSCCLGWSAMP
5489	19390	A	5529	411	142	PRFSFLFSPPRKKVFPFPKILGGPRFF PPPRFLKPPPHFFFWGPKKKKKFPFPPG EKFFFFKGAFFFFFFFFFFF
5490	19391	A	5530	174	401	QVQPQKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKASPGGGKKKK ERGGGGERKNI IWVPLLPF
5491	19392	A	5531	410	0	QPQSKKKKKKKKKKKKKKKKKKKKAS QKKKKKKKKKKKKKSSGGGFFKEV
5492	19393	A	5532	383	145	GGFFFNPPAKKGSFPQPHNLGGPVFSP PPVFKTPPRNIFFGAPKKKKFPFPGAK KYFFKKAPPPPPPPPPPPPP
5493	19394	A	5533	418	328	KTGFRHVGQAGLKLASSDLPALASQSA GL
5494	19395	A	5534	169	3	IILIIHPCSHVPRRETGLKACTFKNL WPGMVAHACNPSTSGGRERRITRSGDR
5495	19396	A	5535	1	254	PTRPCPPQTSPNSGKLSFSSNGCMNTL HISSTNTVGEVIEALLKKFLVTBPAKF ALYKRCHREDQVYACKLSDREHPLYLHD
5496	19397	A	5536	43	404	QGGTLVLPRLVLNSWPDKRSSLGLPBC WDYRYEPPHQAN
5497	19398	A	5538	2	212	KENHLNPGGGGCSELRSCRCTPAWATER NSVSKKKKINFRGGGLKGRGPGFYPLEK KFPVGVPFPKTNLV
5498	19399	A	5539	2	387	IFQEHKNCGEMSEIEAKVKYVKLARS TYGVSFFLVKEKMKGNKLVPRLLGITK DSVMRVDEKTEVLQEWPLTTVKRWAAS PKSFTLDFGEYQBSYYSVQTTEGEQISQ LIAGYIDIILKKKKKD
5499	19400	A	5540	317	407	GLSHHVFPFEEGKLKKPRIKDKDKVPEP DN
5500	19401	A	5541	120	3	NFFFFFLRRSFALSPRLECSGTISAHCN LHLPGSSDSP
5501	19402	A	5542	430	0	QKAQSNQPEKQEKRGVIONFKRTLKSKK
5502	19403	A	5543	172	2	FIENFLHIFSFWFTKFGCFIVLFLRQS LALLPRPGVQWRDLGSLQPPPRVRPRV
5503	19404	A	5544	149	2	EKDQLBLSALHQADLIDYRTLRKST FFSAPHRTYSKIDHIVGSKAL
5504	19405	A	5545	84	276	TLKKRPKEIRNQGGSFQKRAQLGKLQQ KYPVLNFKAPFFGERGDYKSFFTCLD NLPRRGK
5505	19406	A	5546	2	914	RPAWHHEQKSKNEPEDTEDKEGCQMDKE PSAVKKKPKPTNPVEIKBELKSTSPASE KADPGAVDKASPEPEKDFSEKAKPSPH PIKDKLKGKDETDSPTVHLGLDSDSESE LVIDLGEDHSGREGKKNKEPKPSPKQ DVVGKTPPSTTVGSHSPPETPVLTRSSA QTSAGATATTSTSSVTVTAPAPAATG SPVKQRPPLPKETAPAVQVVVWSSSK FQTSSQKWMQDSSSSSSSSSQNQQQQ QSSQGTTRYHTRQAVKAVQKEITQSPS TSTITLVTSTQSSPLVTSSGSMST
5506	19407	A	5547	2	244	TRLIFVFLVETGFRRVGQAGLKLITSGY VGTSASQRMTHLCLPRCWDYRCEQLHP AQRFFKRMLSVAVDAALLHTSGGM
5507	19408	A	5548	406	1	FFFFFSETESCSISQARVQWCNLSLKP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
5508	19409	A	5549	417	43	IRPARKGCSSGLFGAPLAGGGAPPPPPP RQTSPPPPHTKGGGGPHKPPPKKRPP PKKGGGKKNPKKKKKNTPPPKSAPP PAAKTDPPPLTVPPFLPPYIFTKKIPF LKSYFFFFY
5509	19410	A	5550	3	136	QPRFPTLTNNENNPTLLNPIKRLAAGS LFAGFLITNNISYHSP
5510	19411	A	5551	75	194	NKELSRNKKKKKKKKKKKKKKRGGG LKKKNGGGAKT
5511	19412	A	5552	343	493	IIFSFFFFFFLKGSEVFPAPQAGGHGNGF GPLKFPPLGLKEFSLTLSSW
5512	19413	A	5553	148	3	DAVSLFCPGSLEHSDTIYAHYSPDLLGS SSLSASTSRVAGITGICHA
5513	19414	A	5554	407	252	KKKFLKLAGQGGMRLOSLRLRLRQED HSSSGVQSCSELWGGLIYSKNR
5514	19415	A	5555	3	231	HEFVFLVETRFHHVGRAGLELLISSYPL ASAFREAKARREDLLSPGVKDKPGQYRD TLTLKKKKKSFYILGECW
5515	19416	A	5556	3	131	SVVVSWEESKDAKELVGYYIEASVAGSG KWEPCNNNPVKGSR
5516	19417	A	5557	3	131	SVVVSWEESKDAKELVGYYIEASVAGSG KWEPCNNNPVKGSR
5517	19418	A	5558	462	255	RSHHSAQAGLELQASSDPPALTQSAGV TNVSLRAQPIACSSVEVSSRCQVCLHV RRGKCFRAESYR
5518	19419	A	5559	445	29	KSSNILILQKVENGDLNKLKITDPGL AREWHRTTKMSAAGTYAWMAPEVIRASM PSKGSVDVWSYGVLLWELLTGEVPFRGID GLAVAYGVAMNKLALPIPTCPEPFAKL MEDCWNPDPHSRPSFTNILASQAWR
5519	19420	A	5560	225	475	GAVESSTEEHMIPEKAVEGSLTPTPE SRSAHAGVQWNNVSSLQPPPPGFRFS CLSLPSSWDYTSAGEGCAASYRSKVLK
5520	19421	A	5561	248	142	NKNIWVQKCCVFIYLPFFICVCVCVCVC VCVCVCV
5521	19422	A	5562	262	456	NFPLRTTYFLKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKASSPPPLIKRGPKN
5522	19423	A	5563	314	444	LKSMFCFVLFCEFEIESRVAQAGVQWC HLSPLQPPPPGFKRS
5523	19424	A	5564	220	486	LNSSHPESPLFLGLVLQFFYPSPNPKSF NKKNLRIIRMLLTVDGRGNHPSLFFVHS NVDTVFLPQEGPSFLQPLGQGITAEFEH NQAYV
5524	19425	A	5565	176	492	CTKTAVASKARYLQALLYALASVTIAAT ATRLASISGASPIFRSFPYLPQTPAGLV LPSILILVDVGLRKEKGPDTVAHACGPG TLGGRGGRITRSGVRDRPDH
5525	19426	A	5567	24	470	PMDKXPKXXETPLNGGAGENQDDMAK LKEKLFNEINKIPLPPWALIAIAGVAGL LLLTCCFCICKKCKKKKKNKKEKGRGM KNAMNMKDMKGGQLPQDDDDAKTGLTEQ EGEGEEKEPENLGLQLQSLDYDFOANQ LTVGVLAQA
5526	19427	A	5568	45	485	GXDGRLLRGHNQYAYDGLDYIALNEDLS CWTAADTVAQITQRKWEAAREAEQLTAY LEGLCWEWLRLTHLENGKETLQRADPPKT HVTHHPVSDHEATLRCWALGFYPAEITL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						TWQRDGEDQTHDTELVTETPAGDRTFQK WAAVEVP
5527	19428	A	5569	221	422	FFFLTGRVQRSLADLEQKIEVHSMPPPE SLALSPTLYCRGAILGATSASQVAGITN ICHHAQPSYLF
5528	19429	A	5570	401	477	IFSRDKDVAMLPRIVLNSWAQVILL
5529	19430	A	5571	102	36	EVENDDISHHHHHHHHHHST
5530	19431	A	5572	106	407	AGRQGVVLEGCRAAWPTLLTPPATSSR GASREPTATCTPTDPAPATTWQFWPPR PLWAGVQWHDLGSSQPPPGIKQFSCLS CPSSWDYRGERRAVCHH
5531	19432	A	5574	253	363	YHSNQCVGRLRWPGAVVHACNPSTLGGR GGWMIRSGA
5532	19433	A	5575	1	132	MECHYVAQAGLELPGSSDLPASASQSTG ITGVSHCANEGFFFFF
5533	19434	A	5576	18	378	TPGGGGCIEPRWHHCTPAWATRAKLSYK KKKKKKK
5534	19435	A	5577	21	232	ILRCTTIETLLKVQDNHLNPGGGSCSEP RSHCTPTWARERDSVSKKKKGGGAALW DPGGGQPSAGSQTR
5535	19436	A	5578	377	2	LSLIQTITLCLGATTLFAAVCAVTOND IKKIEAFSTSSQIGLIIVTIGINQPHLA FLHICTHAFFKAILFMCSGSIIHNLNNE QDIRKIGGLLKTIPLTSTSLTIGSLALA GIPFLTGFYRTRG
5536	19437	A	5579	2	227	IESWLEPVRFLRSMFANNLVYDTSDD YHLLKDLEEGIQTLMGLEDGSRRTGQI LKQTYSKFDINSHNHVDAA
5537	19438	A	5580	113	3	NFPFFFFLRQSLAVAQAGVQWCDLGS LQ PPPPWFKQ
5538	19439	A	5581	184	3	IMPPHSRLSPTARFCLQKKTNNNTPIE MASIQCPGWSQTPGLKPPSCFVLPKCWD YRCE
5539	19440	A	5582	381	3	FFFFLGDRAAPPGGGEKNPLGGGLKTPGKP PGWGVSPPPQKKKMPNFPFPGKKKS FGGGGPIFFPGKNFPPTQKKKRGGGG FFFFKKPGGFFFFFPFFFSFFLGLK SFIKISFKRRRG
5540	19441	A	5583	314	389	FSCLSLSSWDYRCVLPHLGNFLYF
5541	19442	A	5584	131	1	FPLWTSEQGVGRNKQTYVTWQADCKENA GGDYWTFFPQPTFV
5542	19443	A	5585	484	3	MTEILLKQAMVGIVGSIGSAIGGAVGGG ASASGGTAIQAAAAXFHFATGGFTGTGG KYEPAGIVHRGEFVFTKEATSRIQVGNL YRLMRGYATGGYVGTGSMADSRSQASG TFEQNNHVVINNDGTNGQIGPAALKAVY DMARKGARDSNSAGDQIFHH
5543	19444	A	5586	136	48	NTMQPGVVTHTCNPSTLGGQGGRTGSG R
5544	19445	A	5587	306	479	DSFFPGVGSALFYQVAAVVTTYFKKRV ALSTDIAARSEMLTFLAPFTKFLIDVC DW
5545	19446	A	5588	201	2	ILETGFHHVAQAGLNLASSNLPASTSQ SAGITGVNHAWPSFLIQGTHKHSFKNSK PVFHIKLSKN
5546	19447	A	5589	30	477	TPSLARGVYPCWLYTGFLHDFLSPKIE ERFMDVGLRATBPSNSLFAIYSTPIE LAIKSWHIIGDGLSIELVAVERGNRTTI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						ISRLPEFEKSSLSLSDQSLVTLTSGYFAVY RVKLTAKKLEGIHEGAFQITTDYEILTI PVKARNALC
5547	19448	A	5590	208	91	KGHFWVTGKKKVPCCPPRFFFFFLDGI SLCYPGWSAVV
5548	19449	A	5591	325	467	ADLCSPCDILQDFRHIRKTVDTLLALG EKAPPPTSALRSRDLISFCF
5549	19450	A	5592	332	403	LSLCVXHTHTHTHTHTHTREIFTY
5550	19451	A	5593	292	26	FLLDMEGAEAGAEGLGLYHCLLCAWETPS RLAVLQHLRTPAHRDAQARRLQLLONG PTTEGLAALQSILSFSHGQLRTPGEEE GTGE
5551	19452	A	5594	387	51	LKKIFLGRGQGVSLFFSPPLGGPGGRFL GLEIGALFGLPGKTPPPFKIKKNYPGLW GGALFPLPLEGLGGKMAFPRKGGAPFSQ KNPPPPPLGGKTKPPPLKKKKKKKVL
5552	19453	A	5595	88	362	AETSPGQGSYQDGLRRPGFAEGPPAGR PRRKTQTDRRGGSAGSQPQACADGVRL CTRLQCSGAI SAHCNLCLEPGSSDCPASA SRVAGIT
5553	19454	A	5596	92	366	DQWPGQLPGRSPEAGIRGGSTSRKKPQ EEENS DRSPGRQGI PASGVGRCAALY QAAVQWCHLGSLLQLPPGFKRLSCLSLP SSWDYSH
5554	19455	A	5597	3	138	TRPRTRGVGQAGLELLTSSDPPTLASQS AGITGVSHRAPQSSS
5555	19456	A	5598	150	3	SCVIYSWMKFFSFLRWSPTLVTOAGVQW CDLSSLQPPPPRFKLFSCFG
5556	19457	A	5599	148	3	TOHLNLAKKSQITPGMVHSAHAGRQW CDLGSPKPLPPGLNRASCLP
5557	19458	A	5600	195	1	MVYFKKFCGFFLFVRSRIACSAVQVGMQ WCNHSSLQPRTPGLKQSSHFSFSPRWN RHMQPCPGA
5558	19459	A	5601	228	415	VNVSIPKDVFLLIILFFFGPAPQAGG RGCNLNSLLPWPPLGKQFSCLTLPERSWN YGLPPP
5559	19460	A	5602	405	2	AATGVDRHAQRTQAGLPLKTPQTPCPNF TSKARGTPSAQHPSCTRQRHQASNPTQR RRRRPQAEHSIRTDHAGPLPASGHMAG ERPTRKAQSRDVS VLRQLALLPRLECT SAISAHCQNLTGSGNPPVSC
5560	19461	A	5603	3	236	RQENGMNPGGGACSEPRSRHCTPAWATE RNSVSKKKGIKIKGHCSAMHHQYLSPF GWRQVCSHCVCPKPWLLVRGH
5561	19462	A	5604	184	2	RPFLRIQKKIRMFSGSRFIFNFILETW SHSVQARVQWCHRSSLQPKPLVFKSSS YLLP
5562	19463	A	5605	261	2	GWFLKGPPLFLGPKKPGGLGFFQKLV QKNPPFFGIGPPKNLKTPLFFFFFLRR SLALSPRLCSTISAHCNLRIPRTSNS PA
5563	19464	A	5606	134	2	GSPPKNLVFFLGQSLTSPRLCSTIS AHCKRLPGPHQSPAS
5564	19465	A	5607	3	269	RQESHSPGGGGCGEPRSRHCTPAWLAT ERDSVSKKKRKNFLNFIGKKKPCLP KPKLTKKKKWGGITLVLYKRAIAPK TGGY
5565	19466	A	5608	36	380	PPFXPPGGGETFGGTGPRGPPPKKKKSPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KRGGGGKKKPPRGAPPKHLGGKNRGG GTPPPPRKTPPLNPKKKRGGGKRGVFFP PKGGIFQKRGFFFSRGGGGGAPPHPPPP GGG
5566	19467	A	5609	3	411	SSRSRAAALFYFFFFSRRGQKEKEPFLG GKTTPVFVFFPGGVGKKNRGFPFPPAG KGPFSGGGGREQTPIWSPPPPGRKMGK PPKVTNPNFNLGRVGLGKNPSPGGVC PPPKTPIFFFGRRPPPGGFVWGGGG
5567	19468	A	5610	364	483	ISWVLFLLFLKWSFVLVAQAGEQWRGLG SLQPLPPGLKGF
5568	19469	A	5611	399	285	GGCSEPKSRPCTPAWGTERDFVSKKKNK NNYLVKKSN
5569	19470	A	5612	408	3	KEVFSFPPGLEHGGVFYSLPPLPRVKG FSPPPPPGGGGPRGPPPPGYFLFPKK GGFPPLPGGFSSPQIWPPRPPQKVGVP GAPRPGPNFFFFFFFRESFFFLARGFPKK KKKTCWNVTISHSASVQSSVLL
5570	19471	A	5613	1	112	LAQHVFLLNTSISPADSSELLMEVHG NGKRPSPER
5571	19472	A	5614	2	389	FVREGERRKKEKRKKEKKEGTKEKKE EGRKERKKEKVRKKTVDRRRPQVTFQA VNLESEGAPGNCGTAPPGGHIWLKQVE VQTHLENRCHRLKATVTITTRPGAEPRS PPFIITCGEIMNVFSDM
5572	19473	A	5615	385	3	KPPFGDPGKTFFFLKSQKITGGGGGAPL FPPQKVKAKKRGYPRRQSFKRARLGPC PPSRGGKKKAGFKTNPPTKKKNQTKKPM KAKTSKLLQENRSGPGTVAHACNPSTLG GQGWIMRSGDRDTK
5573	19474	A	5616	218	402	RSYSFSQLVGTVIKARKPESSCWLCPN RKNAFWPGAVAHTCNPSTLGGRGRIMR SGDGD
5574	19475	A	5617	2	235	KSFGCASRLQMHGRTHTEKPYCKQCG KAFGCPNLRHGRTHTEKPYCKNQCQ KVFRCSQLQVHGRAHCIDTP
5575	19476	A	5618	347	421	IYLXXXXXKKKKKKKKKKKKQKKKK
5576	19477	A	5619	92	1	ENLALLPRLECNGTILAHCNRLPGSSD SP
5577	19478	A	5620	3	402	APPPSFFFKGLIMASPTLGAIKLINF LFFPKGKKKKKPPLEKKKKKKKKGGGA PLKKKKFSPPGGGRKIFFGAPKKISRA RVKKQRRGEKTRGNPKKKRKKRPPFN TVSR
5578	19479	A	5621	420	3	HPPPGGSANFFPPPRKIGINGPPPPAGI IFVFLECRGFQVGGGFKIRPPNKKPPP PPPKNLGLQKKSPPPPPIFFFFLWRWG LMTLPRLVSNWLKQSSHLGLLKHWDYM SEAPHLAKNFLKEYEVVLSLHFVEGS
5579	19480	A	5622	246	132	EVAPHLLGCTISPTMCVCLCVCVCVCV CVCVCLCSW
5580	19481	A	5623	219	424	ILNVMLVIGTGFGRLLGLEGRALTNGIK ALIRDMGPGAVAHTCNPNI LGGREGWI MRSGGDHHPQH
5581	19482	A	5624	32	454	GLEKVHSMTXDRNSRLSVQLRDWDGGGE LLQFSVHLGDGTAYSLQLTAPVAGQLG ATTVPFSGLSVPFSTWDQDHLRRDKNC AKSLSGGWFGTCSHNSNLNGQYFRSIPQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1. 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QRQKLKKGIFWKTRGRYYPLQATTMLI Q
5582	19483	A	5625	166	2	LFGLVKLTALKGLKMLPSQVWMLTPVI PTLWEAKAGSQGQEFETSLANTVKP
5583	19484	A	5626	120	406	GEAATQENLAELRPEPELLSPSTVLSRE PELPSPSTVLSREPELPSPSTVLSRKPD LLSPSTVLSRKPDLLSPSTVLSRKPDLL SPSTVLSRKPDLLSPSTVLSRKPDLLSP STVLSRKPD
5584	19485	A	5627	324	16	LSPPPPFLKFTAPRPQKKNPPKKKKPAP PKKKNLFFFFFFFLVFFFIWCSWRLAE WNETLGECDMRWGQAVGTGTSRELPGG SRSQPRRLAGKELGPHCAP
5585	19486	A	5628	378	72	GRGGERPPPPQKSGAKKKPGVLPFPQR GKRSGPPGPPGFFKIFSQBAPGFFSSFF WGRSLALFPPSWGARGGFLVPANLGPPAG APKGNPPSKKKKEKIED
5586	19487	A	5629	3	204	QESCLNMGGRGCSEPRSCHCTPAWATEK DSVSKKKKKWFGGFYEVIGNFLHLFPK WSYPSPFRIF
5587	19488	A	5630	177	1	SFHEMRFWKLIFIRIYVHFERRSCPVP QSRVQWHDLGSLQLPLGPKRFSCGLL SNW
5588	19489	A	5631	154	3	KWPMGSRSVTQAGARQCDHSSLRPPTP QLKRSSCLSPGGWDYRHVPPC
5589	19490	A	5632	239	17	EGVRNYLILQPRSLCRLNCSFFPNREKE LCHHSSFSFPLAAAKESQGEKGRLLSQD EGLLVVEVFVEDVEINS
5590	19491	A	5633	2	110	GCSEPRSHHCIPAWVTEGDSVSKQPPP QKKKCIAG
5591	19492	A	5634	433	0	FFFFFFFFFLKKIPPEGGGF
5592	19493	A	5635	306	433	FSISIERSSSGRAQLLTPVMPALWEABA GRSRSQEIKTILAN
5593	19494	A	5636	2	285	QSRTSVIFNSEKAERGESTTEEFSEAR GWLVKFKERSCLHNIKVQSEASADVEA AASDPEDLAKIIDEDGYTKQHIFGQALC LMSNPTTLGG
5594	19495	A	5637	160	1	LYCGKIYVVKFIRLNFFLSQGLTSPKL ECTGTITAHCSLKLISPSNPPARAA
5595	19496	A	5638	3	261	KIQLNPGSQGCSGLSLCHCSPAWATETL SQKKKKKNPPFGFKIKGEIBPLREFGTK KKKGGFLKKFPPHPLGFFLEPFTWGGFW N
5596	19497	A	5639	2	121	SELRSCHCTPAWRQSKTTSHKKKKNIKK KNKFPLPFREN
5597	19498	A	5640	370	180	VEMEFCHVDQSGLELLISGDTPTSASHN AGITGVSHRTWQPSFFSFKERNLKS V TSLNVSP
5598	19499	A	5641	254	1	FYILRKVFVFLFPAVSYGKGTIFYAVDAS YSAKDTYSKPDNSGRKHMVVRVLTGVF TKGRAGLVTPPKPNPHNPTDLFDSVTNN
5599	19500	A	5642	292	106	NFVILFYLFKQGSYVAQAGLEPLSSSD PLATASQRAGITSVSHRAQTQAEITYV PFSLFT
5600	19501	A	5643	3	100	DTFFEVEVEMEKEVCRDLMCTSPKDEEG FLLI
5601	19502	A	5644	1	282	EKVPEAKRLYGKRGDPFYEAQENHNLI VANVFLECLFCDVKLQYAVPIISQQGEV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						STGQPWRTMVVQVFCFGLFWFSYLSV LEVDQETKAN
5602	19503	A	5645	142	67	NKNRPGTVAHACYNTLGGQGGQIT
5603	19504	A	5646	350	213	GLELLTSSDPPASASQSGITSMHRPW PPLASRLDLCCGTYLI
5604	19505	A	5647	3	180	EHNAERAFLAQAHLPAGPCTPGFPST PTQFPFRSSGLPNIPVQTIISRAAAEKL FG
5605	19506	A	5648	366	1	RSWFTTYKERSLLHIKQVREASADIE TAASYSEDLAKITHESGYPKQIFNVDE TAFYWKMIPLSTCIAREEKSISGFKASK DRLTLNLGANAIGDIKLPKIVVHFKTP RALKNYASSL
5606	19507	A	5649	1	355	QIQSSQSGKGLLLTSFIDEETKLEFFGN KVVFCIPPGEGGKLCFKKKKIFGLYPGG GGFWGPQTPLAPTFFPPGFPFPPGPNFS PRGPFPMGPAALRGPGKKKKPEKTKPA KGGTGP
5607	19508	A	5650	348	124	RAPPVFFWVFLGQFPKKKSTNSPRGGP PRSFQPFSLPFFFRNVFKKKPPFFFBG GRGPPAPPFKNPFFFFSRL
5608	19509	A	5651	194	43	KKKFFFFFYEMESHVPTQAAVQWHHLS LQPTPTTFERFSLTSLIAIP
5609	19510	A	5652	27	244	KKQOSTLFLFYFLSFLFFLVKTGSHY AAQAGLELRASSNPNTSVSLPKSWDYGH EHTVPSPTWFLAAKTP
5610	19511	A	5653	38	429	GLFLSCLFFFFLEKGVPLTPPGATGENP APKKKGTGQKLLKNRDFLLKAMFGKQK QKKFFAPTITGDQAPRVFKGPGAQKE PFAQKKKERGGGKTRAAPNKKKKPGAF FSLKKTPLWAGGGPPPPF
5611	19512	A	5654	391	68	NLYPHGGVPGVSPGKSLPKAPNPLGGI PPSGEPPPLEFPQGFPCLPKPKRLGKAP GPFFFLAILLGWFIQISNTDSCVQVFI IQTIWIIIFTIIGKCHLHFTFLF
5612	19513	A	5655	159	34	GARLFFSPVLSPLTEHCVCVCVCVCVC VCVCVCVCVLCACMCT
5613	19514	A	5656	88	388	SIFCFIYVFFLRQSFTLVAQAGVQRDL GPLQSPQKKKGKETFSLGENRYLQPK NFFTFLTQVCFFEKIPPNGLINGKRPKW IPGCEFLKTLVVGPPV
5614	19515	A	5657	176	371	HFYFCFSDINLAAEPKVNRGKAGVKRSA AEMYGSVTEHPSPLRSGLTLLFTTAL CPSVGIFSF
5615	19516	A	5658	3	113	CSEPRSRHCTPAWATERDSVSKKQQTKN LSYKKIHW
5616	19517	A	5659	409	67	SSSNKPPTRPVFILPFFGHGVPRLPFGK KPPGPPPPPPQVEQMYGRKGGFALNL PPRRQNKNNMLYSPELGEK
5617	19518	A	5660	2	377	GRISCSRNTPLRHRSMLIVCGLRMLPS GFLPWVGQVFLALIPVNPQPSLGVRTI MDMLRCCRDFIYGQFWGFMARLWGACS QQYTEFFRFKIIIFISSLLFNIVLEVLR AIRQEKELNGMLQ
5618	19519	A	5661	256	381	NFNTGQAWMLPVLAIWEAEAGESRGQ EIETILANTVKPHL
5619	19520	A	5662	19	313	LYSSLAILGFLPLLINFIIIIFFFFER DPGQQNQNFVSLKKRETPPPPSLGVPG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid- residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KRSLLEPPPPGPKHAGPPVLPAGLWGGPE PPTWGRGAKQKREI
5620	19521	A	5663	78	365	ETGRKRKETRWNLKKVCLLKMSLQGEKE ERKREKYRRTEMKRQKNSKQRGREKSK KSKYQRRRKKEKKGENQTKPKPKVESS SRQ
5621	19522	A	5664	159	28	DTSTLPTPTGFKRFFCLSLPSKWDYRRP PICLPNFFFLVVTGY
5622	19523	A	5665	350	151	IRCLCPDKFLAFCDGVLCCSGWSRTP GLKRSPPCSLPSKSWDHRLCLADIYYIF LKDTSTIMSF
5623	19524	A	5666	394	248	LTPGGGGCGKRLRLRHCTPAWATRANLPL KTKKKRKRFLFLAETSKVY
5624	19525	A	5667	1	194	RLNPGGRCSELSRHCIPAWATRKLH LKKKKKGDOGFRGDHTKNIWLFPRVFLP LHSLNLTk
5625	19526	A	5668	2	312	RGONSARGIIIIAILKKVCVYIYRCGLT LSPKLKCRGTIIAPCSLELMGSCDPSTS ASQIARTADMHHHTRLIIASLTFCLLKK KKNVFCGTYNHCPPKGFYL
5626	19527	A	5669	1	245	RLNPGGGGCGEPRSSHCTFVWATRVKLS LKKKKKKRPFFFFGIRQPPQGGPFQTL TPLNLLKNLTLLGAKKFFFTGGK
5627	19528	A	5670	1	135	ARTPSPSLSESEDEKPTKKHKKGKALR LKRRFWVVLMSALPCIH
5628	19529	A	5671	97	2	KKFTHVWPGVVAHACSPSTLGGRGGRIT RLN
5629	19530	A	5672	362	173	VFSPPPPFKTPPPPKKIPPPKKKKTPP PKKKKLFFFFFFFFFFFFFFFFGTRIVIDN ILSGNRV
5630	19531	A	5673	237	13	SPGGGGGFAPYWMFFLDFERQSCSVAQA GVQWHNLSLQSPPRFYFFSRDGVKNR VPVRYAPSPKGISLRPYK
5631	19532	A	5674	245	14	ANFLKAHIVSTLGLQIIWSLLQLLNFAI VFYFLRQSFAVAQAGVQWRDIGSLQPL PPRFKRFAQRFSWEAEVAVS
5632	19533	A	5675	2	249	SHPTSHPOHLPLTPTWNWSSTPVDIF RKAPPVFPWHQHRAGPGTSLIPTDAQ EASPPPPYSSPSTPTIPRETFLRQ
5633	19534	A	5676	115	241	SSTLGGQGSITLAQELRSCHCTPAWATG QDSISKKKKTLG
5634	19535	A	5677	460	2	RLGVTGRWQKLKPQERMRAWRENGKGP ALPASWEGPTVNLLWKHEHRAWVSCD SGFCAWCQGLGSEQSLPSLIPSWDGLV LTSFNPNTGPPPLKTRSVLRGDDVLLP CDQPSNLARALWLLNGSMGLSDGQGGYR VGVDGLLVTDQ
5635	19536	A	5678	2	346	ENCLNSGGEGCSKLRLCHCTPAWVTERD SITKEKKKNFKPVLEKGEIFFLKGWK FFQLNPLKSSKEMEFTNTLPLEPCFNG NKPFWAAKIWTLNFFQTQKGSI FKWGG KK
5636	19537	A	5679	181	4	PKEVRTLFGRFFFFFHESHVSVQAGVQ WCNFSSPPPPPGFKFSLSLPISWNS RHM
5637	19538	A	5680	549	410	FFVQTDFFCHVAQAGLQLLSSNPASAS PKYWDYRREPVCWPSSGF
5638	19539	A	5681	111	403	SRQINGFFVSRKVAIGQFLVGPSVKI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FENNNEICMIKSIQSYIVLNHKLKVYS SNIWQLKNILLRGGAVAHACNP SILGGR GRRITRSRDRDHP
5639	19540	A	5682	189	3	NNNRKASWKKKDRVLLYCPGCNWCGLGS LQPLPPGFKRFSCLEKPKCWDYKHEPLH PAPHV
5640	19541	A	5683	2	227	IHVCVCVRVCVCILREDSAQPARCVCVC VCVCVCVCCLDPRELSPTSQLESSCH PLYVPSGGSRINRPPYGGC
5641	19542	A	5684	318	421	DVPCFPVAFCCDCKFPEASPAMLCESM KPLSFI
5642	19543	A	5685	213	398	SLCCLLFCCCYFETESRSVVQAGVQWHD HSSPQPGPPRLKSSSHLSLWRHDHSSPQ PGPPRL
5643	19544	A	5686	398	1	SFPTSSSTYSSSVQGGGQGAHSYKCTAP TAQPHDRPLTASSSLAPGQVRVQNLHAYQ SGRLSYDQQQQQQQQQQQQQALQSRHH AQETLHYQNLAKYQHYGQQGQGYCQPD AVRTPEQYYQTFSPSSSHRE
5644	19545	A	5687	2	288	SDRPRSFPSPFPSSPAGVGRASSIPFPL SAILLLGGVCVAASRVYKSKRNIILGA GILFVAAGERQREGATGAHLGAHVCVC VCVCVRARARA
5645	19546	A	5688	314	2	CRPGSQLQELGDGGGGESFVGGHQQHP GAPQGRYQLPLLMCGASPHASPRQPLA ILAAGVKFRVLRHEAGRPLRLLMQINPL PYSRVVHTYRLPSCGLCTCI
5646	19547	A	5689	122	3	MGGGEFSKKNININGQGVVAHACNPSTLG GRGRQITRSGV
5647	19548	A	5690	144	1	EAVKKYTCPTWAGAVAHACNPSTLGGRG GWITRSRGRDNNNGKHGEIPR
5648	19549	A	5691	377	65	LGVFPPFFFLRGEGLSPPPPGGLVKNQF FFPPGQKGPFGTPERGFQFLGPKFFPP LPPQGPKGIFFLKKKKKKKIPICALAVL TYQHFCYRTGQERVDGLREL
5649	19550	A	5692	12	147	YERRFCHIGQAGLELLTSGNPPASASRG AEITGVSYHALMRNIS
5650	19551	A	5693	183	395	GHRFGFLHPPPPGFGGFFRPPPKTEGK RAPPPPPRFFFLGCGGFGSGGPRGVLF LEHENPPPGAPKGVG
5651	19552	A	5694	177	283	THFLNRTDGRRWLSLASLSSGYGTNTPS STVSVSA
5652	19553	A	5695	266	460	LSQRKYAFFFFFFFFGKKIFFSSPGGEI RAQFFLTEPSPFWVKGFSLPLPKTWDY IGRDPPPLG
5653	19554	A	5696	1	412	MQPLKVNLLQKNLGLFVAPFTWIHCP SYWSIAYNVYFSQYSFIWFTCTMFITVN IPSKKKKKKKKKKKKKSSSPGSP GYAPKKAPKNKKK
5654	19555	A	5697	379	0	FFPPSQKKKKKKKKKKK
5655	19556	A	5698	1	187	PTRPPTFRFENGVLGGGCGEPRLCH CTPAWVTERDSVSKKKKKKKAUGGPMF FQKKKV
5656	19557	A	5699	374	0	DFLQKKKKKKKKKKKKKKKKKKRGG
5657	19558	A	5700	219	413	PFCPQGGGGPNFVFLGPPPPGLKEIPP PPPRGGKKKPPPPRGGFFFFKKKGV PGGGSPP
5658	19559	A	5701	381	249	FHRAGQDGLDLLAPGSAPLGLPKCWDYR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						REPPRPAFFFFF
5659	19560	A	5702	382	197	LANFCIFSRDGLPCCPGWSGTPGLKQS AHLCLFKCWDYTHKPPCPAPQVIKPSIN ILIVN
5660	19561	A	5703	1	381	ERGSKHPPRGLKHIRGRTCFVLKGCMIQ LCVVPPGQKKKKEGGGKKDKKREEE GREKKKNGNQGERVKKKSKRKKKKRSS SS
5661	19562	A	5704	291	167	NGPPFFFFFLVKMGFCHVGQAGLEFLTP GDPPALASRLGL
5662	19563	A	5705	367	23	KNPCPPPPPEFFLAPKKKGPFRKTRF VPPPLFLIKGPPFKRGKGGPPGGFPPLF CPLGKRGGVFLSPRVGKPRGKGNPLF PKKKKKKRRRRKKEGKKGRKERQYIH TV
5663	19564	A	5706	411	116	FLKRWGSYAAQAGLELLDSSDLVPSAS QSAGTGTGVTCHSRLSYSALACQLCPVW RIPWRGRGVGRETSFRGWGRRYGRWSS SGGGAESLPGLSPG
5664	19565	A	5707	162	2	SYCFPNSDDFIPFQPLPHTWFLWPRPFF IFKTAHGWARWLTVPVLPALWEAEAG
5665	19566	A	5708	1	416	LPLLYKIPPPPAIFLFLIKDSPPPPPPP PPPPPPPPP
5666	19567	A	5709	403	142	LSKEKKWGWPRGFSPIFEKPPPPKIFF APPRKKIIPPPPGKKKFFPKGAPPPFFF FFFSFFFFFDYCNSSTWNSAWHIRCSI SIC
5667	19568	A	5710	339	461	PSTFILFILRRSFALVAQGGVWRHLS PQPPPPGFKRPA
5668	19569	A	5711	408	42	TGARIIFSGPPKKTYPSPRAFIIISFK RAAPQLIYFYLNLFAVKRLVLTIVIMR RRPTFFLLLPKTLFVVEPGFCHVAQAGL QFLGSSTCGSLPQCWDYRCEPQHLAKRS TFIKSESAY
5669	19570	A	5712	277	9	GVCVCVGGVVPPMGLQTPSAPWGLSLA PPLGTLCSVQWLAESIHLICQALVEPL RRQLYQVPVRKLLASSIVSGFGDSIWN GSYLR
5670	19571	A	5713	411	0	FLQILLFLIDIAFFLVFFFFFWKK
5671	19572	A	5714	205	400	HYLIQSSSSMASESQLDVVMKIPLTWP GAVAHTCSPSTLGGRGGRITRSGDGDHP QOHDEAPSL
5672	19573	A	5715	1	89	FFFFKTESRSVAQAGVQWCTLGSLQPPL P
5673	19574	A	5716	176	392	GVHLVLEWKLSMVCAEDDELFPPLCSWKK FFFFLFLRQSRSVTQAGVQGRNFGSLQP LPPGLKRISCLTRPSS
5674	19575	A	5717	1	89	FFFFKTESRSVAQAGVQWCTLGSLQPPL P
5675	19576	A	5718	306	42	GSGLRRCALNSVKCLNTLECIILGIYLR QIKICVYTKTCTCKFIVTLFIIAKKYEY PSVHQLINKMWHIQIIFLVIKRNEGCGG SCL
5676	19577	A	5719	1	263	PTRPGRFFLILGDRGSELKSCVCTPAW VTEGDSISKQNKQVELRSPAHLGLGL VPNRPOASTRIGDPCTKKLLELISKFSK AAA
5677	19578	A	5720	3	278	NQEILKNVESSRTVQPHFLEFLLSLGWS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VDVGRHPGWTGHVSTSWSNCCDDGEGS QQEEVISSEDIGASIFNGQKKSMHIKQ IKYFLSH
5678	19579	A	5721	127	3	KKKKKKKEEEQGGRRRRRKKKEKEKK EKBEDGEGKEKGE
5679	19580	A	5722	204	96	VTSRSSLFSTPGIKRASCIGLPKCDYR PQPPHLA
5680	19581	A	5723	3	261	QIVRQWKYNDDDDLFYTRVYLDPLGR VGKAEWAHPAALWEWRPQAEWDLGSKG GCKEKNVCLGVVAHACHPRLLGLGRRI A
5681	19582	A	5724	134	358	PPPPPPXLLFFVSAVPPSPSPSLFPP HRPCYSPSPSTLSSLPPPLFPFPPSSP PPPPRPSAPSPSPSPSPSPSPSPSPSP
5682	19583	A	5726	248	470	LLNVQNGIRNVCSCPHYTFPHKVVKYL S VFLTEVDSSQLRRQLCGGSOAIERMIH FGRKVKQILHLALYFLV
5683	19584	A	5727	1	281	NQHNRGFFDSCDGFFTNYNWREHLERM LGQAGERRADVILGVDVFARWNVVGGRF DTDGKGGGFLSKGQRPSASPSTSPFHGP SIPVCTSKE
5684	19585	A	5728	460	3	SQTRTLTLDRITLPSGGTALISLVDGS GNPVSVEVQSVTDGVKVKVSRVPDGA E YSVWELKPLTLRQLRFRCSIRENDG GT YAITAVQHVPKEAIVDNGAHFDGEQ SG TVNGVTPPAVQHLEAETADSGEYQV LA RWDTPKGGPVT
5685	19586	A	5729	70	465	SQCSPHHSVLCQKQVQDLESGLTQSNW KK ITPWDENVCVCVCVCVCVSMCVYV CV YVCLCVCVCVTVMCMVCLYIKGLL FLA KKETAGSFFHSQTLCLGVPCAPT IHPVP FLPQCRSHCVSGGRFWGVL
5686	19587	A	5730	281	427	SWLTAAPNPLQMESRSVAQAQAQWHD L GSLQAPPFPQSAETQKQMI
5687	19588	A	5731	418	194	TKFHHVGHAGLELVTSGLLSSASQSA R ITDMHHCWSPASVLSMNRPSGSTRCL RN GIFGLPKDKFPNDLTQ
5688	19589	A	5732	229	2	PGGAPPLVRSGFPFGWGGAPPFVFPN GE PPKNFFFFFDGVS LCRPGWSAVAG SQT ASSTSRVHAILLPQPGIVA
5689	19590	A	5733	435	138	PPRYPPFLWGAPPHLSRGGGSFTPLTP Q GKPRFFLKIKINPGGGPPPYSPFPGG GG PRNFFSPGAKPLVLISPLFFPPGDQ KK NSFKKKKKERERE
5690	19591	A	5734	113	409	KDVCQGVLTGLSGVLTSPPEYNNPN SM ECHWVIRAGPAHVKLVPVDFQVEG NEE CTYDYVAVLGGSSPTPVHQYCGS ISAPY LFFLAKNIMSYSLEN
5691	19592	A	5735	3	122	GGWQVQFVSEPCSLSINGVIFGLTST DL LFHLGAEEISR
5692	19593	A	5736	14	428	FLALRWGHIRLPASGPRDTATLFTLDT QLLMTLYVGKDETGFYVSKALVHTGVAL VPRGLTLAPADGPTTDEVTLQVSGEREG SPSTAVRYPGSGVALPSQWLLIGHHELP PVLHTTMLRVHPTLGSGTAETRPEN
5693	19594	A	5737	415	1	QHINTLGGQFWTTKAFLEPRMLELQNG HIV CLNSVLALSAIPGAIDYCTSKASAF AFM ESLTLGLLDCPGVSATTVLPFHTS TEMF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QGMRVRFNLPPLKPEVARRTVEAVQ LTQALLLPWTHALVILKSILPQAA
5694	19595	A	5738	335	152	GVEMGFHHVVOAGLEFLSSDDPPASASQ SAGITGVSHQASPFPLPLSGITLPLSIY SSGSD
5695	19596	A	5739	35	462	IDASDFGECSQAAINDNVVIVYELLEEM VDNGFPLATESNILKELIKPPTILRSVV NSTTGSSNAGDTLPTGQLSNIPWRRAGV KYTNNEAYFDAEBIDALIDKSRSTVFA EIQGVIDACLKLSGMPDLSLSFMNPTLL DD
5696	19597	A	5740	429	325	NPGGRGCSELRSHPCTPAWVTEQDAILG GRSGRIT
5697	19598	A	5741	344	423	FWPGAVAHACNPSTLGGRGGRITRSR
5698	19599	A	5742	431	103	RGPFPRPRQKKGSGPGGPPQNKKNKP PLHTGGAKGGSFFKKKKKKVPPKGGPL FFPGPQGRKGPVGAAPPVLIPIRLGPPR IPGWEPRQIIFLAPVFFPSKPK
5699	19600	A	5743	31	224	EEMGFYHAEQADFELLSSNDPAALAFQG AGIASMSHCSWPGKNFMFCCIWKMKRL AIHWE CIA
5700	19601	A	5744	217	400	HSVGGSPSFFFFFFFFFGEKGLFFFCP GGPNLGKGNPPPPGKKGFP PPPPKGGN NGAPP
5701	19602	A	5745	4	455	DGLEFPGRFRGRQRCSSPFRGRGQVEA LLTSQTGRGRGAPHVSDGRRGRDAPH FLDGLVAGKRRSSLPIDGGRRAETLLTF QTGQPRGAPHVDDGRPGREAPHFPDG VAAGORLQSRHFGGQGRRLGGGCIEPR SRHCTPAWAP
5702	19603	A	5746	381	212	PRGGGGGRVSPPPGGGGGRNSFVPGGGG LNKPHFGPCPPPGGPKMKPPPQKKKSL
5703	19604	A	5747	334	432	MFCENYKELAWPGAVAHSCNPNTLGGRG RHITC
5704	19605	A	5748	190	1	IPPKKGLNFFSPPTPKKGVKSKPPQK VFFFLRRSFTLVTHQGVQWRDLGSPQPP APGSKHE
5705	19606	A	5749	425	297	ESAFHHVAQAGLELLGSCDLPVSASQSV GVTGMSHHTRLYCS
5706	19607	A	5750	425	0	KKKQKKKKKKKKKKKKKKKKKKRT KSDE
5707	19608	A	5751	136	3	AQSSRPALIFLFLVETGFHNVOAGLE LLASGDLPTSQVPRRP
5708	19609	A	5752	3	237	GCSEPRSRHCTPAWVTEGDSVSKTNKQK TQRLKLSIALFPPIHSLPVIKLAMPI LAMDIFFPHIVEFSYHVWQM
5709	19610	A	5753	1	358	GDRGCSELKSCHCIPAWVTEQDLPSKKK KKKKGKKTTRNGPQTCCGDLPPPPLGGG KNFPKGETFWFHSGKKRFFSLGKGEKC FFIFRAPKGPCKTLGGPNRGGGAKKKLK RPPGFPVY
5710	19611	A	5754	2	191	QGCSELCSYHCTPAWETRAPVSKKKKP KTKNQTKKNRLGKKPPNLIFFPFQKKKK WVQIPGK
5711	19612	A	5755	42	408	KHAAPPASLSLSLLHHGQKRACFPFAF CRDCQFLEGSAMLPVQPAKLTFRSTPP HPCSLENDSAHFFN
5712	19613	A	5756	179	410	LQAFLRPSPPVLFLLYADLSNQNLPWGM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VARACNPPTTLGGRGGRT
5713	19614	A	5757	166	2	GRPGPADFRVRPQLLQRFIFYLFTEME SCSVTQAGVQWCNLSLQPLPPGLPD
5714	19615	A	5758	334	3	EEKVFGLPSPILLKSGQGGAGSGPPCPI SPRAMGPQKKGWETMVFITKAPPSGPFV LVKQSPGTGPVPRNFFFLRRSLALSPR AGVQWRDLGSMQAPPFGFTPFSCNLN
5715	19616	A	5759	373	470	SSCWSLRNSSPGAVAHACNPNTLGGRGG RITR
5716	19617	A	5760	210	384	EALDTTIFFFFFFFETKFCFVPOAGGQGO NLGSLGAPPTGLTPFSCLTLRKTWDCGP PP
5717	19618	A	5761	257	400	SLGSEYTWVCFCVFETESRSVGVQVQW CNLSLQPPPPGPKRFSCLR
5718	19619	A	5762	400	2	ARAVGSVGEDEPLGTGSPARETWAV VCRACRGSQLLWGLFILRHWDLRKVLA RNGTDECLKQLWSQCGAGMGRGPPQGL KGKPVGCLCSSREVFYLFYLFDRDRVSL CHPGWNAVKQTRLTAASASQ
5719	19620	A	5763	34	440	RVRAPLGWEEGNYFVLRAPRSGKRSCL PFLRCGHQEPILLWGISTASPLRHLVGAS QICGVFLCFQVSLKPAGSWKVIGNNG ERKAQRLCPLRATRVEGIFCFRFFVFLRW SFTLVAGAGVQWRDLGSLQPPPL
5720	19621	A	5764	297	468	LVGAGVPTGCGQRNGVNVSHKSVQAQWL MPVIPALWEABAGGSRSQBIETILANMV T
5721	19622	A	5765	1	205	GFKLTDSFASGAKAILRSQQLGRLRQEN RWNLGGGGCMGLKWHNCPPAWAIEGNLL FKKKKKKGGGTF
5722	19623	A	5766	307	1	KERDPPTTFFGKTFFFFFFFKRNFCFFPP KEGQGGILGPRHPPFSRLSFLGRGVPRG PPPGPRNFFFFWILVKMGVPHVQADFK LLTSGDLNKTASQNAIGK
5723	19624	A	5767	2	319	LLNGEELSRRFFQRSSQAWVFESSAGI FGGKAGATGLEKLTGSFQQLTGHPDPT PEELGDPEKSSASEKTRGLQEANGVPEI LKAVTYTQAWPEAKVDPIITP
5724	19625	A	5768	787	1118	EAARELEAERQALQSOLQREQEELLAR RKAKEQLSEBIAALQEHDEGLLAES EKQVREPWRLCCSLSCSSSGAGPCSA TWQLGALQATALLGASVSLPAGGED
5725	19626	A	5769	2	452	NGAGTMSVSLEADENPFAQALKSEDCF ILDHGKDGKIFVWKGKQANTEERKAALK TASDFITKMDYPKQTQVSVLPEGGETPL FKQFFKNWRDPDQTDGLGLTYLSSHIAN VERVPFDGGLNLTFTAMAAQHGMDDGT GOKQIWRIG
5726	19627	A	5770	2	130	GTQGIKIVDLVKELDRDTVFALVNYIFFK GKWERPFEVKDWKS
5727	19628	A	5771	422	8	HIARWGARAPQGGWALLKABLCLNPAPP PIGARTAPLWPGCCFSLRPVFLLLPFPF SLFIQSFRILYPQWPPLQGRRTTLRSM GTTDHVIVLASTNRADILDGALMRPGRL DRHVFIDNPTLQERRKCMRRLGASRN
5728	19629	A	5772	432	3	YSLNLKKRWVFLTHNSVHYKSSSEKSA KLGTVVINSLCSVVPDEKIFKETEYWN VAVYGRKHICYRLTYKLLSEASRWSSAIQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NVTDTKAPIDTPTQQLIQDLKENCMTSH VVEQIYKRKKILRYTHHPCIAAAVEDHD ND
5729	19630	A	5773	20	432	SRAAALLEAVTETLFYYEVAEKIWSNRA NRQCADCGSSRPDWAAVNLGVVICKQCA GQHRALGSGISKVQSLKLDTSVWSNEIV QLFIVLGNDRANRFWAGTLPPGEGHLHPD ATPGPRGEFISRKYRLGLFRKPHPO
5730	19631	A	5774	433	2	RGAFQTLQKKDLQAFVLSSVQLQVLTGS CFKLRTVHNIIPVPSNKVDDECPLGYGFL HVI VHPAKGFKQSATLSCALEVDSFGYF VSKAKTRVFRDTAEFKWDBEFIELEGS PSLRILWYEEYNKSKVNNLYSAAVGFS AWQ
5731	19632	A	5775	133	436	MLISLPHPSTHLTSLFFCADFGTRQTG AASHVLTLSAHSSVCSPPLMGATTSR AQDLPADEHTAFAPHELEAPALSKGQGLS ILRALTGHLPLGQEVNL
5732	19633	A	5776	397	58	KGTISIGKLEEKLRGAARQALADAIIEF QLLPASLCTEDTPTGMQVRSLSGRECH RSKQDSVAGERAKVGFGRSTSENYIIRT TYSQLSVSLSGHHPGATLAAVNGCSCSP T
5733	19634	A	5777	1	324	MRRCVSAGGVELEYYPAFLDMVRSMLE GSIDPTQYEDTLREMFTIHAYVGFTMDK LVQNIARQVSRAVGPAALRTAEMALPSF HSPLGRRGPVVSTANLSCFFLIETK
5734	19635	A	5778	1	398	RLGSRPPLHDQSPLELRSEIQELKGDVK KTVKLFQTEPLCAIQDABGAIHEVKAAC REEIQSNAVRSARWLFETRSLDVINQDP SQVRLIRGISLEEGARPDVSAIRWIFDT QSLDAIREILVDEKDFPPSP
5735	19636	A	5779	281	12	VACNLGWRVRTPTPASYPFCVPQLSVRG KNRKELLGGFLRNIVKSADREALITGMSG LKEVDDFFFEHRTNLLEYHTLYCGRSED HATSR
5736	19637	A	5780	406	23	DSQATGPGISRGRRISSPSSLCTRFSTS IVKCSPLEHVLKYLDPPTTRCSRPA LRSSPKHCVQQQFIACRFGAAAPPPPP AQCNPNGPAAASARHEPKWGSRTGEGPA RARREGTGRRKKRR
5737	19638	A	5781	415	18	TSQAGDDLHGSLLRRGPEMGYLPFYDP DPTLATPPAGQTLAVPSLPRATEPGTGP LTTAVTPNGVRGAGPSAPELLTPPGTT APPPSPASPGPPLGPEGGEEPPPTII TTTTVNTVTISPMYCGRSEG
5738	19639	A	5782	168	432	GMRRQTGLDQSGRVGKNWRVDFFPSS LSFFFFFGKESYFVLKFGIHLKFGYL EPLSPGLKEFSRLSPPKGHLKCRPPSP LFFF
5739	19640	A	5783	1	423	TDDDLNWLDSRTFREQGVDENETLLLR RKFFYSQNVDSRDPVQLNLLYVQARD ILNGSHPVSEKACEFGGFQAQIQFGPH VEHKHKPGFLDLKEFLPKYIKQGAEK RIFQEHKNCEKISERSAKV
5740	19641	A	5784	273	400	DSVLLMLSPGVCPHVQWPISCTLGAT FGYVAGLVISPLWI
5741	19642	A	5785	445	28	DTNRAPNHMEIKSGSGTEAKVNGADSID

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KEAAGDETMEARTMEAEATGAKPTGVEA TGAKVTETKPTGAEVREMEESTEEANME SKPTGAQATDTETTGVEAMGVEATKTKA EEAEMQAYGVGAGQAEPPVTGTVLRPL
5742	19643	A	5786	380	2	QRQQESPEASSLHILEROVQELQQLLVE SQEEKESLGREVESLQSRLSLLENERGN TSYDVTTLQDEEGELPDLPGAEVLLSRQ LSPSAQEHLASLQEQVAVLTRQNQELME KVQIMENFEKDECI
5743	19644	A	5787	663	2	FGVERRATRTIRLTRTVLDLYSFLAGVS ENLRHATQDDASRTRAPGLSSQHPKPD TVSGDTETGQSPGVFNTKESGMKDISE LAEVKDTLKNKSKLEELDGKVKGYEGQ LRQLQEAAGQPTVTMTTNELYQAYVDSK IDALREELMEGMDRKLADLKNSEYKLT GLQQQCDDYGSYLVIELIGEKETSLR KEINLRARLQEPSAQANCCDSVY
5744	19645	A	5788	398	1	TRCYHSALRYGGSFAELGPRIGRLQQAQ LWNPHTGSCQHRKVLPPLEQVWNLHL EYKRNYGAKRGCPVKRAAEPVVPVQVP PAALSGPSGEEGLSPGGKRRRGCSQET GLPPGLPLPPPLPPPPPPV
5745	19646	A	5789	116	371	RHPKIWGLRGPPGLTLEKRGKEEPLDP RSWGFKEAETPPRPFTRGKGTPLRKKK PKERKTRERGGKKEGKKKGKNEGKTNP L
5746	19647	A	5790	406	284	RRGFFHVDQAGLELPTSGDPPTLASQSK PGPLCPALLHTF
5747	19648	A	5791	200	3	GDALIYMEPEKQVMSRSSDECVVALCDQ WLVSYSKKIPLVNLTLFDLKKNISICPL PGTWIMEMY
5748	19649	A	5792	372	278	LQIQSPAGQSRCCGFLVREDFVLTAAHC WGR
5749	19650	A	5793	1	167	VAPPKLDPHSGRVRAQAGLELLTLCDPP ASSSQTAATGASHHTRQVLGSYKALS
5750	19651	A	5795	112	3	SSWGKVGAGAGEYGAEALERMFLSFPTT KTYFPHCI
5751	19652	A	5797	356	238	FLFCNNGVYSLEHFRCLAENAGDDAFVK DVTVLQNTDGR
5752	19653	A	5798	379	60	VKIRHCHTMVMSLLKNIRLILEEEQVE GNYSFCVLDNQNLQQLWDWDHRSLLTKA GKMYFAFNPRLCVSEIYRMEVVTGTRGR QSKGDINTRSNNGHRASCE
5753	19654	A	5799	377	3	KVAFPGEGRQGESWSAFQGHTRVVS DLK WAVYEPDLMTSSVGTYIYIWDIKDTRK LTVALFVVAGASQVKNKNANCLATSH DGDVRIWDKRKPSTAVEYLAHL SKIHG LDWHPDSEHNLY
5754	19655	A	5800	143	316	CPTSPFRLPYTEFFGGVSGLTVEQFRKI NGFPNAPFWGGGEDDLWNRYLCRSFGV F
5755	19656	A	5801	390	2	LFFFFFFFLRQSLTLVQAGVRWRDLSS LQPPPPGFKRFSCLCV
5756	19657	A	5802	342	465	VIFFFFLKQGLTSLPRLECSGTITTHCG LDLLGSSESPTFT
5757	19658	A	5803	1	378	VYSSEFENIKEEYRGRGFPTICYFEKGR FLIQYDNYGSTAEDIWEWLKNPQPQ VPETPWADEGGSVYHLTDEDFDQFVKEH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						SSVLVMFHAPWCGHCKMNPFEKASEA LHGEADSSGVLAHV
5758	19659	A	5804	152	1	KPEIFFFESRSVTQTGVQWCFNFSLQFP PSGFKLFSCLSLPSWDYTAHV
5759	19660	A	5805	207	31	LYLQLLQQTASSGNLNTLSLHPMGGKC FTAAEEQHPGQQTQLTTVLGVWHRFCE NIF
5760	19661	A	5806	199	2	GSECSCLLSRGGRMHVSLSSPKVTFSCD AIIHFSPLFFWRQEPSPVQAGVQWRDLG SLQPPPPGV
5761	19662	A	5807	385	239	QDQPLQKMCVCVCVCVCVCVCVITC KSCIRLSYMKMPINFGKLN
5762	19663	A	5808	39	184	GRIIKFFGEMRSHHAAQTGLELLGSSD PPTWASQSAITGVSLRIRP
5763	19664	A	5809	376	2	WAEPTSFFHVCITSYTOFFRGLTAFTRVR WKCLVIDEMQVRKGMTERHWEAVFTLQS QORLLIDSPHNTFLELWTMVHFLVPG ISRPYLSSPLRAPSEESQDYHKKVIRL HRVTQPFILRSV
5764	19665	A	5810	271	120	FLCFIGKTSESGSFLYSRDTGLPGQV SLMIKKSNEVMFKHINKGSINR
5765	19666	A	5811	367	3	DKSPKWHKMLEDANAPTEERDERIAGL YEEIERDLMLLGASAVEDKLQEGVIETV TSLSLANIKIWLVTGDKQETAINIGYAC NMLTDDMNDVFIAGNNAVEVREELRKA KQNLFGRCI
5766	19667	A	5812	294	37	FRGENPDDGVRGSPPEYRLRQVASSLF RGEHHSRGGTGRLASLFSLEPQIQPVY VPVPKVSHPAFFPNSLEPLTYKAIFLP TA
5767	19668	A	5813	184	3	IIISYLNKYLFSPLQRQNFVLLPRLECS GTITAHCNLKLVGSGDPPAPASQVARTT GMRH
5768	19669	A	5814	468	1	DDMEYEGSVSVFTQVPRKSVNKGDLTYL MVAGEFGLGKSTLVNSLFVSDLYRDKL LGAEERIMQTVIEISKHAVIDIEKGVRLR LTIIVDTPGFDVISTECGRRAMY
5769	19670	A	5815	24	314	QAPFGPKCFNVNLCFSLSLSKGEPEFHY IAGAHGNEVLGRELLLLLVQFVCQEYLA RNARIVHLVEETRIHVLPNLNPDGYEKA YEGVMALAHLTQ
5770	19671	A	5816	474	3	TTLRKGYSRHKGLLHSIRQEVQATPLEG IIIVSGQMSTMNLSSTLWSPKRVRLCI GRTLRLRIRPCKRTPLQTRMPQKMRA LYGDPGDSFPLRSRAIPASSPGSTGSFR ARPPHPLHPPHPLTREGEPPPLPVLPQR RGPPPLPLHSQASRPV
5771	19672	A	5817	511	389	GMCTEGREVVPTRFNEIEIEEDHCGRV SASIIILTHCSNR
5772	19673	A	5818	510	2	PLSCEVPNPLFPVPGVRMIQHIEACAQ VRGMQEIIVLIGFYQPDPLTQFIEAAQ EFILPVRYLQEFAPLGTGGGLYHFRDQI LAGSPEAFFVLNADVCSGFFLSAMLEAH RRQRHFFLLGTTANRTQSLNYGCIVEN PQTHEVLHYVEKPSCIAAAIEDQASSRQ R
5773	19674	A	5819	282	152	FSLFLFLQSERHFMQVVCATQCPDT RVSRLYEKSVLHLS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth' od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5774	19675	A	5820	347	1	EPHEVTPPAVGTSRYNPLIMDRNRSAV TPPSHPPQQPSSMQTGMNPSAMQGPSPP PPPPSYMHIPRYSTNPITVTVSQNLPSG QTVPRALQILPQIPSNLYGSPGSIYIRQ TKV
5775	19676	A	5821	482	13	IYEKLITGCYNILANHADPNISGLDESIL EECLQYLEKQLESSQARKAMEEFPDSG ELVQIMMATANENLSAKFCNRVLKFFTK LFQLTEKSPNPSLLHLGSLAQLACVEP VRLQAWLTRMTTS
5776	19677	A	5822	608	7	FRFAEKVVEGMFIIVNSITIKIHSKAPH ASFELWQLQGYSVNPNWQSDLRRLTRIT DPCRGEVLTFFEITWQTLRIEADATDNG DQDPVTTPLRLITNQGRIQIALKRRTKD CNVSSKLMFLDDLLWVLTDSQLKAMM KYAESLSEAMEKSAHQKSLAPEPVQIT PPAPSAQQSWAQAFGGSQNSNSSSSPV LRPL
5777	19678	A	5823	328	3	AEVASEDCSLPCFLAVWNRIIEPVAAMR KEADMLRLFPEYLGESLFGTLVHAVLR IAESLPGVESCQNYLFRYGRHPLMELPL MINPSGCARSEHKILLTHYKRPSLY
5778	19679	A	5824	69	308	TSVPSCVRCRYIILRTSSALTNILGTHS NSSFFHASSALHSCCFPFSSWLQTLDI NVKAPALMTKAVVPEMEKRGYRE
5779	19680	A	5825	424	2	LQRAFSEIRKLRGYQGADRKQIYHRR SFANHSVRPSADEKCNNSFFEQRHGGSH QSSKWTVPVGPAPSTSQSQKRSSGLQSGH SSQRTSAGSSSGTNSSGQRHRESYNNS GSSSRKKQHGSEHSKSRSSSPGKQTV
5780	19681	A	5826	107	2	SSLTAGVRMGVPAQSTQGTVNGSSPQMS GTAALTS
5781	19682	A	5827	2	437	FPTEDSRTSKESMSEADRAQKMDGESEE EQESVDTGEEEEGGDESDLSSESIKKK FLKRKGMTDSPWIKPARKRRRSRKPS GALGSESDKSSAGSAEHIGPCDSTGDM VSSGLPGSRRPENPVFLCIWVAVRAICP GFLWS
5782	19683	A	5828	487	22	MPEPVFPLSHFRQFIAAIKLOFQARLSR CVRDLVRSIAAPNHDTRLMLFQHLCRVI EHGEQNRMSVQSVAIIVFGPTLLRPEVEE TSMPTMTVVFQNRVVELILQQCADI FPPH
5783	19684	A	5829	2	871	RGICSRWRREGSQSRGFLVITSPSGS LVTASSAQTFPIAPMIVSALPPGSA LQVVPDLSKKVASTLTEEGGGGGGGGS VAPKPPRGRKKRMLSEGLPEMNDPYVL SPEDDDDHQKDGKTYRCRMCSTFYSKS EMQIHSKSHTEKPHKCPHCSKTFANSS YLAQHRIHSGAKPYSCNFCESFRQLS HLQQHTRIHSKMHTETIKPHKCPHCSKT FANTSYLAQHRLRIHSGAKPYNSCYCQA FRQLSHLQQHTRIHTGDRPYKCAHPGCE KAFTQLSNLQ
5784	19685	A	5830	463	1	LPESRLPSPHKREEGSRARVIMTSYPT PHERKGLADVVATLQKQKLEBEMTRTE QEDSSCMEKLLSKDWKEKMERLNTSELL GEIKGTPESLAEKERQLSTMITQLISLR EQLLAAHDEQKLAASQIEKQRQMDLA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: In USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						RQQQEQIARHQQLY
5785	19686	A	5831	462	2	MILFDSSLYFLCGWYLSNLI LGTYGVRK PWYFPPTASYWKS VGFVLEKROYFLSSS LFFFNENFDNKGSS LQNREGELEGSAPG VTLVSVTK EYEGHKAVVQDLSLTFYRDQ ITALLGTNGAGKTTI ISMLTGLHPPTSG TII INGNLQTVY
5786	19687	A	5832	396	2	VPSTPASKRKGIVPRCDIFIYDRGGALP KDIHVAGILFASAWMNWVPLLSAIEFHS AWAMGMGVNFFVASTHHVSLNMSGSGRY APNGRKVYHYDMKTEMGELLSEVD SHP LSSLAYPTADNWNAYATLY
5787	19688	A	5833	384	137	EEICLNPGAGGCSEPRLWHCTPAWATKR DSSKKKEKNCLSKNKEKEKEMFACVVCV CVLFSIYAFPSKAQELSNPCKHYGNF
5788	19689	A	5834	171	2	FVEGINISGNFYRNKLYLAFLRRKMNT NPSRGPYHFRAPSRI FWRTVRGMLPHMY
5789	19690	A	5835	278	404	SVLIKFEKTKLYKAIWP GAVAHACNPS TLGGRSGITRSGE
5790	19691	A	5836	417	3	SKGKEGRCEWQYDLPSGTHAVFQFLKQ QGRVPGLTQAVQVAKMSLIDLASERAS STHAKGERLREGANINRSLALINVLNA LADAKGRKTHVPYRDSKLTLLKDSLGG NCRTVMIAAISPSMTNEDTYSTHV
5791	19692	A	5837	409	230	AGRAYCYNGMCLTYQEQCQLWGP GKAL LGSTALPSPPLPSQPLALRVVWNLGFK WHL
5792	19693	A	5838	3	409	LRSVPCDYLTQNHYITSPLEEEAAPP LAYVMVIHKDFDTFERLFRAIYMPQNVY CVHVDEKAPARYKESVRQLLSCFQNAFI ASKTESVVYAGISRLQADLNCLKDLVAS EVPWKYVINTCGQDFLTTTRPV
5793	19694	A	5839	385	174	GLAVEIGSRRIAEDGLELLASSDPPTSA SQSAGSTGVSHHAWPDTVSSVYWCFLCC TKQVVVGALSIVSL
5794	19695	A	5840	260	2	PLPRYTAACSRLLVQYKAAPRQVQGEI SSIDEFCRKFRLDCLAMERIKEDRPIT IKDDKGNLNRCIADVVSFYITVMDKLRO CI
5795	19696	A	5842	299	3	FSGIKYICIFLFCVFFLYLLGIGSPYV AQAGLTLLGSSDPPPSASQSPGIIGVSH YVQPIHTVAQLSPSSI FRTFSSFTETV PIKHTSHSPSPSLY
5796	19697	A	5843	391	2	APHAPAFLRARGEPODPLSHPRVPAVSA NCRMWKHLPVHSSPTPRLTPLWKLQARW LLPQLVYLQGWGSYSLLRPAALISMVLL AREFLYPAKMSVSEVCSSGLSSP LLEQH KTNLI FYASGDIC SANV
5797	19698	A	5844	479	59	FVGMEPGVGHASLAMHGLHRSLOKIKL RKRKCTLPFNTQEKSAARRGHLLGENIY LLLFAIALRILNCLLVQTSFVPDEYWS LEVSHMVFNYGYPWEWTERLRSYAYP LICASIYKVLHLLGKDSVQMLVSGNKSS
5798	19699	A	5845	406	548	SVQTKFFFE TESHVPVQAGVQWHNLC SL QPLPCRSKQFLCLRLPSSW
5799	19700	A	5846	2	394	TLCHRAKDPTVHHESGRIMYLNGLCFLM GPAQLTORLSVSRQGE C
5800	19701	A	5847	472	201	LSILSDTSLCLGRFFTYBNGCAYFHEE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						REGIARICRLSIHSRYEDFVVDGFNVLY NKKPVIYRSAPARPGLGQSLCNQVMWYQ VAILNK
5801	19702	A	5848	127	3	SSNVKAAWGKVGAGHAGEYGAEALERMFL SFPTTKTYFPFCI
5802	19703	A	5849	238	1	MAETHPNPTGLPLAPALPCLAGSATHPC LFSPEISLDVDADRDGVVEKNPNPKVPS FQGRHHPEPRASEDTAPDPAGMY
5803	19704	A	5850	423	2	LSPLGNWSSANQKVVDVSVKPSRKDLFA VDTQVGTVPVSLTAGEQGGFDGKGGRAGE QATQAAGDWSSNMWGSGLSHSAPLTV PQPLLTGPQGPCLCRPLPNQQTSPALL PFSTQLCSMCPCGPASARPPPLLLKPTMY
5804	19705	A	5851	326	682	PSYSLLSLLQVKNEVEKLPRQQRKESMK QKMEHTOKKQLLVSPWPQLGSAGAGAR PGMVTRPPLCLCPAPQIPRSEYLNLA SSFMAPLSPPPCSLHRLSCLHLEVRNSI SGYPNCI
5805	19706	A	5852	263	30	HEKTDDERGPQGSARSGAITKPPGPPLP IEPHETTPPEHPAPSGTIPEPPLPVELHE TTPQHPVPSGTIPEPPYLLSQ
5806	19707	A	5853	389	2	GLPTQREKFGASMRTRMTIQSIADVTSF VCLVGEENNVOGFRASRCRWYDPRHNR WFOIQSLQOEHADLSVCVVGRIYAVAG RGYHNDLNAVERYDPATNSWAYVAPLKR RCMPTKAKRWRGRCISP
5807	19708	A	5854	379	2	GRSLRYSGSCSGEENSTNNSAGQSRVAVI AAAARRRGNSHNEYYYEAEHERRVRKR RARLVVAVEEAFTHIKRLQEEQKNPRE VMDPREAAQAFASMARAMQKYLRAAQ QNYNTMESILQHC
5808	19709	A	5855	374	2	SDAGAPVNIYEFRRHPQCLEDTKPAFVK ADHADEVRFVFGGAFKGDIVMFEAGATE EEKLLSRKMMKYWATFARAGNPNGNDLS LWPAYNLTEQYLQDLNMSLGQRLKEPR VEIWNSTIPPCI
5809	19710	A	5856	516	18	PYECKECGKAFNCGSSLVQHERIHTGEK PYECKECGKAFSRGCHRTQHQIHRGET PIKCKECGKAFSWGSSLVKHervHTNEK SYECKDCGKAFSGYQLSVHQRFTGEK LYQRKEFGKTFTHGSKLVHERTHSNDKP YKNKECGEAFWTTYSNEKCIASAK
5810	19711	A	5857	392	3	CERGMGGSFPRALGRHWTSFLKRLNCSV PGDSTFYFDVLQALTGPVNLHGRSALFG VFTTQTNISIPGSAVCAFYLDIERGFGB KFKEQRLDGAWTPVSEDRVPSPRPGSC AGVGGAAKFTSSRDLLY
5811	19712	A	5858	391	3	ARRTTGMVPKAGGGKGRGAVFRSYIRE TEELRSKLVSEAMNESLRRLSRASDR SPYSLGASPAAPAFGGSPASSMEDASEV IRRAKQDLERLKKKEVRQRKSPKBAF KKRAKLQEQENSEETNGE
5812	19713	A	5859	409	3	SLPGGDPFWWAGQEEELLFVQEGKLSLPV AERVLLRIACRYDPRNSNWAELAPMKNC REHFVIGAMEEYLYAVGGRNELRQVLPT VERYCPKKNKWTFFVQSFDRLSCHAGYV ADGLLWISGGVTNTAQYQNRQCI
5813	19714	A	5860	405	135	NLSRLSLCRQPMTLVTWVLLFYDSEKA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						FWLLVALWKRMLPDYINTRVVGECPRVL PRLGLQVPAGSMRVAALPRPSSRLHVGS LGVRG
5814	19715	A	5861	389	2	YYSELEEQLTDEFNAELNRVPLKRLDLI FVTFQDSRMAKVRVKDYKYVQCGVQPPQ SSVTITVKSYWVMTMAPHPKDIWKHL SVRRFPWWARFIAINTFLFLFFFLITTP AIIMNTIDMYNVTTRPCI
5815	19716	A	5862	525	0	SHLPESERIHTTVGQKEQVMDTSKTRP NNDVPEPPMPIADQVSNDDRPEGSVEDE EKKESSLPKSPFKRKISVSVSTKGVPAGNS DTEGGQPGRRKRWGASTATQKKPSISI TTESLKSILPIDIKPLAGQEAUVDLHADD SRISEDETESKGGDGDTHDKGLTIC
5816	19717	A	5863	399	2	ATRRNRNRVPSGMTRTNVREMIAAVGGP PSPYPLPPPPEGTSSIEYSNQGNTCOGH GNFDFPHGNPGGTSMDNFMHGPPLSH PDMFNMMMALEKPI SHPMQETMPHAGSS DQPHPSMQQDKARNTPOPMY
5817	19718	A	5864	3	714	RRPFFIALCLSNVAFMLPWQFAQFILFTQ IASLFFMYVVGYIEPSKFQKIYMMNIS VTLSFILMFNGSMYLSYSSSLMTWA IILKRNEIQKLGVSCLNCWLIQGSAAWC GTIILKFLTSKILGVSDHICLSDLIAAG ILRYTDFDTLKYTCSPFDFMEKATLLI YTKTLLLPVVMVITCFIFKKTVDISRV LATNVYLRKQLLEHSELAFHTLQLLAFT ALAILLRLKLVL
5818	19719	A	5865	423	1	APPVSTAVAQSNSEEEAREVGSQAQEF KYQKSLPPRQRRQQQQQQLYMQHW QPVYPPPSHPQRTFYPHDPQLGDFPRW MMPSYMDPRITPTRTVPDFYPSALHPS GLMKPMMPQESLNGTGCRSEDQNCVPPC I
5819	19720	A	5866	497	2	AVGAGQKGGRGGGGRELMPQKIWGGGA FTNNAHVGLKIMPRILRTGMLEIHL PGVVQGLFPCVDELSDIHTFLSOLLER RRQALCPGSTRNFVIHRLGDLISQFSG HSABQMCKTYSEFCSRHSKALKLYKELY ARDKRFQFIRKVCYCGRCRGSQQGR
5820	19721	A	5867	382	74	LALSRLKCSGQIIAHCSFDLLGSSDPP PSASRVAGTTGARRHARLPYSLRHYHFV LRLFNPSKHSKCLKHFFHPIIRNPGKVGS YSFQMSDLLQSRRARQOS
5821	19722	A	5869	378	3	SFSRSANLIHQRIHTGEKFFQCAECGK SFSRSPNLIAHQRSHTGEKFPYSCPECGK SFGNRSSLNTHQGIRSGEKPYECKECGE SFSYNSNLIRHQRIHTGEKPYKCTDCGQ RFSQSSALITPV
5822	19723	A	5870	375	3	IHVIVFNQATGHVMAKRVFDITYSPHEDE AMVFLNMVAPGRVLICTVKDEGSFHLK DTAKALLRSLGSQAGPALGWRDWAFFVG RKGEABCHWADTELNRRRRRFCSKVEGY GSVCCKDPTV
5823	19724	A	5871	373	1	QPEEVSGALSPPSASAYVKLVLLGLIMC VSLAGNAILSLMVLKERALHKAPYYFL DLCLADGIRSAVCFPVFLASVRHGSSWT FSALSCKIVAFMAVLFCHAAFMFLFCIS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						VTRNMAIAHLY
5824	19725	A	5872	382	2	KSFSQKSQLI IHLRTHGTGERPFCEPCG KAFREKSTVI IHYRTHGTGEKPYECNECG KAFTQKSNLIVHQKTHGTGEKTYEACAKCG ESFIQKLDLI IHHSHTGTGKKPHECNECK KTFSKSTLI IPHV
5825	19726	A	5873	370	3	MGRVRAQNISGVMSGPQKMLMQSQFPTQ GQQGFCEGKEPYQAMSONMNTQDMFSP DQSSMTMSNVGATRLSHMPLPPASNPFG TVHSAPNRGLGRRRSDLTISINQMSPG IGHLNSTTCI
5826	19727	A	5874	362	2	GGKFLVLGNLPSKLEESMVQYYRLVTA SLVRGQISEYNISLRASDGGSPPLSTET HITLHVIGINDNPPTFPHLSYSACIPEN NPRGASIFSVTAQDPDSNNARITYALT EDTLQGVY
5827	19728	A	5875	369	1	RIRPRPTARLASARTLHEVSLQESIRYA PGDAVEKWLNDLLCLDCLNIARIVSVCP LPEACDLSYVNRDTLFWCHKASEVFLQR LMALYVASREFKNSPNDLQMLSDAPAHRL LNKCLLCPPPV
5828	19729	A	5876	119	39	VIQDYTTTPNEELSRDLVNKLKPYMR
5829	19730	A	5877	461	2	RRGWTSSRRPKEDPSGAAPVEMPCKSSK IASFIPKGGKLNKSAKKEPMAPSHSGIPK PGMKSMGKSPSAPAPSKEGERSRSGKL SSGLPQQKQLDGRHSSSSSSLASSEGK GPGGTTLNHSSISQTVSGSVGTTQTGTS NANSVQLPQELCI
5830	19731	A	5878	503	3	PSPQVPGECPSPKILGARAFTTPDPAP LSPQSRVASSGSEQTEBQSSSRNSFQED GSGMKDVPSWLKSLRLHKYALPQMSY EEMMTLTEQHLESQNVTKGARHKIALSI QKLREQRSVLKSLEKDVLEGGNLRNALQ ELQIIITPIKAYSVLQATVAATLY
5831	19732	A	5879	421	34	LVHKVLSASNVLDAGETVKITDYSISK RLADICKEDVFEQTRVRFVSNAMHYRTG NKGDVWRLGLMLSLSQGQBCARYPVAI PSGLPGGFQDFLKKCVCLDDKKSMESPA VETKQNKSPANVLRPL
5832	19733	A	5880	379	3	AQGLLLAWPNLNRQHCPCSCSHNLSTFI QNWKSPGLSLKTRAPGQGSVLSSDLPR AVLTGTFAVMSVMVGSVTESLAPQALNG SMINETARDAARVQVASTLSVLVGLFQV WNSQEVVPPTTCI
5833	19734	A	5881	429	1	SLVSYMDTESTAEKLGKELGLQAKELSA VHSSHHEIGVNDNLFSLEMREPLESSN TKSFHSAVEIKNRSQHLEPCFQHHGIDT PTSLQKRSACCPSSLRLLEETASSSQDG DPQIWDDLFFSES LNKFITVLESEIAVT QCI
5834	19735	A	5882	436	3	WSLVSYMDKSTAEKLGKELGLQAKELS AVHSSHHEIGVNDNLFSLEMREPLESS NAKSFHSAVEIKNRSQHLEPCFQHHGID TPTSLQKRSACCPSSLRLLEETASSSQD GDPQMDDLFFSESLIKFTVLESEIAV TQCI
5835	19736	A	5883	195	353	DSYSYVRSTAPAVAYDSKQYYQOPTATA AAVAAAQPPPSVAETYYQTGGFS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
5836	19737	A	5884	432	1	LSAKVPVASVSDQAAAMHLSQCCKNLAT SLAELRTASQKAHKLCPMEIDSALNTV QTLKNELODAKMAAVESQLKPLPGETLE KCAQDLGSTSKAVGSSMAQLLTCAAQGN EHYTGVAARETAQALKTLAQAARGVAAS TTDP
5837	19738	A	5885	313	1	GKSPHLLILQTSPLSKAPQLILLLLYW SWVGVSVTAAARETEAGIQVSSEEPGP RNVSPHSRLQDETNRLEAENNLAAAYRQ VREVQGRDREGKGLMATLY
5838	19739	A	5886	432	3	GSGFCSPIILCLWWVEEAVGIIRLHLWL ELGCWHSFSLPGTYSLEFLSTCTQVLPY WSGGLLFASGNLYLSYLVPSTRAETDSRG SQPLPVARHGVGACKCKPRQTRPGLSPO VCVEKLMPLSSFCSAFQNTYNKQPMSP PV
5839	19740	A	5887	417	2	ASLMVAPDYAEISPLAMPASSGVVCTP IMSTSSSEAMSTPLMLAPDSGELSPILM QDMNPGVMSTQVPVAPSPFAMSPLOITD EDTEAMSKVLMTALASGEISSLLMSGTD SEAISSLIMSASVSGTSPQPTSTLY
5840	19741	A	5888	420	3	KPDLIKLLDKTMSSYDLDEASDGGGL SGKCSVSVKVLDVNDNFPELSSISLTSP IPENSPETEVALFRIRDRDSGENGKMIC SIQDDVLFKLPSPVENFYRLVTEGALDR ETRAEYNITITITDMGTPLKTEQSV
5841	19742	A	5889	321	414	FNMRIWPGAGAHACNPSTLGGRGGRITR SAD
5842	19743	A	5890	415	1	PGLPGTSVRGIPASKQSPHESPTLHLK TSPIIQQLGLYLSHTAIRVHPQETLKEF VOLVCPDAGQAGQVGFLNPNSSQDKV HNPFLPTPLMPPPPPPMARPVLPVPD TKPPTTSTEGGADYPTSPYSTPSLY
5843	19744	A	5891	193	3	KPSSKVSRRDPFLSSVQPIKDAVIT VPVFFNQAEARRAVLQAARMAGLKEMQLI NDNTACI
5844	19745	A	5892	412	2	KHQVSDNKDSFYVSLYPDFSSLSRAILD VVQFFKWKTVTVVYDSDAGLIRLQELIK APSRYNRLRLKIRQLPVDTKDAKPLLKEM KRGKEFHVIFDCSHEMAAGILKQALAMG MMTEYHYIPTTLDLFDLVEPSV
5845	19746	A	5893	413	3	ELLCSNTSCRCFCVCEVLVGTGTA AEAKLQEPWSCYMLPQRCCHGVLRKRD WVRLQAFFTSDTGLEYEAPKLYPAIPA ARRRPPIRVLSLFDGIATGYLVKELGIK VGKYVASEVCEESIAVGTVKHEWR
5846	19747	A	5894	424	3	CSGRREPSVRGVQCKGDQGHHSARMAPS EAPGTRSCTPSHGQNTAAEATPAQKTPA KVYVVFSTEMANKAAKAVLKQVETMVS FHQNISSSKTERSTAPLNTQISALRND PKPLPQPPAPASQDQNYSONTRLOPCI
5847	19748	A	5895	400	1	ASVQNPALRLVTREFAIMQTPAGELYD KSIIQSAQQDSIKKANMKRENKAYSFKE QIIIELELKEVSTRRLRKVAELGGLKL VAFPTAHMLFTWNILRPMHSSDAPDQC LVVHHTFSPSLLHSFFHPQLY
5848	19749	A	5896	421	3	VSSIQMGAVNLGGGLDSLGLGDLGGGI AGSPAVGQSFIPSSVQATCAPSPTPAVV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SSGLNDLSELSTWIGMAHGGYVAPKAVW LPAVKAKGLESSGTFTRRQGHYIMAMDF TNKALQHMTDSAIQFTKNSFGVIPSCI
5849	19750	A	5897	384	1	PRASRFIHEAGIVPLPMRTHTPKPFPTC EVAGVQFSRNVKVKIHRKHTGERPYSR QSCSVRFVHSYDLKNHMLHTGDRPYEC HLCHKAFKEDHLQRHLKGQICLEVTRR RRRKDDAPPHYPPPCI
5850	19751	A	5898	429	2	QDIAAWQSLTQVLTPESWRKANIMTEPQ KSQERYKGIYVKEKLYRRARHDESLNWT SCDHHSQECKGEDPGRHPNCGKNLGMK STVEQHHVHVLPQPFCTCNCGVAFADD TDPAHPSTHLGEKSYKCDQYGKILSOS LY
5851	19752	A	5899	424	1	GTMLQALAAHDAGSRAHVLSLSQQDGI EQHMDFDSDRYTLLELFAETTSSEHCMA FEGIHLPQIPGKLLFSLVKRYLCVTSLL DQLNSSPELGAGDQSSPCATREKSRGQR ELEFSMAVGNLISELVSRMGWARNLSEH V
5852	19753	A	5900	135	459	YFMLKAEHVISYVCSSENSLMVVNMRF LIGLIHIQEFYFFEMEPHRAIQAGVQWC DLCSLQPPPPGLKRCSCIPSSSRDYRC APPYP
5853	19754	A	5901	418	10	GRSPKPGDRLWESVHLSFPGPADSLSGG SAPASSYEPSQRSSFSNNRSQRGSTSTR NSSQKSSVLSIKQKGRKRELYMEKLQEH LIKAKAFTIKKFSQNLVAQLWYFVKCV YFGLSAYQIPRGYPTVLGNFLTK
5854	19755	A	5902	402	2	GYRHPLEIKSVDFGQGPVKQVILSLV RSNRKGEVGFVEDRRINVDVTRARRLV TVICDYRTVSSHAFKPLVRYFTQHGVE RTAFBYLDDIVPDNYSHEDSQGSSQAAT RPQPGTSTRTKKQREQGMY
5855	19756	A	5903	346	1	GICPLSHIKMTDARCIYEMKGGKESPK DTGKEPGHSEAKTGPPQVLAVPAQPEA PQPGPNTTAAFPVDSGPKAGLAPETTETP AGASETAQATDLSLSPGGESKANCSPED PMY
5856	19757	A	5904	139	212	EVENNDIDSHHHHHHHHSHNSKS
5857	19758	A	5905	2	345	PCGCWGRCALLLISAAKAKSKCGPTFL PCASGIHICIIGFRSKGFEDCPDGSDEE NCTANPMLCSTARYHCKNGLCIDKSFIC DQNNCQDNDSEBSCSSQGVGYVCGFK KA
5858	19759	A	5906	432	17	PQTTPHRTFGGGKAAVLLAVGGQFLLC WSPYFSPHLYVALSAQPISTGQVESVVT WIGYFCFTSNPFFYGCLNRQIRGELSKQ FVCFKPAPEEELRLPSREGSIEENFLQ FLQGTGCPYKSWSRPLPCIAALRV
5859	19760	A	5907	407	1	PYACGECGKSYRQSSSLVSHRRHSGVR PHHCDECGEFSRKYDLLIHQRVHSGER PYKCSRCGKSFHSCSLIAHQRIHTGMR PYECSECGISFIHSCSLITQQRVHLGTR PYMCSECGKSFQSCLIKHRSV
5860	19761	A	5908	419	3	VLAKKTIITKSARDCHEFGNLIHLSTNL VASIQRPDKHESFGNNMVDNLLDFSRSS AENKYDNGCAKLEFFHTEYEKTPNGMKPY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GYKECGKGLRRKKGLSLHQRINKGEKPF ECTACRKTFSKKSHLIVHWRTHGTGVY
5861	19762	A	5909	441	57	KVMGIFKSSSLFQALVDIQEFYEVTLINS QKSCBQKIEEANQVLQKWEKTSLLAPCH DRLQKSSSLQSLIGQHSSLETTDGPQPW LFPRGSEGHGRGKTYDHCHSIGLQIAVDQ RKMLHVLSSKIKKIRV
5862	19763	A	5910	3	317	CLLMLWRRWGSRSRQRRLQATPSWEST KTADGGDRRESGSQRHCSSPHQSKST TTSSVPAAREGAQAAQGGPRKGQTSRP QVSTRQCAMPARHRKLEND
5863	19764	A	5911	183	1	QNSDSKDSLNRVASRDHAKPNLTCHVSP AIQGTGSISESSIPSVSDTSTPRRSRRO LPPCI
5864	19765	A	5912	395	1	KTIQFNICVKVFHFRFSNSNKKDKTRYAGD KTFCKCECGKSPHVLRLTQHKRIHTGE NPYTCEECKAFNWSSILTQHKRIHARE KFYKCEECKGKGFTRSSHLTKHKRIHTGE KPYICEKCGKAFNQSSSTPV
5865	19766	A	5913	449	2	FGSHLEKEDEKKQELVDKAKPSTEATL ESIQRKLQYKRAESSRPEDIKDMTKAQI ANEKVALQKALLYYESIHGRPVTKNERQ VMKPLYDRYRLVKQLSRANTIPITIEEE EGSEADSNVKPDMVNKKTDFSAARMVKR PLGGSARPD
5866	19767	A	5914	464	23	SAHMTETRSKSFYDGSLSLTGFSAPAPV APPARVAPPERRKCFVLRQASLSRPPET ELEVAPKGRQSEEPQSSSKPSAKSSL SQISSAATSHGGPPGGKGPQDRPPLGP TVPYTEALPVFHHFVAQTHKHEKPYLPP LYCGRCG
5867	19768	A	5915	366	1	LVSFINFFTSVLATLVVFAVLGFKANIM NEKCVVENAEKILGYLNTNVLSDRDLIPP HVNFSHLTKDYMEMYNVIMTVKEDQFS ALGLDPCLLEDELDSKVQGTGLAFIAFN EAMTHSPACI
5868	19769	A	5916	246	366	TSVKEQQMPGAVAHACNPSTLEGQGGRI TRSGVRDQPCOH
5869	19770	A	5917	400	3	NDNAPEFYQSVYKVTVLENAFNGTLVIK LNATDPDDGTNGDIVYSFRPVPVAVVY AFTINPNNGEIRTGKGLDFEEKKLYEIS VEAVDKGNIPMAGHCTLLVEVLVDNDNA PEVTITSLSLPIREDTQPCI
5870	19771	A	5918	410	200	CTPPQPVKCRFLNRDRVSSCCPGWSQIP GIKRSSYLSLPECWDLRPVILLFCFLSH ISSKQPYFLPPSYR
5871	19772	A	5919	214	407	MYFYIDRASLLSPRLECIVVTIAHCSLE LLCSRDLPASASQAGITGIRHHTWLKT HFYSSFKT
5872	19773	A	5920	476	39	VPYGLFVGSTGRGLPYLRGTSHPLRGC LHAAALNGRRLVQPLTRNKHEGCAEFP ANDDVALGFCGSHSLAALPAWGTQDEGT LEFTLTTSQWQAPLAFQAAGWHGDFIHV DIPEGHLWSMVEKGQGTVLLLSNVPVTD AQPHM
5873	19774	A	5921	430	2	SLRPSSTGSPSPGGLSEEPAAKDLDNRM PGLVGQEVGSGEGPRTSSPLFNKAVFLR PSSSTMILFETTKSGPALGKAVSEGAEE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AKLGVSGSRPEVAAKPALPTQKPAGTLP RSAPLSQDTKPPVPQEBAGQDHPKAS RC
5874	19775	A	5923	411	2	MSLKVDVEALENSAGATYIRKKGGKVTG DSQPKQQGQVLKKKKKKKKGMVKNYD PKVTPDPERWLPMPERSYRGRKKGKKK DQIGKGTQGATAGASSELDAKTVSSPP TSPPRGSAAATVSASTSNIIIPRLY
5875	19776	A	5924	402	2	LQSGAIMNKFYQPEAHIPYLLQLFIDY NLYGMNLINLAAVKFRKARRKSNLHAT GSCKNHLSGNSLADTLFRWEQDEIPSSL ILEGVPEQSTCELEVDAAVADILNRLDI EAQIGGNPGLQAIWEDEKQRR
5876	19777	A	5925	215	403	AETSTYFFFFLERQFPFAPQLGGHGRNL NSLNLPRGLREFSRLSLPGGWYGGAP PSPTFFC
5877	19778	A	5926	320	1	PGRDRWIWGQGECEYLLASMTQWCER EISSIAPGELCCLLSFLPQEECQNYVR VLIVAGRKVFMCGTNAFSPMCTSRQVGN LSRTTEKINGVARCPYDPRHRV
5878	19779	A	5927	400	1	VVATDGGGLPLLASSATVVALQDVNDNE PQFQRTFYNASLPEGTQPGTCFLQVTAT DADSGPFGLLSYSLGAGLSSSGSPFRI DAHSGDVCTTRTLDRDQGPSSFDFVTVA VDGGGLKSMVYVKVFLSDEMY
5879	19780	A	5928	398	62	HNTEVLVGESVTLCSATGHPPPRISWT RGDRTPLPVDPVRNITPSGGLYIQNVVQ GDSGEYACSATNNIDSVHATAFIIVQQG YPSSVPEPGLSPILTPPLAARAIPDAP
5880	19781	A	5929	403	1	LASDGGDPVLSGTSRICVKVLDANDNAP VFTQPEYRISIPENTLVGTRILTVTATD ADEGYAQQVVFLEKSPGETSEVFELKS TSGELTIKOLDYEDATFHEIDIEAQDG PGLLTRAKVIVTVLDVNDNANV
5881	19782	A	5930	408	3	VASDGGDPVLSGTSRICVKVLDANDNAP VFTQPEYRISIPENTLVGSRILTVTATD ADEGYAQQVVFLEKSPGETSEVFELKS SSGELTIKOLDYEDATFHEIDIEAQDG PGLLTRAKVIVTVLDVNDNANV
5882	19783	A	5931	126	391	PVLTCAPHFHSAGAGGSYFMISRLGPE FGGAEGCLYLATTFATAMYILGAIQIL LVSQAEPWSTLAMIKQFLWTPNRRIMVL IPTC
5883	19784	A	5932	436	359	NKEWLPQSKVPEKSINDVKNTSGLL
5884	19785	A	5933	365	3	LIIGMLTATIGDLASHFGCTIGLKDSVT AVVFVAFGTSVPDTFASKAAALQDVYAD ASIGNVTGSNAVNVFLGIGLANVAAY WALQGQEFHVSAGTLAFSVTLFTIFAFV CISVLLYR
5885	19786	A	5934	394	3	FQYFSRTDRVLKHERMCHENHDKKLNRC AIKGGLLTSEEDSVFSTSPKDNLSLPKKK RQITEKRSSGMDKESALGKCDLKKVKND YSPLYSSSTKVKDEYMAEYAVEMPHSS VGGSHLEYASGEIHPPCI
5886	19787	A	5935	393	1	REDLIAGIDEFLDEVIVLPPGEWDPNIR IEPPKKVPSADKRKSVFSLAELGQMNGS VGGGGGAPGGGGGGGGGGGGAGSGG AGGTSSGDDGEMPAMHEIGBELIWTGRF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FGGLCLDIKRKLPPWFPSCT
5887	19788	A	5936	410	126	PICYYKKAGRARWLTPTVIPSSWDYRHOA QLIFVFLVETGFHRVQAQAPELMTSGDP LAYNFLCSYPNEVFRSQASASDLQFVLR NLEPPDAGNV
5888	19789	A	5937	426	1	DATFHEIDIEAQDGPGLLTRAKVIVTVL DVNDNAPEFYMTSATSSVSSEDSLPGTII GLFNVDHRDSCQNAFTTCSLPEDLPFKL EKSVDNYYRLVTTTRALDREQFSFYNTL TAKDGGNPSLSTDAHILLQVADINDNAP CI
5889	19790	A	5938	438	3	ADPTKGLLRNGSVCVRAPGGVSQGNVSN LKNSKQACLPSGGIPSLNNGTFSPKQW SKESKAEQABSKRVPLPEGCPGSAASDL QSKHLPKTAKPASQEHVRCISAIGTGESP KESAQLSGASPKESPSRGPAPPQENKVV SPVV
5890	19791	A	5939	3	191	YSVCLWSQLLRRLRQEDHLSFGGGGCTE PVVINTERLSKNKTKKREREKQCGFHS WYCNLK
5891	19792	A	5940	399	1	QYSDNDMSWKVTRAAKCLDAVSTRH EMLPEFYKTVSPALIYRFKEREENVKAD VCHAHSLFKQTSVPQSWLCGLDAMDQ GTPLAMLSQSVANIVKAVHKQMKESVK TRQCCFTLLTELNVNLLGAVY
5892	19793	A	5941	411	3	SPCEGPRRFQCKSGKRVDDGGKVCDDVQ CRDWSDELLKVCWCGACLRPLAGLSLLPS PSWYLGSRPSSAPCPDTFCGPGPLGFM RPMASHGAFRPQASGLHLYKVLACPSQ VLKNYVFSHKLGLSSFLPRSDHV
5893	19794	A	5943	431	26	KAVVGIPGDMGPPGIVTRPGYNGLEGNP GVQGGKGEPPGVPLPGLKGLPLPGIPGS PEEKSGIGVPGVPGEHGAIGPPGHQGI GEPGPPGLPGSVGSPGVPGIGPPGARGP PVGGQPPGLSGPLVIKGEVSRVR
5894	19795	A	5944	396	3	PLPVELIRVPAFLDLFMQSLFKPGARIS QDLKHXYIHILAYASVVETCKKNKRVS INKDELKSTSKAVETVHNLCNENKSGAS ELVAELSTLYQCIRFPVAMGVLKWVDW TVSEPRYFQLQTDHTPTV
5895	19796	A	5945	465	32	ERVTLADITVCTLLWLYKQVLEPSFRQ AFPNTNRWFLTCINQPOFRAVLGEVKLC EKMAQFDAKKFAETQPKKDTPRKEKGS EEKQKPPQAERKEEKAAAPAESEMDCE EQAMAAEPKADPPAHMNKSTFVLDDCI AAAL
5896	19797	A	5946	414	2	ATPPVRCIRKEIRNWYVDIQPVQEPKAQ ACGNHGIIIIAETSTGCLFAGSSLGKR GVNADKVAIEAAEMLLANLRHGGTVYFY KQDQLIVFMALANGVSIIRKTPVTLHTQ TAILYDEQIVKVNCKENHSVDEQVY
5897	19798	A	5947	411	1	EPCVVRRRIADSSVQTDDEGESRYLLSR RRRARRSADCSVQTDDESAEWEQPVRR RRSRLPRHSDSGSDSKHDATASSSAAA TVRAMSSVGITQISDCSVQTEPDQLPRV SPAIIHTAATDPKVBIVRYISAPCI
5898	19799	A	5948	153	409	LPFFFIILLPFISFFRYRVGLLSFKLKCS GVIIAHCSLELLGSSNPPTSASRVIFLY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						LSLCLFVFEMESCSVAQAGEQWRDLGSL Q
5899	19800	A	5949	21	447	RAAAMSRRNFRFLSSHRELYFGVDLPSG NLVVREPADREQLCRACAACVLTLDLV EDPLELHKIRIHVLDNDNSPLFPAGDV QLHIPEFLTGPARTLPNAQDDDEGSNG ILSYLSLSPSQHFRMDMGSRVDSGEYPEL VL
5900	19801	A	5950	268	19	QDNWAYCYCTVBYCKTKLNILANWLVIN YLSGDFYFFFIFFLDGVSLCHPGWSAVA RSQLTATSSSQVQGRFSCLSHCIAAAL
5901	19802	A	5951	389	3	QQMDLARQQQEIQARQQQQLQQQHKKIN LLQQQIQVQGHMPLMIPFPDQRTLA AAAAAQGGFLPPPGITYKPGDNYPVQFI PSTMAAAAAGLSPLQLQLYAAQLASM QVSPGAKMPSTPQPMY
5902	19803	A	5952	2308	307	RRRPARKKTVWRDGGPHQGL/YPQLPSA VLQPTQPGHGFRAKGRELESWQGKRP GK/GQTHRRKTRGTASPAVYFSVEWGD\ SGGCPMTGKGAQQRAGLGAAPNPELSG EQGTGRGRAQDSQGHGGGKRRGQHPPG ND/PRGVSGMGQESVHSPEARPTGGGTG /EMLGRTWRHQQGLVGGTGNLLETGSWS GSGSWGRCVLRPQEGQVTGMGLAGR/ YQPARQRAVELSPGAQGLRORRGWSP PQETRQSGVPGG*GSWPLESHQGEQ\PA AGQKQSLQMLEGGFPCCWS/SGMGGGPQQ LLESEGAGPSFGGGRHHGKGRVAVTTTP REGD\RGQSPGGHTLQLFPCPLWS*ETQ GQGSRTVQHQEWGGEGRGEGAGSDQSR ALGIA*ICPHILRPTSMEPQSTAPAPGQ PPGPSPWGHGRHGMGYGGRCPCQ/IQG RGRAQLGSTVG*RDG/QRG*MQGRDQQG PRNGAGVGSCHTSQK*IPPSSLCT*N SSHGPASG\QLWWSSPFIHSPGETNIPH TLTEPHSVPCWCWDTLRRHGAGQGHGPM ARSGTGEGQ/QRGRY*ERGRRRRQQKQ KKQGLKEPG*RAAPTLLKATRPLCRCLR KVQKPKQDGDVGS*LLKVFRAPGALGTK PORTCRGPADFFHALSGLSNVHRSYCST NSGFGACM
5903	19804	A	5953	461	117	HPRDIIGFVHQGLPPSPQPPFPCKQAPT TPSS\M*P*TNRHDGLSGPVQVPGADW KPLNAP*LPELAFGEPCRPQVDPDPYV WLPDSAPHEHCVTWATSPGLSDLLSYPRR KQA
5904	19805	A	5954	845	610	FFETGSY/SVAQVGAQWCNFGSLQSOPP RLKRSCHLSPPSSWDYRGAPPRLARFFF FCIFYRNGVSPCCPGWS*TPELQ
5905	19806	A	5955	1	378	KTPVSDR\ATKCCSESLNRRRPFCSALE AYETYVPKEFNARTFTLHADICTLSDKE RQINKHTALAEVLKHKPKARQEQQLKVM DDFADFVEKRCMADDKETCFVBEG*TLV AASQAALGLLHRIK
5906	19807	A	5956	723	343	GCQEGICSPSPCPVIPATREAEAGESLEL RRRLH*AEIVPLHS/KAQRSLCSSDFI RILVIFSGMFLVFTLAGALFLHQRKRYR SNKGESPVPEAEPCRYSCPREBEGSTIP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5907	19808	A	5957	55	491	IQEDYRKPEPACSP AQHFNPHNWPVT*LLPHFTNEGGQVTRA RCLKWQAR\CLVPMQKVPNAMPQT**PS AEVTPPVCNQHHWPQVEGIPSS/APAFQ WPLTMGHPC\WESAPRQDASTSPRPGTA SHCPSAVAFQERGSSPCPPHSDSGLCL LPRLLPAP
5908	19809	A	5958	2	413	KKPDQ\AE\REHLCTSL\WGRNTDKNG EELHGGKRVMERLKKAVKIANQCMPSL QMQLYIEILNRYIFYEKEYDAGTIQVL NQLIQKIREDLPNLESSEPEQIT*HFH NTLEHLRLRRSPESSEGPPIYEGILLYE
5909	19810	A	5959	871	564	WMCHATFGSHLN*AWRLRPVNSG/LLM/ PSEKAKKESTLMVGVTNPD\MKGKIRL LLHSDGKDEYVWNAGHPDILG\HPLTLQ CPIIKIKKKL**PKSGRTADGPDHSRIK V*VTPLGKEPTTDEVLABGKENME*VTE TC*IDMN*VLQGGTWNLQR
5910	19811	A	5960	390	271	GINFFSRN/RSLTT*SRV*NSNAQVIV LPWPSRVLGFOA
5911	19812	A	5961	333	922	GLSCRVFGRITLSCPPCILRHLSEVETLQ TLQKKEIEDLYSRLGKQPPPGIGAPAA LSSRRRLSKGSFPTSRRNSLQRSEPPG PGIMRRNSLSGSSTGSQBRASKGVTF GDVGRM*IQRSHVSPPHQGPWNLCSQ NLMLSDQON*ARKIPTLKG*KA\GGHGE CSSIIIVKSQTYVNCLLCGGVSSAAYHLH L
5912	19813	A	5962	705	387	CVAQTGVQ*HDLGSLQPLPPGFKQSSHL SLPSSWDYRRVTPRLPNF*FFVETDFC HIAQAVLQLL\SSNNLPASASQSGVTG VSHRARPTLTLDIAEIPDLKPSG
5913	19814	A	5963	425	182	ASNQ*DSVGVGPSEPGAGYNLLVRFKLC \LEKHSSWVGVTQFSRCHLSPLSLTRKG NSLTPTCTSRVRQCLALLWLTHGSRTH
5914	19815	A	5964	388	14	PPMYTQLCSIRSTQAFQVFFSRDE/SL ALLERLVLSWVQAILLPWPPKVQG*QA QWLTLLVIPALWEAMAGGLEPRSSRP ATQDLISTKENKTKSLASDAELCVH WRLKI
5915	19816	A	5965	1	373	DDQRVKSVINLLLAAYTGDVSALRRFAL SAMDMEQRDYDSRTALHVSAAQGHVEVV KFL\LEACKVNPFPKDRWNNTPMDETILH FGHHDVFKILQRYQVQYTP*GDSNDGKE HHTVHKNLDGLS
5916	19817	A	5966	3	329	HEETSRYEIYELIHVHPYAVKQSFLEE YSLSQSTLEQVGHF*GFVSSMVVYKTF PGSCRGSTALFSSLYFLPPFQVLELSK EQELGDFE/EDFDPSVRWKLPPQEEP
5917	19818	A	5967	2	47	MEDRRLVRGIPCPQHNRQCFAVPPGIQ AYGAAPFEDLQVDFTEMSKCRGNKYLLV LGRTYSG*VEAYPTRTEKAREVTRVLLR DLLERFELPLRIGSDNRPAFVADLVQKA AKILRITWKLHAYWPQSSGKVERMNQT IKNSLGKVCQETGLKWIQALPMVLFKIR CTTSKRAGYSPYEILYHRPPPIRLGLPG TP*ELGEIELQRQLQALGKITQTI/YSP SKWPSLFPVHPLSPGDRVWIKNNVA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SLCPLWKGPTTVLSPPTAVKVE*IPSW IHSHVKP*TA
5918	19819	A	5968	2	150	KSQSI*QSSLLSYFEKLPQPPQPSA\TS TSKQDPPLATRLWLAEGSDDH
5919	19820	A	5969	3	371	HEGKSGPMTGVVLVAVGEVAMKILLCL CLILLRVRSCRRKAARAALGMEADAVT D*SPDSRLLPD\PPHPVPPQSERCFLC RLCMVCPLLDSPDPSFPCHTSPQTLRA KDSAALDTLHV
5920	19821	A	5970	396	58	YWVLSKGPVTCMLLNSVFSFQASSCLSF LINS*AP*PGIFLGMSVILPFFVFGVQ AGLELLTSGDLPDSASQ\ARITGVSHCA QPHTALSQYLEQCLAPSRLISVSLILR
5921	19822	A	5971	442	120	ICMKQGLALSPRLDSSSAFNTVQPMPP RFKSSYGLSLP/RSWDYRCTPPHMARSG NGV*P\FMVETGSW*AAQGLELLSSSN LPP/SAFQASAGITSGHCTRPVFLVC
5922	19823	A	5972	459	434	MWPLPWFSISSPSSPPT*VSSNNHPCA VPRAYPGADIPGPGWQRLPPPHRGLSGP PESCLLTTLTLCSKHPNGCPLTQNRSLP GPRPCLITYSTSPSP*P*Q/L/YAAPSP*L YTVVREALIR
5923	19824	A	5973	681	1758	VANKCQIPDIKAKTYICNTKEKRSYLK T*NLHRGF\IKKQIEEFNIGKRHLANMM GEDPETFTQEDIDRAIAYLFPGLFEKR ARPVMKHPEQIFPRQRAIQWGEDGRPFH YLFYTGKQSYSLMHDVYGMLLNLEKHQ SHLOAKSLLPEKTVTRDVIGSRWLIKEE LEBMLVEKLSLDYMQFIRLLEKLLTSQ CGAAEEEFVQFRFRSVTLESKKQLIEPV QYDEQGMASFSEKGRKTAKAEIVYKH GSGRIKVNIGIDYQLYFPITQDREQLMFP FHFVDRLGKHDVTCTVSGGGRSAQAGAI RLAMAKALCSFVTEDEVEWMRQAGLLTT DPRVRERKKPGQEGARRKFTWKKR
5924	19825	A	5974	1232	980	SLSLSPRLCSGVTAHCSRLRLPASSNSC FSASQVAGTIGACHHIWLVFVFLVETGF HHVGQTGLELLT*VICPPWPPKVLGLQ A
5925	19826	A	5975	1	259	LTSYDYRRALPCLVN\FCVYFLKREELA LLPKLFWNSWA*ATLLP*PPKIFGLQAQ VAMRLKFPACLPACLPAYLPPLFSFI PP
5926	19827	A	5976	24	223	PYLTQISTNESSVCSHARAEFLDHQNL /WLGTVITYCNPS/TLGG*GGRIT*GQE FKTSLGNTARPCL
5927	19828	A	5977	395	136	GSWDYTHVPPRSANF/LVETGFRHVA*A GLELLGNPPTSASQSAKITAMSHCTWPS SYY*CEYNARFGSLHKRSGMTIYIKSYK RQN
5928	19829	A	5978	1	785	GTRLKSGTNTKKALQAVYSMMSWPDV PEGWNRTRHVIILMTD/GSEGTLLSQP PHLLRPACGP*VHL*HYTHGWGPECDS* LAVHLSCDPS*GILPKPCDQLSLTLPOL AHPAMCIPAFSQIFLISYPHGPVSSAG LHNMGGDPITVIDEIRDLIYIGDKRNP REDYLGE*PA*DPAPHFLRAWTLILPFY PSDVYVFGVGPLVNQVNNALASKKONE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QHVFVKVMDMENLEDVFYQMGREIQGNK EPNSPQVPLK'
5929	19830	A	5979	2	419	KATAPIDSDSSDGSQGNKLT*KEFIIL NAIKSIYDSWEVKISTLTGVNKKLIPI LIEDFEVFK\ADLVEIARERELEVEGBL /LQSQDKT
5930	19831	A	5981	1	154	KKC*MMLTWCMMPVG/PTPRAEAGGSPE TGNLRL*CTMIMSVNSHCTPAWAT
5931	19832	A	5982	12	311	RKSLNFVEGCNIRLNKCRHTNFVPQTIF FFLLFL*LGQC*VVVVSFFFFFCCFV LFFVVCVVFVFCFCFF/GCLEFVFL /YFVELFCIVIMCYLR*YV*IVYMLF FVCWIFVLYLCFHY*LFLEFFVFVFLF ICGVFVVFYELFCIVIMCYLR
5932	19833	A	5983	3	203	IGQKRASEDTT*GSAD/PKKSSAGPKRD ARQIYNPPSGKYSSNLGNFYERSLQK YRWRLGHTRKS
5933	19834	A	5984	368	138	STVGKMLSGQHPCYRE/IL/REQKSQSM *QISLLSYFKKLPPQFQSATTALISQQ PSASRQNPAPAKRL*LAEGSYDH
5934	19835	A	5985	2	155	LANF*ITYFC/RDKCLPVLRLVNSNWPQ VILPPWPKVLGLQGMSPCAPRHS
5935	19836	A	5986	325	403	FIYFLFLLSSLYLIITYALFLSSF*R*V VYHVMVLLKVVICHFLTLFFSFRSLI LYLFFILFM/YLLIFVLFFIQSFYLPF FYLFFYLLFFNDYCFDLIFFLCLIIYYHF QSYFIS*FIYFLFLLSSLYLIITYALF LSSFSI
5936	19837	A	5987	81	651	KLQVAGCRTLSQIDVKFKPSVHSSLAVC LRANYFTSQPNVIMQVTLTRCVHSHK LGTVSYSWYIKLLFPKSHFIYLFILRR SLAPVAPGVQWLDLQSLQPPPGPKRFS CLS/LPR*LDYRHPPPLANF*FLVEK GFCHVGQAGLELLASSDLPTSASQNAI TGVTPAPSPQKATLNLILGGQFHI
5937	19838	A	5988	301	341	FCFCPCKNRVSLW*WHAPPCPANF*LF IYLFVETGFSHVQASLKLTLDDLPA AASQSAGIPGMSHHDGLFL
5938	19839	A	5989	71	1252	TKEQRSLRSQQLGVRQQRSHRLKFGGGG APSARGVGSWSLATRLGFVSTANMSRP VRNRKVVVDYSQFQESDDADEDYGRDGP PTKKIRSSPREAKNKRSGKNSQEDSED SEDKDVKTAKDDSHSAEDSEDEKEDHN VRQQRQAASKAASKQREMLMEDVGSEEE QEEDEAPFQEKDSGSEDFLMEDDDDS DYGSSK/NEKQKDG*EVQT*KKRKENAQ TQTKGYSDAKSSERQRESGSP\QASKAS KERTPSPKEEDEEPESPPEKKTSTSPFP EKSGDEGSEDEAPSGED*K*WGERFY *KKKEKKRKRREKKEPT*DRTWFWLWL DSWGFQCFPPFVESNISLSLFFFFFFK ANHCMCKCLSYLFVYWSLCQSPFPFMA MSN
5939	19840	A	5990	630	316	RWNVNSVA\QAG\IQWCDLGSTGNPRFP GF*K*FSCLSLLSSWDYPTHTMSSKFL YF*WRRGFTMLARLVSNWLVNS*PSDP PASAAQSAGITGMSHRAQPTIYLS
5940	19841	A	5991	2	182	WQEQKAE/CLRDVWTAMCTAALTIKAG

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						R\NIPCPMMKEWVRKMGPIYTFEYYSAV IMQVILKF*HATGMPDDVISEVCQS QDK*KRILLSCNNAGNS
5941	19842	A	5992	79	278	EAK*RVNGCSKPTWHMYTYVTNLHTYV/ IKPAHCAHVP*KLKYKIIITIIK*RWG LTILPRLVSNWAQVILLPWPPIKILGLQ A
5942	19843	A	5993	22	274	AGDEHRAWGYQPAM*ARLEMTGPGDT/ MPAMASQRAGITGVSH*GCPFFSLLNKI WRSH*VAQAGEQRLFRE*TPGLSCYSCS LPSN*DYTSAPLCPPIYDT
5943	19844	A	5994	347	195	YMHTKHTHTHTHTHTHTHP\EKHLKA PNEV*KSKNNV*IKPKQSQSCFS
5944	19845	A	5995	1	122	RYELEDLHLQMTTQLHALKENNYQLR* SSHSVIPST*GYRHVPSCPANF/SSLTM FPSLVSSCWAQVIHLPWPYKVLGL*ALK ENNYQLRTIIIDCTLNNIF
5945	19846	A	5996	365	229	RPPPCPANF*\FLVETGFHHVGKAGLEL LTSSDLAPALHQVFYA
5946	19847	A	5997	357	17	ILVDKINNWNLFQNNLVVC*RGWGYK* DRSFHLLKTVAAB*WVYEGSLY*SLSSY YLF/C*RQGLTMLPRLVLNSWHQAILLP WPFSLLLCILEVFQNRRELKKNQGKPM GS
5947	19848	A	5998	1	207	PILYNLFQKIEAEGILPNSFYEASVTLL PKPKDITR/ITTY*FILLT*NILNKVL SNQIQLYIKRITY
5948	19849	A	5999	603	269	EDRVLVLLPKAKSAVAPRLTATSASW\ VQRSEFHPSPSRWDRHVPPhSANFCCV CL*RQGLSLLPGLVLNSWAQVILPPWP\ PKVLGITSMHHARPLSFYGFHYIQK
5949	19850	A	6000	3	150	DYRHAPLHLATFKK/FFCRD/RGLSVLP GLVSNWPQTVLPP*PPKALGLQA
5950	19851	A	6001	365	62	AITAHCSLNLGSSNPTASATRIAGTIG EAAMSYF*ISSTLTHFSYT/C*LHHVWL IFKFFVDEVVYVAQASLELLSSSDPPAL VSQNAFTGVSHCTEPV
5951	19852	A	6002	537	236	DRVSLCCPGWSAVARFQLTATSAFR\VQ *SSCLSLPSSCDYRSAPPANFLSFCR DEGGGLPGLPRLVSNWAQAIHPPQPPS VWITGVINGTWPKIPLS
5952	19853	A	6003	22	368	NFFLQNKENIKRKIF*ERKHLMQRTSL LSYFQQLPRPPTTSQQPSTWRQDPPPAK R/LRTYKGLDDR
5953	19854	A	6004	327	335	NQSIFFNNYPRPF/CCKFKFN/TLHL WADKVAHTCNLSTLEGQGGRIA*GQFBE ATLANMVKP*LLCKVK
5954	19855	A	6005	2	367	WQFLKKLNTKLLYGPFV/PYLGIYKQEK WKHVHAETCTQMFITVLFIIIVPK*KQPK CPSMEE*ID*M*FVHMLEYRAIKENKLI HATWMNLRLTMLSEISQTQITTCMNLH KMFVKVTETES
5955	19856	A	6006	1	176	PGFKQFFCLSFWRGIFIFMGFHHVG*A GLGLMSGDPPASASQSAGITGVSHCA WTY
5956	19857	A	6007	1	289	EVLTKIPR/FFVEIGKLIQDLKDTGPR IA*TMLTKKTEMGRIVHSDLVAYYIVAV IKMVWYYW*RDRHINQ/WERLEISEIDS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						QNMFNWVFTKMQLF
5957	19858	A	6008	439	223	FFSPGSH/SIT*ARVQW/PHHSSLQBP PSLKQSSHLSPSSSDYRCAPHPADLC RDWVSPCCPGWSQTLGLK
5958	19859	A	6009	1	252	MVSIS*PRDPPALASQSAGITGMSHHAQ LFFLN/CIS/ELISSTVTPGLKESACLG LPKCWHYRREPQHPACTVLYLQFQSDQ LK
5959	19860	A	6010	131	514	PWPYSLSSSGLLSSFEN/VEKWVPEIHH HSLFLGTTIDLRS\EPCTEKL\KDK YNPLTPQADMMVCDLKVV*LECSAFM WKRLK\VFDEALWAALEED*RSSCRKET STLLQSTPLLVSYALPCTP
5960	19861	A	6011	625	141	ETGSRFVTHAGVKWHNDSLHPQPPRLK *FSYFSLLLSSWDYRHVPPRANLVYPL *RGPPSMLPOASLEF\LDK*IPPCLQ PS/AKVLGLQVSHRPSPKVTFHQRAKEG DVVSHVVSRGKSI PDRGNSQCMHRSIPC VFEEQKGGQCYCSIESKEETSRI
5961	19862	A	6012	302	42	GLAMLPRLPGTGPKQSSCLSLPSSWDY KHLS*PAVY/C*FLKNK
5962	19863	A	6013	363	82	VSVLSLSPSLKTKVNYAVASFTIAKIW KQLKCPMDKQMK*IWHIHTMEYSA/I KQKIMSYSTIWMNLEDIMLSEISISQAY KGKHHMIYGI
5963	19864	A	6014	329	99	HIFGNTYFFQVASSFIYLRDSVSLCRP GWSAVA*SWFTATSG\FRPSACGLPKC /WDYRREP RPANVLFMSRVTH
5964	19865	A	6015	324	238	LAMLSRLVSNWPQAILLELPKVLGLQ A
5965	19866	A	6016	2	308	FWKAIAGIEGDSSDKCRQ/SKLKTIWKK FISLDAMRNHDS*EKVKMSIFWKMIPT PRDDF/EGLKTSVEKRTEDVVKARQ*B LKVDRT*TDEELLLDQQRK
5966	19867	A	6017	2	457	FFFLRWSL/DSVAQAGVQWRDLGSLQAP PRGFTPFSCLSLPSSWDYRRPLRPANF FYF**RRGFTMLARMVIS*PRDLPALA SQSAGITDVSHRRAERVISQRIVSVMM KPLPEIHIPCILNLSLRFNHRSVAGLRN SLIVRMLSILTHG
5967	19868	A	6018	389	142	AHMLFAAQGDSSIPMLVAPLFTVVKMWE QSKLELADEWSGFW*HIHVTEY/YAIKR REILTHATSLKALCYVI*ALTKGRTL
5968	19869	A	6019	384	232	LNLPSWDYRRAPSHSA/NFSYF*RDGG LTML\PGWQVQIMPRPLKAL*LQA
5969	19870	A	6020	333	84	GLIDQEFATDTTKSTLSLT*T/IPSRC SLCLRGSDDSPASC/SQPPASVAGITDT CHHAHIIFVFLVTRVHHVGRANTEKPR LH
5970	19871	A	6021	106	366	DTISFFFFLKAPIEPVPIIFIPYFFFI FFFI*FFLLFLFLFIYFVF/IFFFIL LCLFFFFLVLLFYLLFF/SLFFLFCFV FCFF*FCYFYFLFFLFFFFFLALF IFFFFGSSFLFIVFLFLFFLFCFVFCFF F
5971	19872	A	6022	384	18	REKKPGPGTGKPKKKGGPKFGPKGPKK RGEKKKKGGP/NSFFPRGGTGGNF*R GFPFENQKGRKKFFQGGKRGANPGIP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PLLGPKAEGGFIPGKKKKKKNSNKKSK QTKKALSRTSHS
5972	19873	A	6023	3	191	LVKGGKIRSWEETWVKTW/RFPYPGVMAH/TYNPNPLGGQGRWIA*AQEFKTS LGNVV KPHLYKKKI
5973	19874	A	6024	364	142	IINGLIHHLNFKINGHTLSTWYTFHIL CVCVYIYICLC\CIYVSVCLCVCVYTHI QYTY*INKHIC*RLEAK
5974	19875	A	6026	338	102	WGPTILARLVNS*HLVICHLDLPKFWN YRHEPPCLALFLIFVGT**VYIFMGYRR Y/C*YRHAMCNNHIRVMVSVGLNF
5975	19876	A	6027	99	77	REICTPTTFEAFSIEAGWK*PKQPLTN EWINTMWCIHMRGKF*P/YAKTSMKLED VFHEISKSQDKHYI*FLSPTYVKIQIA
5976	19877	A	6028	2	328	TITYRGAKIRITSDSSSETMQAREE*SE IF*VLK/EKKTH*PKILYSGKLSFKSK GEIK/YF*GKQN/LKEFVSSRPVLQGM LKVVLRQREGKLYRSETQTYKKKEKASEKE
5977	19878	A	6029	8	241	GFAPLPRLECSNTNMAHHSNLNLSGSSDS PASANFSIF\IETRFQGHVAQAVL*FLSS SNPPISPSPSVEITGVSHARP
5978	19879	A	6030	108	362	CCYLMVTEISAHQNPAAQGLA/HTAPP* KTFPLKVSWTGTVAHV*KPSTLGG*GGR TS*SQKFKTS LGIMRPPSLQIKKVF KI YP
5979	19880	A	6031	1520	77	ASSSSSSSVILSS*NIPNYNYIVIFM/ CL*IIF*AASSSSIIYVPGICYIYH\IL CVCVICMCIYVCICIYSIC*YIVVYSI YYIHY
5980	19881	A	6032	405	100	EGFFLP PRGGGGR/PPGPLTPGGPGNP RPKPPQKWGKPGPPGGGPF*WVLLSPS LPPGGQVESPGAVSGPRQVPPSGSRPFSP TAVGTTVTFLSKKKKQV
5981	19882	A	6033	42	309	CDKFFHKASNHIVSTYIWFQICVCVC VCVCVMCILC*AY/CGCLGIMIWFLEVL *CI/CYCCY*SSLFSVIIICIFLMCFVSY ERRFILFA
5982	19883	A	6034	397	2	KGPPP*GGPDFF*\PRGGPPQKNPFFPP GGGPPPKNGVGGPPQKAPFFGPKRGA PQKGGPPGGPPRGEKKSLCPPPNWENT PRGLKKGPPPPPPPPPPPPPPPPPPVLR STGLRAPFQSVFIVELVEDMS
5983	19884	A	6035	343	2	LWPPQGSFKTAAPFFFFFLFISDFITF HFLYM\YVFFIPLFLL*SFECIK*IFYY VTF*FLQSFSILFSSVFL\WLL*SLLY SF*LIRIYFRFILT*FQ*DTETLEFFYS IP
5984	19885	A	6036	319	68	SLGEICAPK*FFPPAQKKGPFQKPPSCK FSPSPVFKTRPRAKF*KGPP*GKKFYVA NPGKI\GPPKGSFKRPPLFFFFFFFFFF F
5985	19886	A	6037	419	191	RIHTIPITALFAVAKR/WQSKYPLVDE/ MDKIWIHTMED*AAYGKKEIMSHARTW INLNIMLSEISQSQDKDYFFFI
5986	19887	A	6038	434	401	YGKNFSFSLKV*IFCEGLVLVFFPPKKK /FFFFKNFHRVFFPLVFF*TGRGVVFFK PPFLEKIFFFLTRVNLGPPRGGF*GAPF FFFFFFFFFFFFFFFFFFFFFFFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspond- ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NFFYFMN IFTVI
5987	19888	A	6039	12	346	SFSFVRRSLTQAGVQWNCNLGSLQPP\ LPPSFK*FSCLSLQSNWDYRCLPSCLSN FCIF/M*RRGFSMLARLVSN*PQ/CDP PASASQSAGITGVSH/SHLV*NA*SPKT ESHF
5988	19889	A	6040	275	45	KDVQHQWKIVQPLWKQYGSLLKASTESPH DPSILLGLGTYPRKMK*THIK\TCIRMF AEALFLISK*KLKCLLADK
5989	19890	A	6041	355	1	FGTIKNFFFYIFFFKNYF/FFLYIIFPK KKVLEFF*KKKIFFLFIPNKKIFWVFFF FFFFFFFFCPRFFFFFFFFFFFFFFFFFFFF FFFFFFFFVIRHLF EMRKN
5990	19891	A	6042	635	209	PLNICKTFFFLRQSFTLVQAQAQWHDG GSPQPPPPRFK*FSCLSLPRSDHRRPP PRPANLVF\DFLVETGFHRVSQDGLDLL T/S/GDLPALASQSAGITGVSHCARPTL EFLKVKEMIFCSTTVKAVLDHANFLILR FSIT
5991	19892	A	6043	12	348	ESRYSSICLPFSSVYCSRIISLQLYSYV LLVYILFFF/CFLKREFGFCPLGVQGP GLGSLNPPLG*KQFSGLIFPGIGNTGL APPSPPNFGFFRKKGVSPCGPNRPAISK F
5992	19893	A	6044	192	1	IFHRFCT/HITLP/TTALNNN*PWLGTM AYAYNPNTL*G*GRRIV*AAQAFKSSLGN MTRPCLYKK
5993	19894	A	6045	338	42	WKTAWW/FLKKLD/MNYC*DPAILLLGI YPKELKAGT*TDIRTSMTAELFAIAKR WKQNVLDKLNLRQNECRQFIWAKVEGNWL PSWFGEWSIQHRLQAGF
5994	19895	A	6046	300	3	RLDCHYLHSHHTHTHTHPAGIYTHH/ HCWNLHHPGGILGVALDL*MQFLNLR GWSWGGEQMAWPCPGHVMWLGDPGKMI LKPPPLWVCQLQGSSYDG
5995	19896	A	6047	332	3	SLESAGFT*YKMYFYIYKIK\YIYKSI FIILFL*IFFFDLFFIFFFFIFFFFF FFFFFFFFVIRHLF EMRKN
5996	19897	A	6048	2	152	KNLKISWT*WLMPPVVSAT/WGGSLLKPGR LRLQ*AVIAPLHSSLGDRARPYL
5997	19898	A	6049	1	288	PIIIYVLLLLFFETDHSVT\RL*CSGA FSTHCNLCPLPGPDSSASDS/RVAGVAP ACLF*PYRGFSGPATLAFRALDPGLPLH PGFSLQRPSCSRGG
5998	19899	A	6050	358	1	FSISILIFDPLGGFLKFFAFFYGVDFL RFPFFYR*PFGPKSSFIPPHVF*R\WIW FLLSSWFLKWSFDPQFLKRFPPPPFF FPKGFFYKRVFFFGFFFSNLLSSQG KGVNLI
5999	19900	A	6051	308	45	ADLSAEAL*TRREWDDIFKVLKEK/NKG QPKILYPSKLSLINE/NEIKSFPDKQKL REFTTRLVL*EMLKILHMEAQQOYLPS *KHTKV
6000	19901	A	6052	2	124	IFCVLVETGFHWVAQAGL*LLSSGSPPA S/DLPNAGITCVSH*AGITCVSH
6001	19902	A	6053	1	330	LC*PGWSR\ELTS*SACVGLPKCWDYRR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EPLHLVFFFFFFFFFT* IYLG FYLNPRK IFKNFFPLLKNPFGVPPKIQFSPINL PSLVVPMNVFFKRVLGKIFRGFFFP
6002	19903	A	6054	34	293	SPILFLCLRHQSGCHPSWTAVAQSELT AASNSWAQAILPHSWDYRHAPPH/LNLF GWSHAALPRDSNF*PQAILLPQPVLG LQA
6003	19904	A	6055	319	217	YHFTPTGMAISKNRQKTGDNKCC*GCRE IGMLVCC*WQYKMWLL/WKTVHSLKG IK/L*ELPYDPAIPL*GIQRVSNKPIPH SSEG
6004	19905	A	6056	341	151	VHAGGSPES/REFETNLGNKARLHLYKK *ISQMWWCIPAVPATHAGPSLHFNLYYS PWLQCDY
6005	19906	A	6057	2	558	FFFFLRWSFTLIAQAGVQWCNLSLQPLP PRFRKFSCLSLPSSWDYRHVPP\RLANF FVFLVEMGFLHVGQASLELLASGDPSPG DPDLR*LAFQSLGITGVT/HHAGQIFLF /CLETESPSVAQGVQWCNLSLQPLP \GSE*FSCLGLPSSWD\YRHALTHPANF \SIFSRDGVSPSWPGWSQMPDLS
6006	19907	A	6058	320	21	EICMTTNHPSVSNTIW/SKMTLASVYLT LLPISKTSKTSGLPASKEVNRYLGTCAI RYFVFFYFIIMLFV*RQGLTMLPRLVSNS WAQVILPPWPPKVLGLQA
6007	19908	A	6059	294	50	CYFSLSFGL*QFLSLNQSFVTLSSHCDR DTFE*SWSVI/PGIGVYSSE*E*TRGLAM MPRQVYNSWAQAILMPWLPKMLEVQT
6008	19909	A	6060	616	354	ERVSECHPGWSAVALSQPTAALTWS/VK QSSHLSSLNSWDYKCMPPLLANF/KFFC RNE/SLMLPRLTSNPWAQVICPP*PPK VLGLHA
6009	19910	A	6061	214	11	AASRPSAWQPPLLGSEELCPATTPSG RCTQQ/LH*ERAMMTMAVLWNRKGGKVG KRLRNRLVAMSV
6010	19911	A	6062	349	54	QSKSAFPKKRINRISDSSEGYGQSKLKT FWKGFTILDAIKNICNSSEBVKIATLMG V/WDDFEGFRTSVKEVAADVC/ETARQL EVEPESVTG*QQSHVQP
6011	19912	A	6063	332	3	SQPASGQISKVTQSTLRLCLKMSVQOVKS CYKCTATYLCAPNSHEFRSSGVCENPV SYFYTHSIRSKIL/WPGMVAHTCNPSAL ESQGGCMT*QHCETSMVMNVTPRVSRA
6012	19913	A	6064	174	416	NENELFFCFFFXIFFFFKFFKFFKFFKFF FFFFFEGFFKFFKFFKFFKFFKFFKFF FFFFKFFKFFKFFKFFKFFKFFKFFKFF
6013	19914	A	6065	826	571	DGSHSLA\RLCSCGVISAHCNHLPGSS DSVASAS*VAGTTGTCHHARLIF/VVFL VETRFHNLGQAGLELLVIHPWPFPKILG LQA
6014	19915	A	6066	1	284	GTSFFF*NRVLFCCPG*RAVPQ\SWLTA ALTSWAQSS*NHRLKP/HMLSFFNFCK QGLTMLPKGALNSWAQAILQPPPM*LG LQACTYAWSLGP
6015	19916	A	6067	36	384	VSKNKP IHLFLFFFSKTKSWSVT\RLC SGVISAHCYLRLPGSREGAASAL*LSAT TWLCKVALPLGEDLGALCRNPWAGAGVG SSRESPLGEARGGELPWQVRI RLWGR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
						GEPAP
6016	19917	A	6068	393	116	PQPIFPRY*QNKDPNL*KTF*HKYMPKC PAK\LIIFIEKGFSRFGQPQL*HLSSSN LPALASQSAGISGINPGRARFPLFFFF FFSLLLLSF
6017	19918	A	6069	53	280	FPRFCFC/LLESSEHSVA*ARVHWRLG PG/LKRFACLKLPSSNWNRYRHTPTHANF CIFIRDQGMTL*PSWS*TDIK
6018	19919	A	6070	3	377	HEEPQGCATVPGEFFKFLWRHLITYPR LVNSWAQAALPPQ*METHIIFSIGRLH MVK\RQYWSGAVAHAYNPRLLGS*GGKA A*AQEFETSLGYVMRPLCHKNLKNSPGT VAHPCGSSC
6019	19920	A	6071	337	3	RESQAFFSKKKKKGFTKMVVFQRCERG KGARQQSHLRKSIYV*ETASAKALRRHM PGVFQKQPGG/WPGVVAHT*NPRTLGGR CGWIT*AQELETSLGNPEKPCLYKKYKL V
6020	19921	A	6072	1007	628	FLLLAHSPHSVAQAGVQWGDLSLQALP PGFMPFSCSLPSSWDHRRLLPRLANF\ FIFLVATGFHRVSQMVLI*PCDPPASA SQSAGTT/GARPKVF*IFVYMYFQVRKH SILMSMPQHDLFQYKI
6021	19922	A	6073	27	364	MDLPSVSI*FDLRLWADISRATSTLFWL LFSWNCFLHLLSFNLFSLGQK*VCCR* HIQSCVT*QWRY\WSGLVTHACNPSTFG SQGGWVASV*EFETSLCNMAKPCLYKKY E
6022	19923	A	6074	2	68	ARACSHGTVALTASCFPLQLDYKCLQYS FVCFFFFTKSNFVT\RLKCNGLISVN* NFNLPGLTRSQA*ASREAGTTGTCTYHA* *ILLPSSTRL
6023	19924	A	6075	330	49	KRRFALVVQAGVQWRDLRSLQPLPPVFS CLSLPSSRDYRCPAS/RPS*FFLELLTS GDLPTSASQSAGIIGMSHCAQPLIYPL FQIKVILFFS
6024	19925	A	6076	2	267	ARGVEVKVGKTQKFLNMIRRTLVCWVK CKLIQPLF/WRILPKVKEELPYHLAILP LGIYPKQMKSI*LYICSYI*IVDHFV *AILEPLGIYPKQMKSI*SLNIHMFYIDC RSFCIGTFLL
6025	19926	A	6077	379	236	PPPPQTRTPPPGHVHKDPPPHHPYPP PQEPQPRTPVPNTHPGEEQNHELFNSSL LEPWW\YSSLLPPEQA*EPHII
6026	19927	A	6078	2	290	RRSLPSSPLEDGRSLIAPGLTWEPPSH PPQ*RSPPPPKKKKKKKSPGPKF/HK FKTGKPEKPPRVL*RGHWPPKFF*LKP GLPFF*GTKPPKV
6027	19928	A	6079	1241	1487	KMYCIIFFVE*KPCLSCAIFIRLLKWS*P TVCNISISGGPPHG*IMPSIIL*PLFLET VFHSV\TRVGVQWPDHGSQPGPPGLK* SSCLTASQSTQIIGVSHAWPPSITFEI FKRLAYSMSADGW*KSPMKLDLGALKK KLSFARPG
6028	19929	A	6080	333	1	LCHHVQLSFKFPVMEVSLCGPGWPFK* FSLGLPKCWDYRHDPPHLAFFFSL* FFCRDRVSMLPRLVLKSWSQAILL*PP KVFFLFVCFLLRRVSFHHAEFYAVSSC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6029	19930	A	6081	2	239	ARGKYIYNRDKISFCCPGWNAII/RSIQ P*TSSELKRSSHINRPNWDYRCMPSHLA NF*IFRRDGGGLASLPRLGTGWLKS
6030	19931	A	6082	323	185	SACLGPKC/WDYRREPLCLVSR*VLNS *AQAI CLWPFPKVLGLQA
6031	19932	A	6083	296	2	GERILEECIYARSHRAEITSLHCSLSVS K/HSVAQVVVKWPDFCSMQSMPFRFK*F SCVSVVSSWDYGLPPCAGLHIWRRNVT LALQGLPTTSLALV
6032	19933	A	6084	443	1	QKPK*KTQTWSSISLQSRKMKKKILSV ITFFKT*GEEBEEKEKKR/KEE*EK*K EPSQKKEVEVEVEDEERRGRK*KVDMEV KEEKDKGEEKSGEEQ*KESARAAVRE* VDS/SELVTFAVLPGDSSEEEQGMVPR A
6033	19934	A	6085	328	1	SNILYFKAQVTKHIYSLETCSPPDYGIS QAIKANFSPCTVG*LPSNWAYRHLPCL DNF*IFCRG/RSILCLISNSWLQQVKL QEFPPQLGCHARFQAGFLSHCLV
6034	19935	A	6086	299	46	LDDLHLLSLCLSLFRDRVSLCYLGWSSV A*S*LTVA*TPVILSLRLK*SSHNLNLP SSWDYRVVNS*PQGLLLPRSPKVHLLL
6035	19936	A	6087	266	48	GIEIVRQMRSTGADKVIYVQSPLLKM QKI/WLGTVAHTCNPSNCGRSGRIT*G QEFKQSSHLSLPCWDYRL
6036	19937	A	6088	2	185	ARVTMLPRLISNS/GFK*SSHGLRKCW DYRCEPPCPAEISFISSGYLTRSGIAGS YCNSV
6037	19938	A	6089	520	297	LGYRDFLHLSFPIS/WNYRCLPSCPA/N FFILVETN*FHHVGQAGFEHLTSGDLPT SASQ\SAEITGMTYRAQPAAGS
6038	19939	A	6090	388	187	SQHLGKLSREDCL/RLIVPDQS/GQHSK TPSLKK*F*K*AWVW*HMPVVPATQRAE VGGSLEPRKSKLQ
6039	19940	A	6091	188	329	TLGLKRFFCLSLR*FIYFFRDRVLLYY PGWKAvgiHRRDYSMlySLELLASKDS/ SCLSLRSGWDYCVWLIFFGCM*CKRQDL SIIPWQRLIGQ
6040	19941	A	6092	124	342	RPAPWTQNPISAKNTNITWA*AARVAG IT/GTCQRAQVMFVFLAEMGFCHVGQAG LYPKIIILYDKLSHYKCSHLQMRKALBT YSGIYSLFTIYLV
6041	19942	A	6093	169	2	SH*PFTSSTIRSIWT/GAVAHTCNPSSW GE*GGRMA*DQKIETSLVNMTRPHLYPR A
6042	19943	A	6094	2	324	FFFLRWSL/DSVAQAGVQWRDLGSLQAP PRGFTPFSCLSLSSWDYRRPLPRPANF FYF*RRGFTMLARMVIS*PRDLPALA SQSAGITGMSHRARPAVYILTSTN
6043	19944	A	6095	76	340	LRKKFCFSVYFFIHRWTFELLPLNDFLM NFYFRIVFRFMKKLQR/WPGAVAHAYNP STLGG*GGRIS*AQEFKTSpgniVRDFI STKNM
6044	19945	A	6096	349	84	FLLSLF*DTISLCHPGQSAVVRTMTSQL KQSSHRSLLSSWDCRCVPCPVNFFSPC RDE/SLAMLARLVSNLWDQALVAEAGVS VWARQE
6045	19946	A	6097	346	184	LTMLPRLVNS/GLK*SSHFGLPKCWDY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RHEPCLAKISLYITKFFHILSLPI
6046	19947	A	6098	378	250	FKQFSCLSLPISWDYSREPPQMANS*F LVETRFHHVSYVP
6047	19948	A	6099	3	225	GFKRFSCLSLLSSWDYR/HBPVYLANF\ *FLVEMGFHHIGQAGLELLTSGDPPTLA SQSAGITGVSHHAQPLIIF
6048	19949	A	6100	1129	457	YCVSSKYRRIISFSLIA*LLLTKLGS/V QKVGQWRDLG*LQPPPPG\FKLFSCLS LPSGW\DYGHVPPHPA*FCVF*WEMGVS PCWLRLV\LNS*PSGGSRPSPASQSAGS LQGLI\HRARPEH*F*TS*PLGEGKTLTD EIIYIKTKTFYQFCIVCLKLH*RLMEFAL VAQAGMQWHDLGSLQPLPPQFKWFSCLS LPSS*DYRYWLLYHPALBLKEAPSPFBS PCTH
6049	19950	A	6101	3	296	EIIQALLITIVLGLYRTLLQAS*VL*SA FTISDGIYGSTFLAA\TGLHGLHVIIGS TFLTICFIRQLIFHFTSKHHFGFEADA* YWHFVED*LFLNG
6050	19951	A	6102	1	749	RHEGGLFKTILLI*TSLTIGSLALAGLL FFTGFYSKNHIE\TANISYTNA*ALSI TLIATSLTSAYSTRIILLTLTGQPRFPT LTNFKENN\PALLNP\IIYVAAGSLFAG FLITNNISPASPQTITPLYLKLTALAV TFLGLLTALDNLNLTNKLKIKSPCTFY FSNILGFYPSITHRTIPY\LGLLTSQNL PLLLGLT*LEKLLP\NTISQHQISTS ITSTKK\GILKFYFLSPFPPLITLLLI T
6051	19952	A	6103	377	1	SKAFGPPGF*APYGLKAHCFPPGFRRGV WAPSGFWARPPIGYPPGALIGAPWVSP GGPPKPGPP/GPFGVPKLGKRLGIGGP FPGSPGFLTPGSKKKKSTKKGKPKKI TPLDTSCSRTIVM
6052	19953	A	6104	1001	531	FFLRRSFTLVAQAGMQWCDLGSLQPPPP GFKQFSCFGLLSSWDYRHPPTLANFSV FLVEM\GFMSLARLVSTS*PQ/CDPPAP ASQSAGITGMSHCAQLPKPIFNYL*AID SVTTSISLARDWPNSSENRLLYMGKPS KFKRQEQKMECYRDLAPS
6053	19954	A	6105	376	117	CSDWSAVSRSQLTAAPNS*\VKQSSCHL SLSSCWN/YRCQPRHLANFVLCYVLF* RWALAMPILVLNCWPQAVFLPWPPEM GLQA
6054	19955	A	6106	689	433	LCHPGWSAVVQSWLIATSPSLV\KPSH LSLLSSWDYRCTSPCPANFFVFFY*R*G STM*PRLWNWAQAILPPRPVKVLGLQ A
6055	19956	A	6107	2	176	AREYPANFFVCLFFLILCRDG/DFTMLL RLISNSWLKRSDRSLPKW*DDRREPPH QAY
6056	19957	A	6108	328	69	LYIFSFG*ERVLFCHPGWSAVAQSQLTA ASTFRTQVLSLIGRWDRHVPVPHLAD/ SFYRDGVSPCCSG*SQTQAILLPWPVKV LGFB
6057	19958	A	6109	777	329	FLEMGSWSVAQAGVQWRDLGSLQPPPPG FKRFSCLSFPSSWDYRRPRRPA/NFFV FLVETGF\TILARLVNS*PRDPPASAS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QSAGITGVTPRPALTQNFNLTFGREN RKNPNEDESCVRYLLLSIRQRSPTALLHV ILFQQMIQLVL
6058	19959	A	6110	345	309	ASLIFV*LVEMRFLHSGISLFNSGKNP TAFSQDPPG\SSVSKKAI III INKINK* IQHVTVIQIEVQWHNHVSLQPLNPELNR FSRLSLLSSWDHRHMPHSANF*NFKN
6059	19960	A	6111	332	3	RKVLVCPPLSAVAGFQVPARSAFQVHP LFLEAEVAVSPGCAFAFKPGPQGPFF*KK KEEERKKKGRKKEE/EEEEEEEEEEEE EEEEEGEEGEEEFYFLRAGVKSPRA
6060	19961	A	6112	498	191	STDRLVLLCQKARVQWCDPGSLKPPPPGF K*FLCLSLPKSWNYSHAPPLANF*FL VETGFCVHGKAGLELLASSDPPALASQS VEITGVSHAWPMQEFYFI
6061	19962	A	6113	1381	172	RNIDSKAILSKKNKAGGITLPSFKLYYK ATVTKTA*YWHK/NH/DVD*WNRIENLE MRPHTYNF\LIFDEPDKNQWAMDSLFN KSCWDNWPAILWRLKMDAFLMPYTKINS RWIK/DLNVKPKTVKILEDNPGSTIQDI GTGKDFMTKTPKTIATEAKIHKWDLIKL KSCTAKETIKRVNRQLEWEKIVANYAS EKGLKSSIY*FKQI*KK\NHIKKWAK DMNRHFSKEDICGQSY/VKK/CPASLI IREMQIETTTTRYHLTPVQMAIIKMSENN RCW*GCGEKNMLIHCWWCK/LKLVLQPL WKTWV/RIKTEIPFNPAISLLGIYPKB* KS/C/CYKDTCTRMFVAA\CPSVTDWIK KMWYIHTREYYTAIKRNKTDWAWLMPV ILALCEAEVGGSLVRSRPAWPTW
6062	19963	A	6114	3	155	HEKKISQVWCMPPVP/TILWWLR*EDS LSPKRLRLQ*SYDCTTVLPWATE
6063	19964	A	6115	47	368	STFTPSAFLCLAF/YRQRVLCWPDWGA V\IQHTYSLPT*LSILKQD*PLNLLGT/ WSSRRVAACPENQIYRRNGVS/MLPRLV LNSWTQVILLPWPKV/LGLQA
6064	19965	A	6116	1	592	RQRIFFLECGGAISAHCNHLPGSSNSP ASVS*VAGTTGVRHHAQLIFVILVETEF HHVGQDGLDLL/NLMIHPPRPKVL*LQ G
6065	19966	A	6117	1	306	LWKTWQFVLKLNILLPNPAIVPLGIY PNKMKIYVHTKTCTQICIGALFIART* KQPTCSSIGEW/IKKLWYIQTMEYYSTP ERNEPSSHENTWKNLKI
6066	19967	A	6118	2	284	QTGVHWHQ\NLL*PETPG\SRDSEPSA SQVAGTTGMHQHARLNFFSFSFFLSFFF FFSLGKTLGLGLEFFPRWLQMSGPKKIL RLYLQNPKNKG
6067	19968	A	6119	2	315	SRVAGITGVGHARLIFVF/CFFFFFLB RDLFLVPRVGFQGFNLG*LKFLPLGLFL FSGLTLPKTGD*GAPLQPRVNFWIF*KK G*YCGPGWFEILDRLGSPPF
6068	19969	A	6120	42	392	LQWRNLCSLQPLPPVFKQFSCRLRLSS* DYR\HAPRLG*FCIFSRIVFLHGWVR AGSRNS*PDGSAPPQASQLAGITG\VS HHHTWAPHFLFFKNSGCSTQNR*QVHKV GDKETS
6069	19970	A	6121	2	202	VHLSQDQNPCKP*MIEWIKMWHIDTME

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						YYAAIKKDKFMSF\ETITLGEETQEWKT KHRLLSLIRGS
6070	19971	A	6122	355	161	FIXYLFFFFFFFLLFFLFLFF XXXXXXXXXLXVFTGMIS* LWVCLVYM NVYM* IYMF
6071	19972	A	6123	1	133	LC*PGWSR\FLTS*SACVGLPKCWDYRR EPLHLVFFFFFFFTL
6072	19973	A	6124	3	212	HPGLPSSWDYRCT*PCLANF/SCCCC*R LGLTMLPRLASNSWTQVILLNLWLPKLAQ NTSLINNFYIDQMLK
6073	19974	A	6125	156	2	ALLTHAKNAL\WLGAVAHDCNLSTLEG *GGWIT*G*EFNISLGNIVKHHLY
6074	19975	A	6126	345	34	HPSTIHRVCSL*S*SSPQARNNGSCLS SEHFGITGVNHHTWLLFFKKNY/CILIK IETGS*YVAQAGLELLSSSNPPISGSES AGFTGMSHGIRPVSPSLKWS
6075	19976	A	6127	2	328	ARAYLPLCFIIFI*VSVIYFIWLL*G LI*LNKRYLAHPK\Y*LNVSYSVSFCKT HFFPRHKEKAI IQLGVVAHACNPSTLGG QGGWIT*GPEFETILTSMEKPRLYY
6076	19977	A	6128	1	341	GTRKFSDYRGKPPHPAKNRNLLFSIFFY FETLSCSVLLCEVTSSQL/CNSFHFPDL PSSNDPPSSASRAAETTGACHAQMI*F* FFVETGPDWS*TPG/LLAVLPSPRML ELQA
6077	19978	A	6129	264	2	TAISENKVASRSEHRRHRL* LQVI/LI ALQHRSDNDLSH*KN*KKKMLGEVAHA CNPSTMGGQGGWIS*GQQFQTSLSNMVK PPRA
6078	19979	A	6130	1392	1157	LSLPKCWNRYRPPCPALCCPGWS*TPR LK*SSPLGLPKCWDYR/R*TTAPGLPFI SKSSLRSPAYSCVTCTQLSHH
6079	19980	A	6131	383	108	MRLCSQPHHHVDFSVLETESCCVTQGV QWHDLSLQSPPPRFKRFSLL*LGAIL LLPSSWDYRCTPPHPAN/LCRF*HGPVC LYMFGEKVTP
6080	19981	A	6132	307	1	LKTLPALCELESHSVQWRNLSSLQPPP LRFKRLSYLSLPSS*DHSH*AHQANF\ CIFSRDRETGFHHVQENLIMLIVQSS GLGFSIFATLLAVMQLV
6081	19982	A	6133	351	66	RWSFTMLHRLLLKS*LQ/CDPPASASQS AGMTGMSHHTRLHNL*F*TANNLTQSHK FYSFISLTPHFAINVTNYIFLYTTSINI VCIFLSFKFYARI
6082	19983	A	6134	2118	1392	FFCKGK*IFIQCPDWGG/DLCV*QEKIQ KKTHTGDKYV*LF*KVKPITKI*QRI HTSGNTDAQLSYKENHDQGH*QAKNFKF FLFFVVFYLRSL/NSVTQAGVQWRDLG SLQPPPPGFKQF/SCLSLPSSWDYRRPP PRPANFC/IFE*RWGFTMLARMVIS*P RNPPTSASQSAGITGVSHCTROEFKVK GYHFHLLPSGCLFLFYVFLYACLLYVS VYVPLRQQESRKISKIEMFLITWH
6083	19984	A	6135	383	47	HLFLNFYYLSHYNYLYFLHLIPSSP KIFFFT*KIIFLIKFNKVF*NLSE*K KIF/IFSYTF*FWPP*NFF*KPPFFFF FFFFFFF*QTLFLGGCGYNTKLR
6084	19985	A	6136	2	196	TRPSILVTALYYLIYFTTTQWG*\LTHH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						INNIAPSFTRNTLMFHLSPILLSLN PDIITGVCS
6085	19986	A	6137	700	433	FLRWSSASVTRLE*SGAISAHCILCLG SSYPALAS*VAGTTGTCHHAQLIFVFL VETGFLHVGQDGLDLL/NLMICPPRPPK VLVLQA
6086	19987	A	6138	377	298	QMKWLLLLFRYRVLLC/HPWSAVA*LQ LTAASN\FGLK*SSCLSL/MLTMLVLS WPQVILLPWPPKVQEL*ATAAYTIKMV
6087	19988	A	6139	1	199	LYTTYFVTKLLTSLFL*IRTG\YPRF RYEQLIHL*KNFLPLTLALLI*HVSIP ITISSIPPQT
6088	19989	A	6140	381	28	STPNRLIERQEDPPES*NTNPPGLPRKT PSFTKNPKINLARWGGPENPPNPEEKPR KVPESPKRKKP*TKIRPLPSSPGDPTKP P\LKKKKKKKSVVPATQEAEMGGPLKA RSLRL
6089	19990	A	6141	1	209	LKLLASSDLSTLGSQSAGNIVGMSHCTQ PKINMGILLKLVYRFNINPVKTPAGLF/ TKKKT*KTEIDKRILKFIWKCTEHRIAK QSLKRTKLEDFLLNFKTYEATEIKTS* YRFNINPVKTPAGLFKKKKHEKQKLTSG S
6090	19991	A	6142	3	282	QGIFLTKRVKNF*RGKFKTLVKKNGQDP KKGKNPPGPKIGKNNFGKTPFWAKKI*K FNLI\PKKTPPPFFQKLKKTGVKFFWAP KGPKGFLSKK
6091	19992	A	6143	382	158	FFF*DSLAVSAPGVQ\WHDLCSL\RLPL PRFRFWCLSLSGWD\YRHVP\QYPAK ICIFSRDRVLPILAKASRNVSF
6092	19993	A	6144	185	316	PCLANF*IFCK/NGGFSMLPTLGLNSW AQGILLPKPLKVLGLSA
6093	19994	A	6145	489	231	SVA*AGVQWHDHS*LQFQ/PLGLKQSSC LSLSNSWDYRHMAPHTNFKKFVETG VLSCCPGWSSTPGLKGSFCLNLPKF
6094	19995	A	6146	179	1011	GTILNPQSLPFPFFSTLIFLKTVLLC CPGVNSNSGSSCRSLPKCWDY*HEPPH SAL*TFPWPFP*LVKDTSIHSTQLLKAE IFSASLDAAPSPTPYIRTHPSSGLQRWL LDAARSPTPYIRMHPASRLQRWCSTCTL LPSPSYHTPA*AMTTASSLISPFFPLPP PAHFSQCRMTFCLFVL/CLFEMESRSVA QGWECSGAILGSL\QPPPPGFK/RGFSC LSLLSRW\DY\GHAPPCPG\NFCIFSRD G\VSLCWPGWSRTDVLVHPPRPPKALG LQA
6095	19996	A	6147	348	3	GYHKTINWHCCMSVFANLTCGFNAIPK /IPAKYFVDPDKLVKFTWKGKRPRIAG TILKEKKVRLILPNFKTHYKATVIKIG W*W*NNRHNHNQIGSPBIAPHKYSQLI FDKEA
6096	19997	A	6148	22	228	THRVALFVRT*NWQPKPCSTGEWLNTL CYIHTIEY*YSAIKRNKLSIHVKT\WI DLKGIVLNENNQI
6097	19998	A	6149	406	279	RSIQGSSSHASA/S*VAGITGARHHTQ VIIIVFLVETGVMAITY
6098	19999	A	6150	406	10	MRYHFTPDERLKSGLKLEYW*GSGETR SLIHCWLEYKMSHPLWK*/TVWLFPIKL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NKNVPYGPAILLDIL*EK*KHMSTKNT YK*MLQALFIITKNWLLSIKRRMTKQIM VYSNRNYSTIKNELPIQTRI
6099	20000	A	6152	367	1	PTPWEAEGGSFKPRR/LQ/CPN*PPMC SCTPAWAPGSPVSKKKMQFHRMRGHV SSAWWPCGADVRLRAGGYVRHRRFPGLPWAAGGRDEVIRCLTVCTACGEDHPGS HLAGPRGGGFF
6100	20001	A	6153	441	38	ILNPGEAITSEKYVQ*FNEMYQKAKRL/QVNRKGPVLLSYNA*POVAQPVSQKLNK LGHEVLSHRPYSLSLSPDTDYHFFKNCINI FLKEKRFYNQDAENAPQEFTE*SA/D FCTTRINTFISHWEKYVDYNSRYFD
6101	20002	A	6154	308	121	GESFPAEKTFFPKENDYRWPSPFFQWSSVL /CKIHGLLMLPRLV*NSWPOAILLPWPP KVLGLQA
6102	20003	A	6155	1	420	QNLQPHWKTLRQF/LYKVKHMMLSPAIP LLDIT*GRCKPCPYK/ESIC/RMFIBAL FIIAKKLKLSKCSAGE*INKV*DIYTT EYYSIAKSNKQLTHTTTWIKLSITPSE *SQT*ETACPTMLLIWHSRKGNIIVTEN RSMF
6103	20004	A	6156	77	415	TLGLKPTSSSHLSLSKCDYRQEPCCPT SEANFFFFFFGGEFFFWSPS*LKQFFVVE MG\FTMLPRLVLNSWPOAHLILP/ASAS QSVGITGKSHRAPQKLTTTTLGGNFP FGPQAGCPGAESNYPEP*TPGLKAFFGL NLSKCLKYGDSPAPGKLEIFFFKWGGV SPSCASRVLNPPRR
6104	20005	A	6157	436	206	LWYIHTMEYYSALKKNAILIHTI\STWM SLEHMLNEIKQENHKRANI*FHLYEIPR KESRMEVNGQLGRRGIWEFTVY
6105	20006	A	6158	416	50	RFFTHPAGFEFFSPPPPKNIFFPPPP*K FWGGGGKASPPQKKFPPLPPQNGVLCF PPHKKK*FFPPPEKTVEPGPLHVGQRPP QS\PFLCYPLSFFLYFCYFIFFPPVVF HFLPFFFFIR
6106	20007	A	6159	443	145	FFFFSIRFLFVVVVLVQG*EYLCFMT* *IGVLLFLFRICEFFFFLLVGILFCMFL /YFFATASPGLEFFCFFFIFFFFFFFFFF FFFFFFFF
6107	20008	A	6160	322	2	TQDKNRHRAHRIYKARKSARD*RSLV HR*K*KVQKRNEY*PEGTLHTCIALSQG NNI*DA/HSQE*WITPVI*TLWEAEGA SRGQEPKTSLANIVKPDANAW
6108	20009	A	6161	421	57	FCEMKFTPGNNAVNIV*PTTKDLEY/WI NI/DKTVAGCEKTDNSYERSSTMGKML\ SNSIAWYTEIFRGRKSQLMWQISLFSFK KL*QPLQYSATIALIRQPTTSRQDPSP AKRLRLPEGSGDH
6109	20010	A	6162	333	41	GAWACHLHVGAALNAPTPGLSRFHEEPG WSCRTAGGGSRLSLSVFFVQMGSCHVGQ VGFFCFICR/DRGLAMFSRLVSN*TOG ICPWPFPKVLGLQA
6110	20011	A	6163	2	423	KINNTKSQCENILKIEKTLNLTKE\ REDTNY*YWE*NMDITVESTDIKRIIRN TT\ETLHKFDNL
6111	20012	A	6164	434	5	ICHIFPSISKLLNILRPVSKLFFSINF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FGPELYYL*THFNP**GKCLSFLFLQNI CIGFFNSFMQI*SYFLRISLFI PVSPI LLG\FVQIFIVSINILYLSI*LRLEFFSF FLSLFLFFYYTSLSRVHVHIVQVSYI RIHF
6112	20013	A	6165	1238	1017	ETGSHSVTQAGVQLHNSSSLQAPPRLK *SSYLSLLSSWDYRRTPPQPAN\FCTFG RDKVSPCCPGWSRTPEFR
6113	20014	A	6166	504	210	FFFKTRSHDQGSLOP*PLGLKGSSCLSR TLPHSWD/YRV/PPHPAKYKNIFF VETEFHHVAQAGLKVDSSNSPVSASQS VGITSISHCAQPILCQF
6114	20015	A	6167	258	65	YKTKNTTSIFSLPSSF*TQILTF*NTYY YYY/CRDE/SLAMLPRLVNSWPQVILL PWPPKVVELQV
6115	20016	A	6168	1	156	LARMVIS*PHDPPAPASQSAGITGVSH CAQLFFFFFWRQPRFFLRAGGQGRDLGK VKPLLSGVRPFLS*TLPTGRKSGPPTH FG*VLRE*FGGSH\PVSSLW*QSAGITG VSHCAQLFFFFFWRQPRFFLRAGGQGR
6116	20017	A	6169	3	285	HASAHASGNILSYVGSFISLTAI/LII IMI*EAFASKRNVLVEEPSINLE*LYG CPPPYHTFEEPVYIKSRRIRSLIDQDA ARKETQOGAAD
6117	20018	A	6170	645	15	LPFTYCSPCRNPNLSFWQERDSNNPLG/ ISLPHSDKITFNP\YYT\IKDALGLTSL HSLKDLHSFPHETS*GPQAYYSL/QPT PLNNPSPHARPEWIFPYCAYHNFSGSGP LTNLGGVL\ALLL\SLHPKQ*FPHPPS YPNKQRH*YFGPLRPITFIDFLGRRPSF ISNRESGGQPVSYPTIIGQVASVLYFT TILILIPTISLIENKILKWA
6118	20019	A	6171	409	25	YTTGGGKIFFKSNPGSKLFPPPF/PPF FSPFSP*KFFFSKPLNFFGGFFPPFP PKKRFFSKNPLVFFSPFKKVFPPFP PLNFAPPVFLKAPPPFFFFFFFKGG EVKNLSEALDCKSKDRG
6119	20020	A	6172	73	52	VQLLKCRHIF*DKVLLCHPGWSTVARS *LTATSRSSCLSPSSWDYRRVPCLAS F/SF*YIALNN*A*AILPQPSKVGLL* AVAHAYSPSTLEG
6120	20021	A	6173	325	470	IFTFFFLAFI*FFCRNR/SLALLPRLV LNSWLQAVLPPWPPKVLGLQT
6121	20022	A	6174	2	228	TLEDNSTIPCKTIQSSSCTPWYVTQKAA CITLLSM*PKKLWYVYTKSCTQMFIVAI FIIAKNWKQPRCLSVE*INKLWYI*TM E*YFVLKRNELSSHEKTW/MEM*IQLLI ERSQS*KAVVCLHKKLHTDVYSSYIHNC OKLEATKMSFSKRMNK
6122	20023	A	6175	3	408	RYLTLAIRDQIITPVSYHFVPSGDYQ KDNNKCW*RG*KMGSLMHC*W*CKMVQ LWKAQWQFLK/DVKRRAILFLGIYPREM KTYVHAKTCMHIFTLALFLYVHLNALS VMDWMLGHPIEISRDSYSCVCLL
6123	20024	A	6176	2	237	WVWNLIPVVLAAWEAEAKGLLEGGSSRL *WIMPLHYSIGNRARLCLKKKKKKFK VFPQKKKKKKKKKKKKGGAL
6124	20025	A	6177	387	154	AVVQWRDLSSLQAPPPGFE*FSCLSL\W

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DYRHKLLTSGDLPASASQSAGITGVSHCAQPLSLFVFFLTNRQFVAALS
6125	20026	A	6178	1	239	FFFFEMECLTVSQAGVQWYNLHSLQPLPGFQKQFSC\LSLPSSWD*RVPTSRPAKF/CVIF*DGVSHCQPGWSAVVQPLH
6126	20027	A	6179	325	50	RKFPLTWRRVSFFSLRSSTDWMTPHRHIGGII CVTQSTDNIGLIQKHPHRHTQKNV*PNV\WHPMAKSS*HPKLTITVYPLSTWHTYTS
6127	20028	A	6180	157	338	SQHFGRRPRQACSSSEVRDQPGQOREFFHLYKN*KEITQVWWHMPPEAQDY/LBPGRSRLQ
6128	20029	A	6181	3	273	HEGQSKLETFWKGFTI*DVKNIDDL/WRGVKIPILTGVEKLIPTLINNFVFKTSLERITEYVVEIGRELEVEPKDVTTELQSHK
6129	20030	A	6182	2	359	YYPALPLLGIHPK*KNSIQMHTCTHWTAVLFTIAKIWNQL*CSSMGWIKKM/WMHTHTHTIHTMEYYVPIK/NEIISFAATWMLGVIIITETIIQAQKKTGIFSHLYVGAKIFDYM
6130	20031	A	6183	3	211	NPGKLSVSINQDCFPWTPCFQMGRCPTLLF\SPYGGQAIPLITPSVGTQIFRLKM/PEVTHHFHSFP*EPLTAAALNQPSLPLSLLVDF/RDRGLFCHLGWSAVD*SHLTAALNS\LVTQLSCPSFLSSWDYRMLPCLGNF*IFRLKMLKSLTIFILFHESH
6131	20032	A	6184	707	384	LQIFPYNRVKCVKNKSTONQFYIFSRIMHANRHGKYEI/WIIKKMEMREG*AVQLRMKVVKIKKNTHIKLGVVVHGYNLSTLGQGGRII*AEFKTSLGNIALRLHYT
6132	20033	A	6185	720	363	FFFWGRSL*TILF*/QTGSHVAQSGVQWHHSHLLQP*TSGLKQSSHLSFQSSWDHRCAPPRVANFFLDFCRDVCVAQAGLELLASSNPPTVASQSAGITGGSHRTWPFWDILGIMYWG
6133	20034	A	6186	439	66	KPKTLGSKKVNPNRPVPGK/PWGVGPLGPGP*MGGSKP/S*NPSPPPLFKTRFGFFPPG*RGHYSGFLQPPPPGGKTFPPSPPKKWGHKKKIPFQKKKKKRRKRNII GSWTTSETVGNPAPW
6134	20035	A	6187	83	287	NKMPKIFRFRF/CGFLGQSHSVTQGGVQWHDHSSLQP*TPGLKRSLPTCWDNRHKPPHLVLFCEYYRL
6135	20036	A	6188	290	609	RRMDPPFFKYFFERRVLVCHQGS*V/K*SSHFSFPCSWDHRCV/PMHPAN/FNFFHTDKSLTMLPRLVSNWAQVILWPLP P*VLGFAGMSPCPQPPSQFCIEAV
6136	20037	A	6189	2	371	RYIFEKVFAYKSELNDSLSILSGKSGILWKKRLSLFS*Q*SYKNFSLGAIYCGMH*KRFLGTSIL/FTE*VETGFHHVDQGGLELLTSCETLASAY*SAGITGISHCAESQSTLKKYIPGSTI
6137	20038	A	6190	531	205	RWRPALVAQAGVQW/HDLGSLQPLPP*FK*FICLRQSRWDYRCAPLRPA/NFFVF LVETGFHHFGQT\NLQLLTSGDPPASASQSAGITGVSH*ARPVVFIIFTALLYK
6138	20039	A	6191	52	375	NRCETSFLFFFFEKFPNFCPPGGGEWRN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LK*MEP\LPPGLKEFSCILTRRGGN*GP FPPLQENFGVFRKKGVPHCNPG*FQTPD PRELARLTSPRGDGGGRPPPRVK
6139	20040	A	6192	3	158	FFFLLLNCGLKKETG/WLGVAHACNPS TLGGRGGWITR*ELKTS LANMAEFP
6140	20041	A	6193	2	54	FFFETESHVAQAGVQWCDLGS LQPPPL GLKEFSCLSLSSWDYRHTPPHPANLFV F/SFLVETGFRHVGQAGLELLTSGGPPA SASQSAGITGVNHRAPVEVFCK*RVSPC RPGWSAVV
6141	20042	A	6194	1	323	FILPSSWDCMCAPP/RPDWVLYFLVETG FHRVGRAGLQLLTASDLPASAS*GAGIA DGVSLTQCSMLPMLRCRGVILARYNLHL PAACLG LPKRDCSLCPAATPSRK
6142	20043	A	6195	619	243	SPETGSCSGAQAQVQWHDLSLQ* LGL K*SSYLSLSNWDYRCA/PPRLANFLFF VQAGSCHLAQAGLELWSSCHLPALVSON AGITGVSHHARLAVAWKRTPLYGLPSRI SNLCVLLKFLFFLY
6143	20044	A	6196	385	19	GGHFGAQEISPPGVQLFRLHFLSNWGF KRPPWPPG*FF/VFL*KRGFPPGRVVP PSLFP/SDLPPPAPFKGWVSGLRPCPRT FFFFFFFFDKEC/RLSCPANFCIFSRDGV SPCWPPWSRTPDLQ
6144	20045	A	6197	498	437	ENLQSSINLVDKAMAWFERIDSNFDRSF TTVKMPSNLTSIINACCGEIFHERKS*S IWQTSLLSYF*KLLQLAPPLLATILIS KEP*TSR/QDRLLAEG*D
6145	20046	A	6198	79	394	SVKLLALFFFFFFGENFCAPQVELKGP LG*LNPPPPGLKNFSGLT/LPKKWELGG HPPPPSKFFFLFF*KKGMAFFSQGWFKT LGLNQFACLTLPKGGNLRREGD
6146	20047	A	6199	2	313	SASHSAGIIGESHCAWPTMPVVSILVNF FFFLEKKPPFVTQLEGQGNLG/SMEPS PSGLKGIFCLGPPKKWELRAPPCPGYF WFF*KKGLPIRPGRFWKSV
6147	20048	A	6200	62	732	AFQQARKGTQ\GRLSSPAAGALP\PVLA PSGPPLPA*\GSSS\PASVAPYPPQAT G/SPPTPPGELRRGWSKGGLDHPNRTF YCWBSEEP/PPN*QGS*APGGVNSEGRG Q/LPPSSIARCVP*TPSHVPPHPLAFPP SLPHPGPASRAP/TGS9DLSASAVSAP GREGHP*GTRMVPQAGRQKPGHRGAS* GSSCSKRTLSPLSPRQSGFQSRCCFHP RQNH SRC
6148	20049	A	6201	424	7	KNMKRSPISCVTTRDPQIKITMR*HYTGI KMANV/RLTGNTKC*GYGAKGPLIQC* WECKIV*PLRKTAWQFSQS/LKIV*/PY DPAIALPGIQLC*KCTS\KKNCM*IFIT ALFIMAKKQKPRYPSIGEWKYLLHL
6149	20050	A	6202	371	144	RWALPRTNF*FFVETSLHVAQGGVK LLGSVSPPISPSPSAVITGVSYCAQPYG HPFELSFLIEYIYLDFF
6150	20051	A	6203	409	110	LRRSS*LCHLGWSAMVQSWPT*FKP*LL GLSDPLTSASRVDRGMPPCPRNFIIFD M*FI*CVVCV/RTWGLIVLPRLVSNFWP EVLHPGPSKVLQLQV
6151	20052	A	6204	15	221	KASRKMQIETTLRYLSPMRLAKMQMLI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino-acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NTSCW/RKSQRTTRTLC*W*EGRMVQPL SKGIWPLYLIQAEYP
6152	20053	A	6205	23	371	KVACTCMFITVLFTIVKL*NQSRCPSTD DWIKKM/WLCVCIYSSVCVCLYVCIDR* IERHDIYVYIMEYYLALK*/DEIMFSAA TRVKLDAILI*S*ITQNVKCCIVSTHSGN LIMVST
6153	20054	A	6206	113	417	SAVTLVLYIYLNLDLKYVHTKTCTQMFTA ALFIIAKI*KQLRCPS/LIWIN*C*KEM SYQAMKRSYARNLWSSKKLWRNLKCLLL RERSQSEKSAYCVIPTI
6154	20055	A	6207	510	167	GLGQAI SPSPKSGIGAYGFGFFFFFK R*DLVCCPG/SLNLVASSQSSCLSLPKH WDHECEPPCLAFFFFLL*ROGLAMLPR I LPLLKALASGGGMAKKCCIRYFSMKIHL QAA
6155	20056	A	6208	418	40	SYTHTHTHTHTHTHTHIP**LTGS/RLQ GICRKGSRKHPRGLSQQLP
6156	20057	A	6209	1	258	SGFLLS*VPSVRDPTGNRTV*LTWQPLP APLEF\CPRLSD
6157	20058	A	6210	229	310	DFSEAQKSRQCGGGISNVNHPGVVLKPV IQHF*DGVLCCPGWSAVV*SQLP*LPR LK*SSQSLPR/SWDYRHVLO/HPANCF VFFVEMSLAMLPRLVSNWALAILLPQP PKVLDDWLEHHTWMIYITYATTLP
6158	20059	A	6211	496	1	CCQESFEILGSINSFGPGLKGGVKNMR PGAGPTLNKRPFSDNPLQPGRRGGCFPF VSQRGSQKDRVPPKWFFFFFSF*DRVSL WPPGPSARKPSWLPVASTSR/V*QSSCP PLWFPGPPTMVSYFFFF\KRQDLPLMLPR LV*NEWPQVILLSQPPKVLRLQARA
6159	20060	A	6212	3	340	VTAGIIIFMI*EAFASNRKVLIV*EPS I*SLQV/*WRGLLLGSPPPYHTLEEPG YVTSKRKRKESNPPKLASSQPHGLHDF KKKRGGPFKRILEGAPFGGGWGHREFF P
6160	20061	A	6213	60	493	KSQONFFCFETESRSVTOAGIQWHFSS LQPPPPGFKVISYL/SLKSNFSGYP*DF PCNGPPCS*GPIRFTYYICVIPSSWDYR RLPHPANFCVF\IKTVSPGWSQTPDLR
6161	20062	A	6214	414	1	LCNGRPGLLVSPPLGEELIPCLPR*KL GPPRVL*\KGGPFL*SSFAPFF*EMESH SVT\RLCSTRAILVHCNLCPLGPSDPPP SAS*VAGRIARAQKVEAAVSHDHAALQ PEQHSETPSQQTNNQTKLTQKYPF
6162	20063	A	6215	2	403	SLLLPLVQLPLRLCFFFFLKRGNFNGAP DKREWGFEF*\LKPWLP*NNFSGQTLR RSGD*RKTPHGGVNLV*EKTGFSNLGR GGLKPPPSGNTPAWPPKGVGITGTPTP PPVFCFLGFCENTNLRAKKFI
6163	20064	A	6216	2	388	KMEQTLWKTDWEFLTKLNILYPYSPAFAD LGIYPNELKT/C/CYTNTCI*KSIAPL FIVARTWKQPGCPLRDGWLNLKGIQAL EYYSF*KRNL*NHNMAKKLKLIFFLLR QEDRFSLGVEQEPKHNGEM
6164	20065	A	6217	363	302	NKEFKTTLANMGEPPFL*KRGFS\MLAR VVLSLFDHSDPPASQKAGIPGVSPPPR PLFFFFFLETVSHYVAQAGQLISNYDL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KLPSCLSLDWDYRH*PPYPVFKLLNS TYKAC
6165	20066	A	6218	576	6	RAVLRGLLVLLTKHTFFLPPRQSLAL LPRVGVQW\HDL\GSL\QPL\PPG\FKQ FS\CLSI PSSWDYRYP PPRPANF*FSV ETGFHHVAQAVLELLTSSDLPALASQSA GITDLGQSETIHGSGSLDKPPDHKVDKG PTEERACLLSYSAGRKYKEYHILPEQGS EPPHHGDLISISFQAASHLAQTPFAHT
6166	20067	A	6219	44	496	GFRVDPVRVRVRLNS*PRDPPTSGSAG ITGV/SSHARP*NIFT*KLGISFLVFW GFLFLFFVFCFFFWKGGFLLVAQVEGK /WPKFGLIEPSPSGVKEFFFNPEGWD \YGLAPPPGVIFWVLIKNGVSFFCRAWV QTSGLSWINRLNLP
6167	20068	A	6220	1	421	QRGLTAISRETSPTLVAQAGVQWHDLG SLQHLPPGFQGFPCLSLLST\TGNCST QAGVQWCHLGSL*PLPPGLKPSSHLSPS SSWDYRL*KPHQGS*VCVT\GAASPEP NTMTAANNKPPDIRMKETLLLPSSSEKM L
6168	20069	A	6221	3	36	AYCIVKPS*PLTGALSALLMTSGLAM* FDFHSITLLILGLLANTLTIIQ*WRDVT RETTYQGHHTPPVQKGLRYGIMLFITSE AFFLAGFF*AFYHSRLGPTPOLGWDWP TGITPLNPL*VPLLN\TNE*LA*GVST *AHDP
6169	20070	A	6222	895	13	ANSWANN*FELATQIAFSGRIPLTDSHL GLLKAHVEAPI\AGLIVLAAVLLKTGGL MLYTASHFSNPLTK\HIAYPPVLSLI EA*FITSSHLPSDKQDLKS\LMAYSS\I SPHSPS*LTPILIQTP\W\SFNGAGQFS IIAHGTYHAYITYSA*ANFKITERTSQC ACINPAAQGLSNS*LQILGLFE*LPROA \SLTMGLTPPLINPTGENCSVASNQRF S/WTQISLLLPYRDSTILGSQALYSLYIF TTTQWGS LTHINNIPKPSFTRENTLMFI HLSPIILLSLNPDIIITGFSS
6170	20071	A	6223	68	405	HSYALVYNPVGIRVKVHLSKCIYTWHI SNSSQEVCEMPNLNKRVP TTLAPRF*N IS*GISQLGAVAHTCNPSTLGG*GRW/I QQLKTS LANMAKPHLLKKKKNFNFPK RG
6171	20072	A	6224	591	283	GTSTQAGVQWCNCGSLQPPPGFKRFSC LNLPCSWDYRRVPPHLANF*FLVEMGF HHVN/OAGLELLTSSDPPALASQSAGIT GMSHCARPRVAF*GEKNHRS
6172	20073	A	6225	302	173	GFFSFFLKC*DR/SLTMLRLVLNSWAQ VILPLWPPKVLGLQA
6173	20074	A	6226	417	81	TQTRGPPPPFLGGPPSPERTVPPPRG GVPTGSRFFFLFRQNPFPALFPKN/EGG F*KKFGPPLPPF*KTPFFFTNRGNPCPF FVGENPQAPPVFGGFNPPFRKKKKRND LS
6174	20075	A	6227	41	474	TDATETFHFTSKH\HFGF*AAA*YNHFV DVV*LFLYVSIY*GSCVPHFA
6175	20076	A	6228	503	28	AAHAPPRVRKVIGH*AFFTORCTNSRH* IIKFPKDKDKARILKGAREK/RTTYNGA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth' od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PIWLAVNFSVETLQ/A/RREWHDMFQMP KEKTFYLRILYPMKISFKHEREIKTFPD KQKPRDFISSRPVLQEMLKSWPGARVHT GNPTLLGG
6176	20077	A	6229	418	175	VSPLSPLKILFFPKGLKFWREGGPKCPP PKKRVLPKK/PPAMF*IPPPKRRKSKLP PPRKIWPPQGIFKSPPPQYFFFFF
6177	20078	A	6230	45	308	ACVRLKH*TDN*QPNINQF/HKSLLP* KKKKKKKKKKKKKKKKKKKKKKKKGGG FKKKPGGGPISWGGEKIIFFFFGGGKKN TLGIF
6178	20079	A	6231	440	209	IQHFRGPSRRGLLGPPEARASPGQHRESR SFLKMQP\NKKFS*VWWCTPAIPASPKV EARESLEPGRRLHLTEALQPG
6179	20080	A	6232	419	2	SSPPPPGGKFF*KKPGKKKFSPPKKRV FSPP\PPKKFFFSPPA*NFWGGGGQKFP PPKKGVSFKKPKGVFKTPPKKKKFFFP PGENWGPFRVF*KGPPPPPPPPPPPP FLSFNVNILEKPVQAPCLT
6180	20081	A	6233	448	112	QSARITGVSHRTRPMLRTSTPLSATDRN AGQKISKDIADLNNNEQDHRDIYRNSTQ *QQNTHSFQAIRNKIDPILGHKKMLTH /CKQSDQTWNKLEISNKYAKPQIKHTI K
6181	20082	A	6234	2	351	MDQGI/SDFESYLLRNTFCQAIVARDG DSSDGGSGQRKIKTFWKGFSLLDAKHTE DSW/EEIKISTGVWKLIPILVDDFEGFK TSVEE/VADVMDLSRELEL*VEPEDGTE LLQSHSQT
6182	20083	A	6235	3	252	FHTYNSLLVCHSNLCYQNSLLFFIIH* / CI/HFHS*AKVSIWKHTYTHTHTHTH MHTHFFQATDRKICVNVIMFSVAYIHK LQ
6183	20084	A	6236	3	294	IITF*LPQLSGYIEKSTPYECGFDPISP ARVPFSIKFFLVAITFLLDLEIA/LLL PLP*ALQTNLPLIVMASLL*IILALS LAYEGLQKGLD*AE
6184	20085	A	6237	381	121	PVPASF*FFFFYRDR/VSLCYPGWSQTP GLKQSSCLGLLSHWDYKYDPPHPAFISF LLSSLLWVL*RPVLLCATVPAFLDIR EQ
6185	20086	A	6238	395	62	PPFFIPKFFPWGPNFFF/PLGPPFFLGF FPGSFAPPSSHFSPPD*NFPRPPKNFPPG GDLEFPQKKGDWFFPKRGVFFFLGGFSK FSGGPPPSLGPQKKRKFIKGPKKCF
6186	20087	A	6239	1066	761	SFFLRWSFILVTQAGVQWCDLSSLQLFP PGFK*FSCLSLPSSWDHRRPPRLANFC IF/M*RWGFSMLARPVSNS*P/CSDPPT PASQSAGITGLSHRAWLVFL
6187	20088	A	6240	390	27	GELPTPIYLAPPASPKGVSGGSPPSRV KFFPLEVPPPPPGC*PGPPFYINPQGG ARVP*QQIRFFSLRW\PPRPTRPKNPHL QVGPLRICLSPETGGGVIKVFRGSLKK KKRAAASRSN
6188	20089	A	6241	366	1	KIKNFDRI/TSKGA*SVV/RNLPTKKS PEPNFGPGVFCPTFKKLTPTV/SKLEP KF*KEGILPNSFF*SSLALIPNPFYPSK KKKTKKNYRAISLMNIDEKIHKY*QT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EFRSTLKVLYTITK
6189	20090	A	6242	23	439	IASGRPFFFFFFFFFFCLPPPPGNGSFS FLKKKKKGGGGGGENPNNPPGKAPNPQGV GVPPPPPPPVFQKNPPPPPPFF*KNPPPS PKGPPGGPPPPPPGGGGGPPPT/PYFL KKKGGWGGPPFF*KTNPCKGEITPLVG
6190	20091	A	6243	20	261	WAQEILKKFSCLSLSSSWNYRCAPPHVA N\FVFFVETGSYHVAQSGLELLDSRDP TGESHHQAQPHFC*ILYTGESQRIL
6191	20092	A	6244	376	76	LLPRLECSGVIKPFSHLSLPSSRDYRCV /PTMNF*KFFVELKFNSL*R*GLTMLP RLVNSWCQVIPLPWPVKVQGCATTG LTDFTTTFKGYRHGDTY
6192	20093	A	6245	222	233	KSFYFALIFEKNFCVVKKSQVGLVFFSK VKVLVRPFFPMVICKNQ/FNPL/RFFF FFFQDRVLLCHPGWSAVV*SKTLS
6193	20094	A	6246	2	358	ETILTFQSY*ENTFNEAITAIDSSD SGSQSKWKSFWKRFTILGAIKNICDL*D *V/KISTLSGVWKKVPSLMDDFEGF\K TSVEEVIADVVEIAR*LELEVEPEDVIE LLQSHDKT
6194	20095	A	6247	3	322	PDHSLQLTPTPGFRSSSHLGFSSSWDYR LEPPHSCVCVCV\PCVYIYFFFLFLEKT GFGFVPQAGLNLGVKRI FKA*PPGVVEI PGLTHTPGPWGGPIKGKGANPAP
6195	20096	A	6248	1425	1280	SLDFQGLALPGWSAVV*SLTEASTSR\ VKRTSHPSLPTNTWYRHALPRLANSVYF L*RWGLTMLPRLGNS*QAILQWPPK VLAL*ADEEMKAKGHISTKWGGQTLNPQ PDCGATSVVSLPIRKFO
6196	20097	A	6249	189	336	HAPFFVSVISLSCQKRRR\WLAMVAHTS NPSTLGG*WGWA*GEEFETSQ
6197	20098	A	6250	2	300	FLPSFMGFNVLGHGRASTVTPSEPLSL PFLPAEPFLFFFLFRKRESIFGA/P GGLEGGQNFLEPSPPGIKEIFWPNPPR GWELKIWPPPPINFCDF*EKTGFTMVAR AGLKL*TTGGLEGGQNFLEPSPPGIKEI FWPNPPRGWELKIWPPPPINFCDF
6198	20099	A	6251	1	198	LTGRL/SKCEVVSWRFDVQLKDLKRWQN HLLSQQLACIVLTSAGIMDHKEMR*KH TGGKSLGFFF
6199	20100	A	6252	11	214	SLRLKSSSHLSLPSSWDLRCELPHAN* KKKKKL/CKN/RLTGLPKLVNSWV*T ILPPRPPRALGLEA
6200	20101	A	6253	402	3	KKGFVLSQVEDKDAISGSFNPGGPGRK IPPPQPPEEVGPPGPPQTRGNLGI/LG N*GGGGGF*PPGAGKSPAPGPQKG\PPG KDKREKPYGPPKLEFFFLRQSLCFAQA GVQWCDLGLQPPPPRFKQFCL
6201	20102	A	6254	362	78	VGVN/MTFFPQHFLGLSGIPRRYSYDPD AYTT*NTVSSIGSFISLTAVLIMIFII* EAFASKREVISVSASTNLE*LHGCCPP YHTFEPTYVKVK
6202	20103	A	6255	357	2	DLSCSHGEATQKHSECKASCCTHMTIT ALFLIAKHWNQPTC/PHIMBYNSVIK/N EQITDTTTWMDLKCIMRHEQRQS*KNS VLVCFHAADKDI PETGQFTKERGLMDLQ FHVAGEASH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN '09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6203	20104	A	6256	2	305	QWCNHSSSLHSNPGERETVSSLLKLPKAWN PRHMLLCPTTSFILRWGFIYVAQAGPDT RGHASL/LA*ASPSVGITSKSQRVRPVH DIACFHRESTMFAENFN
6204	20105	A	6257	335	3	GPFQSPPPGVTPISCFTPPKKGGNRGPP PRRGKFWIFKKNGGSPG*KRRVLFDPDG VPPPRPLKKGGLKGGAWAKIFFFFFLRQ SHSFTQAGMQWCNLSLQPPPGFK*F
6205	20106	A	6258	219	2	PTLSSQKDTKAQRLYSFPLTTTKDERLV TLVS/WPGVVAYTFIPSTLGGQGRWVT* AQKFETSLENTVKPPSC
6206	20107	A	6259	306	117	SFELLGSSDPLTSAISSWDYRCAPSRLA NF*FFVCVEMGSSYIVQ/SWPQ*ILLSW PPKVLRLQT
6207	20108	A	6260	572	269	ETDILSVAQARVGGLHLGSLPAPPPGFT PFSCLSLSS*DYRRLPPRPA/NFFVFSV EMGF\TVLARIVSIS*PRDPPPSGLP*G ALGLPGVSLRPAICLLK
6208	20109	A	6261	357	116	FAQAGLELMGSSSPLASASQSVGTTGMS HCA\RLLLFFCGGRW*GG/LK*FSCLSL LSSWNYRHEPPHPANLCIFSFNTISY
6209	20110	A	6262	3	337	HERHERHERHEQSAETGVSHHAGGGIG LNNFFLFLFFEAGSCTVT*T/GV*WHDH GPQ*PQIPRFK*SSHLSLHSSWDYRHVP P*LGLQACATMPG*FFIFCRDPISINK
6210	20111	A	6263	515	150	FLRWSFTLVAQAGIQWGVSSLPQLBPG FKQFFCLSLPSSWDYRCPPCPTNF*L LVEMGFHHVGQAGLELLTSGDLPASASQ SAGITGISHRAPGTLEFF*AANGGKQV FLLLRVLNGL
6211	20112	A	6264	1	296	GTSFLPSFLP/LLSFLKFLNFFQIVSHC REGWSAVA*SQLTAPSI\FGLKPPSOLS RLSSWDYRCPINFF\SLPMLPRLVNS* PQAILTPQPPKFLGLQA
6212	20113	A	6266	298	182	LHFFEVSKIILIRAEAKWCL*VLFTIA KIWKLR**ICKYLSIDEWIKMWTIHTV EYSAIGNKEI/PVIVTIWIYMENIMLS EIN**QDKCMIAL*GIYIQ
6213	20114	A	6267	402	234	PPPPFLKNPPPPPPFKNPPPKKKTIFF/ SPPVNLAPPKEF*KGPPPPPPPPPPPP PF
6214	20115	A	6268	125	17	KGQAQWLTVPVIALREA/EEAGG*LEPR SSRPAAWI
6215	20116	A	6269	1109	454	GDSAGAEGTMENFTALFGAQPDPPT ALGFGPGKPPPPPPPPAGGGPGTAPPT AATAPPADKSGAGCGPFYLMRELPST ELTGSTNLITHYNLEQAYNKFCGKKVKE KLSNFLPDLPGLMIDLPSSHONSSRLSI EKPPILSSSFNPITGTML/VRLPPPHWP VAGAVSSDAYSASQEEE*AAQATEPYPG SCPPRNTI*FRSQEEKEKRRGS
6216	20117	A	6270	111	86	VVGITGVSHCAWSRNGTLTHCWBECEKV /QPLRKT*QFLMLKI\PYQMI*PLLGI YLRKNKAYIHMKTIL*MFSLFLFEIAK/ TWKQPKYPSASEWIN*LDSFSLYLWGS RTPDLK
6217	20118	A	6271	2	222	RSCESSQTSACYKSFYLYPLKS/GGFK ILERM*PIYFLIPYVVTIFNQRYFYIW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NLKKTRGIYTVLYKMYKSF
6218	20119	A	6272	787	470	LPFFFSFFETGSHCWWRERBSLGVAQVG VQ*CDLRSLQPPPPRLKQSSHLSLPSSW DYRCAPP*LDKFFFCIFCRDGFHHVAQA GLKLLSSG\NLPASVSPSAGTTL
6219	20120	A	6273	2	322	FCMAIAAIDSSSSHGSRESKLKTLWKR SILDAIKNTCDSEEV/KVST*TEVWKK LIPTLTDDFQRFKTSVEEVTA\ELLVVE ITREIELEVELDDVTELLQPHDQT
6220	20121	A	6274	175	406	KNSLGGPNLTGEGKKITFSL*NFFFSLE ALIFVGRLLSSFPVPPKIRFFSKNSRNLF /CPVGEFFKTRPPVNFSSLP*RKSYFF SFPG*IWPP*GIFLKAPPPFFFFFLRE RRVSMPLPRLMSNSWVQVTPPPWPPKVR VLLGIVDVQ
6221	20122	A	6275	2	181	PRVRGRVGRKGGKSFVHCWWQWKL*P LWKTVWRVLKTLK\IELPYYP/ATKLL* SYPLE
6222	20123	A	6276	397	47	PPPSKNFFFPQKDFLGLPKKSPFPK K\FFPKKTPKKNFPPSPFFKPPPPAFI KTPLKKKKKFFPPQKFGPPPKFFKPP PLFFFFFFFFFFITAP*KITKSIPIFYFF TKTFYL
6223	20124	A	6277	2	264	ETESHTVAQSGCSGAI IAHRSNLQGST NPPTTAS*VAGTTDACDHAWMF*FL\V EMGSHYVAQAELELLSSSDPP\QSPKI LGLQA
6224	20125	A	6278	3	204	IRCYRKIFYERKHQWLQQLSLLSYFKKL POP\PL*ATITLISQQSLISRDPPPV KR**LTEG*DDC
6225	20126	A	6279	57	306	INKANRDKL/GTIDFLEFLTIKVRKMN TKTESKRN*ESILHVE*EDTGHVRAAA VCRDMTYLGEKLTDEEDVK\IIREAKYW
6226	20127	A	6280	419	18	SSSSPKACMFVYEWVCTQKCVWIYEYMC VFVYV*LVLCCMNVCACM/C*SACV*M CVICRCVCM*GLSVICEGVCM
6227	20128	A	6281	459	235	FLRNGVSCCHPGWSAVVQS*LTAASNS* AQVILPSSWDYRPVTSHPAKTHNFYMQ/ CGNKKMCTHISIVIFSLQ
6228	20129	A	6282	505	470	GVP*GQEFEPSSLHMRPCFFLKCKINP AWWQKLF*PRRQKFRLTQI/LALAPQG QQKVNFFS/NKKKKKNPNNC*IALR
6229	20130	A	6283	206	374	GGGGGKKKNWGGGKRGGEKKIFFF*SP PRFFFSPPYKKKKFFPPPPFFPPPNFF FYPPPPPPPPPPPPPPPPPPPPPPPP FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFLNHFF\FF*LYVII LFMGHSDILMHVHV
6230	20131	A	6284	431	269	YIKGGPPPEIETFLIFFYYIYLIPIFF FFFFFFFFFFFFFFFF*FVCLKLIFNHI QRF*TYISIPHFMLLM\YTLHLFTFCIC SLFTIIVVFYIFV*L*YCTVKALCNSL LVSELDKYIKNNYNCKQ
6231	20132	A	6285	298	44	YLFFFFFF*VELVFFLCMFFFFFFF FFFFFFFFFFFFFFFFFEEKNKVSFNS CFSLSLFKLYFLKYNFIQLQGNLHFN NI I
6232	20133	A	6286	386	1	ANLHIKVNFFVNFTLLNFSFLPVWFGFH FLVV*RVYLSHRGFYVFFQNFLRIFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SF*VG\FFFFFLLFFFFFFFFFF FFFFFFFFFLCIAIVFY*IWYISYFTKY IEEPRTGRTRGRTRG
6233	20134	A	6287	190	134	LEFGNRRFQFSRMILRGSGLOWRNYADM VKIAKT*YLRNTFHKVIAIIGDSCDGS GQNKLTFWKGFSLDAINGIHNSQBEI KMATLTGVWKK*IPVLKDDFEGFRTSVE E/V/TADMVKIAKT\LELEVPE\EDVT* LLERILF
6234	20135	A	6288	394	2	RRQASLSCGGLHPVRSSRLCLPKQAWA MAGAPPPASLPCCSLISDCCASNQ*DSV GVGPSKPGVGYHLLVHRFLSPLEKRSIR VGVARFSRCLSLPLSLTRKGN*LP\TPC ASRVROCLTLQLAHGALHP
6235	20136	A	6289	233	58	DRVSLCRPRWHVVSRTRLTVASTSR/LQ AILPPQPPPE*LGPQASANRSPRSPKLTG LRG
6236	20137	A	6290	385	48	TLQYLCTPTSTV*KKKKPENIKYW*QCG ANRTLFQ*WQVCKVAQTLWKPVWHYTVL NLNTRIVYDPGMPLLGTTNNNAYMCCIC\ YQKTFTRMFIAALFEITPK*KMHKYLTV VG
6237	20138	A	6291	273	36	RNGRWTPCGGR*IHPS*GTDVYLPVPG TLSSSQASNSHPLLKAPGSRP\PWPTDL GYKDFRGPPSPNPACRRRPSLFHSD
6238	20139	A	6292	394	5	AKIYFSINPLVFSKQ*FLKNVFPNHLHL QFFSNINSLMLIKV*ALLQDFPLVHNVY NKICDTSKDTTTLFMYLMFVFKMTFFS LKAYI/WSGTVTHTYNPSTLGGRGMWIT *QGEFKISLANMVIASLY
6239	20140	A	6293	536	190	RRSFALAVQAGVQWRDLGSLQPPPPRFK RFSCLSLPSSWNYRHAPRPANFVFLVE TGFLHVQAGLELLTSGDPPVLASQK\A GMTGVSHRVQPD*GHGGSRLSSQPFWEA KTGGSPEVRSSRA
6240	20141	A	6294	2	238	HEADLGTQVLTHPSTTAMYFVHYCQPP *ILYGTINT*PPVHKNPIHIKTP/SPC LQASTAINPQLSHINC\NPKDTPH
6241	20142	A	6295	2	447	FFFLMGVSLFCFGL/WSAMGATLGSLAT SCLLGQVQVILLCLSLPSSGKLQVCAYPH LG*FLYF*AEDGGFSPCWPG*VSNS*PQ VIHLFPWAPKALGITSMSHCCPACFHCTF FRHFRONPHNLFFFLGLGLSPPPPSQ PLEGGKPGCN
6242	20143	A	6296	2	133	AEERERERERERERE\REERERERERE R*VERERGGVPLRTYR
6243	20144	A	6297	3	244	HDYSSFLAPPALGYMRPLHPAYFILFY FIS/FYLFFSQDEVLLC*LGWSQTPELN QASCLGLQKWWDYRCEPQCLAECD
6244	20145	A	6298	1	361	GTRRSAMLARLVNLSGPQ/CYLPALASQ RAGITGVSH*GCPFFSLKKRWRSHCVA QAGVQWFFRG*TPGLSCFSCSLPSN*DY KCAPLCPP*DTVF*VRAVSSEVLTITY RGEAGGVNA
6245	20146	A	6299	3	348	HERHELEELIKNLFFFFFGKKIFFFF GGKNGGPF*FIGAFSFRPQGIPLPYPP* KW\DWGPWPCCRGDFWFF*KKTPFSILA RVVLNSPPWGILSPYPPKGVRFPGGTPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						PGPV
6246	20147	A	6300	1	436	VDGEFSCSLSPSGWDCRRASPCPANF/S VFLVGIGFRYVQAGLELLTSGDLLASA SQSPGITGMSHCTRPKHH* IANSSSVL GDFRIDYFQISRKAQWITLGYNPWAESH LLMGAGLRVLPAPRIMISQVDLLPATHP SSGRRG
6247	20148	A	6301	370	70	PKG*STLPASASRSAGITAVIL*SHCTS PPM*LRFKHFTHSSTSTPP/ CFFFGKK ILIFVPQPGKGPNLS*LPKLLSWLRKL PCLTL*RGGDYPGFPFPP\SYFCFFIKK GV*PCGPGGNS*PASASRSAGITAVIL
6248	20149	A	6302	1	285	KHFFLEFYLFRDRVSVCPYPSWSTVVE/S L*SWLIAASN/CLGSK*FSLSLCHHA LLVDFNFL*RRRLRQPRLVSNWSAQAI LSSQPPKALELKT
6249	20150	A	6303	194	351	GTFCIKKPVQ/WLDTVAYTCTPSTLGG RDGRVT*AQEFETSLGNIVRPHVYKK
6250	20151	A	6304	354	211	YRHMP/S*LADFFIFCRDSLFLMLPWLVL NL*AQAILLPQPPKVLGLQE
6251	20152	A	6305	1	346	GTSSQLISLHSSPTASYPPKHLHRLT ELLSVSLMAHVLSVSPATSS/PILQPHP IYPCTWIMFTSHSSGSGKPSQTHHTYT HTHTRMCAHSGGHATLPP*HPLHPRHSA YLLW
6252	20153	A	6306	395	177	WLNTLWYIHTVDYFLAMKRSDDLHSPW MNLQGMILSEKQ\SQR*HV*FYLYNN VEMKKSQKWRTVLWLPB
6253	20154	A	6307	2	718	GVLPYWPWGSRTPDV/HPPTSASQIAG ITGKSHRALP\KFAFLTSSQVMLTLLAH GTTAVVFSKLS*F*EPPMTCAVFSVVTG SCHINSFRIQTCL*YYSVFTSCFYCSMI EKLTTGIS*QKEHELPPFSQSSDIFKLAY LIFFW/CVVMESHVSQAGVQWHNLSS LQPLPPRFK*FSCLSLPSGGDYRCPPPH MANFCIFSRDGVLP*PGW\S*TPDLRM DPPGLRPPQSAGDLTGMEA
6254	20155	A	6308	377	67	PPPKIFFFSQTLFFFWGGCPQIAPPPK KFFF*KNPQGGFFPPPKKKKIFFFPPPK FLPPQKFF*KPP/LSFFFFFFFFFFF FFFFFFFFPTI*IFYSMSFLP
6255	20156	A	6309	1	362	QTYAKMHVTIIFFGVK/LTFLPQRFGL SGMPRRYSYPVAYTT*NILSCVGSFIS LTALILIIEMIREAFASIROELIVEEPS INLE*LLGCPPPYHTF*EPGYLKPKRRR KESSPPKLV
6256	20157	A	6310	2	411	VLPTLWEAGARGSLERSSRLQ*AMIT\ HCTPPWAT
6257	20158	A	6311	59	334	THACGNMLSYAGSFISLTAVLLITFMI* EA\FASKRKVLIVKEPSINLE*LYGCPP PYHTFEPPVYIKSRQKRKESNPPLVSS QPHGLHDL
6258	20159	A	6312	3	22	KPSP*PLTGALLDLMTSLSM*FNHFS ITLLILCLLNTLSIYQ*WRDVTRESTY QGHHTPPVQKGLRYGILFITSEVF\F AGYF\WPFTHSSLTPTPQI*GHWPTGI TPLNPL*VPLLNTFVLLALGVSI*AH D

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \=possible nucleotide insertion)
6259	20160	A	6313	11	182	INKMW*I*VRG*YSVIKK\DEILSFMATWMEVEDILLSKIREAQKVTHPVFSPISGS
6260	20161	A	6314	3	421	IOASTMAGAPPQASLLPCSLILDCCASN S/RGSVGVGPSEPTGVNLLVCLLLRPS EKCSIRVGVT*FSRCRPSPT/TKGHSPT PCTSRMR
6261	20162	A	6315	1	111	DRGMNVFMPANTASVLWPMDDQGVILNFK SFYLRN\TFSKYISAIDS DSSVGSGQSK FKTF*KGFTNLDAIHDSWEEIKIST*TG VGKKLI\PTFRDDFKGFSTSVAEVSADV VEIGREL*LEVKPGDRTELL*SVLWPMDDQGVILNFKSFYLRNNIF
6262	20163	A	6316	440	312	TSSFSLSPFF/CQDG/SLTMLPRLVNS*PQAILPSWPPKVLGLQL
6263	20164	A	6317	5	404	PRVMIVKLLKI/ERNKILEAAREK*HFT SRGKAIWIIVDLSSETMEVRKNLHNFQV LKEK/NKTWEVRILYSARISFQKKGKIK IFSDEGKLR*SFTSRPTLRE**RKFSK* K*NDRRRLNKTFRKKKEYPKELKP
6264	20165	A	6318	394	182	MFIVA/VFSKAKEWQPKCLSTDEWV/Q YM*YIHTMKYSAIKSNELVIHVA*IL FENTVLSERSHIWHGSHI
6265	20166	A	6319	1	378	APSDFFLFQSLNKLPLNCTHFSVVHNVKK TSLT*LNSQNPQFLRDEENGWYHCL/QK YLELDGAYVKK
6266	20167	A	6320	286	314	NRCCFSLPTQVKCFNLVIGICCVCDWGY YRWLNF*NPIF*FILRQFHSVAQAGVQW RDLGSLQPLTPRPANFYILVEMGF/TPL LARLVLS*PSLLKYKN
6267	20168	A	6321	23	397	QKTLNMEKEMNIYIHKM*ITPNRSNIKR SSLRHITVKFSKVKDKQRI/MKLAIBKQ PITYKETTIRLSEDFSAETL/NARR*WD DIVRYWLKKKKKKKKKKKKRGGGLLN SLGGPILTGGGKEIF
6268	20169	A	6322	411	2	TEPPPPGGNF/L*TKPGKKNFLPPKNLG FFSFFSPLKFFFSPPK\P*ILGGGAPFC PPQKKGFFPKIPRGVFFSPP/YKKKNLI FPPPVLGPPKVFVKGPPEPPPPPPPPFG QSGQVKLKSPKCK
6269	20170	A	6323	395	280	MLARLVNS*P\CDPPGLASQSAGITGM SHHVPQVNHF
6270	20171	A	6324	3	359	QHYLVFRETQIKAAVRCHYIPTGMAKII KTGSTKC*Q*CGAAGTLHCWEECR/LK QPLWKTAW*FLI*MLCD*TVPFLQIYPT EMKMCVCRMT\RVFLSVLFIIASSWKQ PKYHKLVN
6271	20172	A	6325	3	174	FFFETGPNFVNQAGGQGHDLG*LQPPPP \GSRIFPA*TSRVAGITGLNHHPHPLGS IF
6272	20173	A	6326	265	13	TASPIRIITSQDVLHS*AVPSLGLKTD AIPVRLN\QTTFS DTRPGV*YQCSEIC GANHSFMPIVLELIPLKIFEIGPVFTL
6273	20174	A	6327	32	259	CYYEHLCTSLCVNWFPHFF*VYT*EWQW PKYLSADEWINKM*YIWTVEYLTIRIS EVL/SATTWLGLENIMLSKRS
6274	20175	A	6328	1	228	PGLNHCSHLSWDHRHALQCPANFG/YFV ETRFTVLPGLVSNDDPPALASQSAEITGV

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						SHCAQP*VCFHYCLTFFSLQ
6275	20176	A	6329	346	1	LPKKKKKKISRGLFPFQLPKKKKDNEKS LTFSSSETMPGRRQWSKIFKVLRGKKQPQ QPRIISLAKLFLKSEDFL/ETQKLRFFV ASRPALQAMLEVL*REGK*YRSLFKKG RALK
6276	20177	A	6330	349	77	HTTPKKKNKH/RKKIKLDVLRYNKVDN SKMSGHLH*QCPSDECDAGVFMASHKQ/F DRHYCGKYCLTYCFNKPEDKAQHCGLS PRSLRPAAWAT
6277	20178	A	6331	319	46	RPRRPETK*ALNK*KDI/PMCSWKQRHN TVKMLILSKLINRFNAITIKISTE\FHR NKLILAIWKCKGPRIAKTT*KGKLEE LLYLISRPP
6278	20179	A	6332	496	309	DRATAF*RQSFTLSL/RAGMQWHDLSL QPPPPGFK*FSCPSLQSSWDYRCPSRT G*F/CIF/VEMGFHGGQAGLELLTSGD LPASASQSAGITGVSHCTWPNILNWK
6279	20180	A	6333	3	173	HHHSRL/IFFCSVLGTSSHYVA*AGLEL LGSSNPDLASQNPGITYGSHYAWPDIP VF
6280	20181	A	6334	339	153	FSPPPPFFKGGFFPPPPPPF/SF*PLRG GGPPPPFGPPGVRPPSPVVSWCSPFPV VLASFFFS
6281	20182	A	6335	32	331	QLLNHSVIVFLLSFDHSYFLRNLSLFLA FKLIGVKNS*YIILSFRYLLHP*HLNLF FFF/CKRQGLEVLTRLVSNWAQGCQP WPPKVRGLRAWSPGLSL
6282	20183	A	6336	226	177	DGVSLLLPRL/GGATSAHCNHDLPGSGD SPVSAS*VTQLQYYFCICLGLFTFTTRL SAYLGTGKLTALPNTPGLLDS
6283	20184	A	6337	302	59	KMLLNTIMCNREIL/RKRKSPRVHQTSS VSYFKLPQPPQHSAASTLISQPPSSK QDPPAAK*L*FVBGRLIAFPPSNNVF
6284	20185	A	6338	197	28	AEKVRFSsavTWHLGSHSL**SKNL/W LGMVDHNCNPSTLGGRGRIA*AQAFET G
6285	20186	A	6339	46	317	EVPSSISSQISLPSGDFSSVPLELSNL FFMPCPEHIIIVTCERVTSNYS/YKWKP EFSYP*IF/CFKMSLTMLPGLSLNSWAQ VIIPPQPPK
6286	20187	A	6340	4	276	QTTLRGTTVQITKNLSSETMNASRCEKK NL*SANGWGMWENNYQPILYSAKISFKN GVEIKTFTN/KQKIKN/FITSITLV*EI LKEVLQAEQ
6287	20188	A	6341	485	2	GVWEFLETESRSVAQAGVQWCDLGSLOA PP/PGFTTFSRLSLSSWDGSPPPHPA NFFFVFFVETGFRHVSQDGLDLMVIS* PREPPASASQSAGITGVSHRARPXHSKI LIAGSRRSIQMFVPKFFQKLAVVENFQN TKDFLNPYSEILLHTSQIHSSC
6288	20189	A	6342	2	339	EDLRVKLKEGYSNISYIVVNHQDPMNL SNGSVTVVALLQAS*YLCILQAS*ASSQ SWTS/VTLAAVSFQRISNQEHPVYQQE ENQTDVWTLNLSKDDFLIYDRGCLVY HL
6289	20190	A	6343	181	12	RWGLESGWDYRSMPLHPVNF*II/CMRQ DFTVLPRLILNSQPPVILLRWPPKVLGL

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6290	20191	A	6344	3	295	QA YWHLSCF*FLAITNKAAMNIRLLWTCAS IFPR*RSRKEMAGS*GS/SLFNFVRNCL TIFSHDCTTL/HS/HQQWGGV/PVLEFP HQHLL*SIFLVFDILIGI
6291	20192	A	6345	334	8	KPSNPGGEGFP*KKGPKVFSFWGKKNF SPKKKKKI*CPQKPKGPPWGAFAFKKK NF*NPRGSPQL*KKRGIIIGPPTLIPESS QRPPPKKKKK/GPPKGALLAFGGIKFF FFPLEKNFLFPKPGKTLAPFFKGLPL PG
6292	20193	A	6346	68	256	WVA\PVTHTCNPNTLGRRGRIT*AQEF KTS LGNIVGPHLYKNLKKKKKKGEEKP GGGFSPL
6293	20194	A	6347	385	60	KKKKKNRTPYDAAI/PSLGTSSKEPKSG SSRDICTPMFIA/ATKRWK*LKCPMSV NI/VKMWFIHMMQY*SAKKKEILS*MH LKDVMLSERMLSQSQKKNFCMILLWGI
6294	20195	A	6348	234	61	CHRIEHIKMVNL/WLDVVVHTCNPTLG GQDTWIA*AQEFKMSLSNTAKPCLYKKY KN
6295	20196	A	6349	2	358	FLSLGIHFNYCLVTTESKLSKLRLTYFF FFFLETEFFPCSPA*RPW\PNLG*LKFP PPGSRTPALTLPRTWNNRRAPPHEANF GFLRKNGV*FFGPGGFKTLDLGGPTRLW FQKGGNN
6296	20197	A	6350	346	27	KMV*SLWKA VQFLIKLNIH*PYDSAVP LIG/IYPT*MTT*IYTKP*TMQLAAVSF IMAKNTRNESNIFNWPIDKLWYIHIMEY **AFKRN*LLINTKT*MNLKC*LF
6297	20198	A	6351	36	158	KNSVPSQE*LYYL\QENRLNSGGTIGCR EPIWCHYTTPAWAT
6298	20199	A	6352	2	146	RSSHLSLPSSWDYRRAPP/H/LANCCIF CRDR/SFTMLPSLVINS*IQTILL
6299	20200	A	6353	74	303	EPSICGQIYLSFSYKIQK*/WPGAVAQ ACKTSTLEG*GGWIT*AQFKTSLGNMMK PCVFSKKKKKKKPHPGGGGRKK
6300	20201	A	6354	3	210	NNKKIWT LKNLKFPRDRVLLCFPDWSTA VHSRLTAAS\TLGLKQTSCLSLVSS*DH RCMPPLALKRKKT
6301	20202	A	6355	2	627	GRVGGFLVPMRDLAEASRGQQQVKLGE MKPSVSCVCGGV*CISKFKLN*L/WPG TVARTCSPTSLGGQGGWIA*AQBFETSL DNMVK\PCLY
6302	20203	A	6356	584	166	RQGHNVAGVQWRDLGSLQPPPPGFK* FFHLSLPSSWDYTRVPPHLANF*FLVE TGFHHVQAGLELPTLSLPAWASQSAG ITGVT/HQARLQLL*KELINPSTLGPTW ELLEAWGRCPSSVVMGDDLALNCFHHFSV S
6303	20204	A	6357	448	202	FTTLVSECI*DIHDSWKDV*ISTLTGAW KTWLIPTLVNGFEG\FKT*VEEV TADV EIARESELEVEPEDVTLLKSHDKS
6304	20205	A	6358	3	237	DRSSL*P*PPGLK*SYLSLPSSWDHKK A*PHPANFCLTF/V*QRGLDLA*HDP PASASQGN*ITGMSHRAGPPLTF
6305	20206	A	6359	49	242	SSYLSL*P*PPGLR*SSYLSLPSSWDHK HA*PHPANFCLTF/V*QRGLDLASHD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PPASASQSTSTITGMSHRVWPPLTF
6306	20207	A	6360	508	223	FVTQAGAR*LDLSSLQLPPPGFKQPSCL SLPSGWYRHYV/STPIVF/CIFSRDGF HHVGQAGLELLTT*STCLGLRSAGITGL SHRAQQERGFEF
6307	20208	A	6361	2	595	AIVVG*GTHFLIPWQKPIIFDHRSPH NVPVITGSKDLQNVNIIPCLIFGPVTSQ LPRIFRIGEDYDERVLPSITTEILKSV VARFDAGELITQRELVSQRQVSDLMERA ATFGLILDDVSLTHLTFRKEFTEAVEAK QVAQDAERA/RNSLATAGDGLMELCKL EAAEDITYQLSRWNITNLPAGQSVLLQ LEQ
6308	20209	A	6362	1	259	LESFYFLYYK*SS*PLRLKRLILFIF ETECPPVA\QLECSGTISAECCLCQGS GNSPAPAYRVVGITDSFRITHCILTCIP SE
6309	20210	A	6363	60	221	NTTKLGMVAHTCNPSILGARGGRIT*V* EFKTSLDNIVK\PCPTPKKSLKIKLN
6310	20211	A	6364	1	393	RPRRPQTGVQWQNLGSLQPPHGFGRFS CLDLPSSGDYRHTPPCPANFSGFS/HHV GLKLPDSSDLPWPPKFVGIARHESHRKC T*RSRRGRIADPLER
6311	20212	A	6365	19	85	CINSKIMQSSRITTLCKMVQPL*RALWQ CLIKLNIHPHYDSAIPLLHFYQCK*RHM NPHN\TFTSMFITALFITARN*KQSKCL SIGQWMKK*CIHTVQ*NSGI*HE*IN SKIMQSSRITTLCKMVQPL
6312	20213	A	6366	2	298	PRLAKVQKFLFFFLVFF*DRVTLCHPG WTAVV*SQLTVTLAHRNLRLPSGWDYRH VPQRLADFVFL/CR/DRGFSMLVGLVSN SRPQEV*ATSPSQSLLS
6313	20214	A	6367	67	636	QDNKKGIYLFVYFRQSFALVAQAGVQW HDLGSLQPLSP*FKQFSCSLSPSS*DYR HAPPRPANFL/QFLVETEFHHVGAGLE LLTSGD*PASTSQAGITGVSHCTGPRI RFLKTFSHLEAPGGFPEKQPLRSERLQ FRAFPQTAPCAHAYLLGCVSHLEMGRN IDIPELSFFLCPLQCLIIYRGKSP
6314	20215	A	6368	3	251	RSRHCTPAWAPLSTQDHPVVFYFPLHPL IGSLFIFACFVSSYFIEFSYCL\YFFVD SFGFYRYTMK*NLNSNYFKLSAELPQ
6315	20216	A	6369	333	193	FKKLVMIAKAKYCKANFFFGVPPVASKN /TGDLEWEEPGWSQTPDLR*SALLGLPKS WDYRHEPPPPRLANFCI/FLVETGFQHG QAGLALLT/S/GDPPASASGALE*LGGS SCL
6316	20217	A	6370	36	369	RPTRPEMRFHVPVQAG/PRSPGLK*SAC LSLSKCWDYRHEPP/*PG*FSFPTYIYI YFFFLFFSFSFLEEMGFHHVVKAGLELL C*NDPPASASYSRIIGVSHQARPFFFF FF
6317	20218	A	6371	2	375	DIQIMDRNIKN/CSTSQSIRKLQIKRIM *YHLTSVRMAITKKTHKC*RCGKK/LH C*WQCKLVQPL*KTIQRFVQKTENNINI *PSNSKN/WKSAC*RDICTAMCITT*PI RAEHGGS\PCNPSTLG
6318	20219	A	6372	75	372	NGNSQKKKKKKKKGGPPLKKPSGGPNL

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						PPGGAKKSFPLKGGQKKPPGGFLEKNPP LGGAFL\GPPPPPKRPRGKTKP*GG*R GKNPAKPWLGGKILKP
6319	20220	A	6373	605	350	ISTGICLGMFIAALFTIAKL/WKAT*PS FNR*KKKMCYIYASYSAIKK\DAILSFA ITWMNLENIMLSEISQTHKOKCCMISLI CAI
6320	20221	A	6374	167	378	KKSQGGTNIKPPAITKYLSOMGG*KKLL TGFLKKKSLGGGAGVTILLT\NRTFST KINDPDGGGDHILSQ
6321	20222	A	6375	994	747	VSLALSPLRECNGVISAHCNLRFPGSNN SPASAS*VAGAHHTOLTTFVFLVETGFH HVGQAGLELL/NLVIRPPWPPKVLGLQA
6322	20223	A	6376	1956	1592	HEFEMESYSVTQAGVQ*HDLGLLQPLPP RFKQLSCLSLP/RWYDYCLAPPCLANF\ *YLVKMGFRHVQAGLKLASSDAPASA FQSAGITGMSHRARPKSAFKIQAIIGEG GVSELHRKINI
6323	20224	A	6377	94	402	KTQELQNKISHCLIRRVDRKM/WLCTVA HTYYPSNLGGQDGRJA*GLEFETSLSNI TRPLRYRKKKKKNVQAWPLWSNFLRR LRREIRAESF
6324	20225	A	6378	463	146	GKLGPPKGSLLKPPPPFFFL*R/P/HPP PRGETPFFFKPKPKSPRGGGASPPFPPL GRVRPENFPFPRGGQSP*PKRGPTPALP PGGQKETLFPKKKKRKKKKYMRLL
6325	20226	A	6379	3	207	LEYQVAQTMCISSRIQLVAEKASVPFV DKTVLS\TMGQL*EAKAEDGFFVPG*YG LAVSPLKFQSTRP
6326	20227	A	6380	328	70	RPRRLGLPRSWDYRHEPLHPDQLLVEI MSHYVAQAGLKL\ITGVSHHARPH/YR F*LGH*SLVRRPWTISYFCLGFPFMW EVSD
6327	20228	A	6381	13	77	VIFLLQPPK*SSCFSLPNRQDYRRVPY PANF*FS/CRHSLTMLPRLLF*TGLQAC ATIPS
6328	20229	A	6382	342	77	KGQGFYPHLFFFFFF*KDSPSLPRVEC CGEISAPCNL*LFGSNDFF/ASHAIVGG KLPKQKGAFFS*GGGFFFF*M*KHSV LNSSRN
6329	20230	A	6383	1	208	RGRVDKIFYLFFETDSQSVT*AGV*WLN PGSLQPLPPGFK*FS*PQVI\TCLDLPK CWYYRREPLCPVY
6330	20231	A	6384	277	50	LVLKLGRCCTSSFI*NFKGPQIAKTILK XNKAGSLT\LPNFKTNYKATVIKTV*YW HKH*YRHGFISGLSILFH
6331	20232	A	6385	2	354	AASTNFRDR/IL/LCHPGWSAVAQS*L TAVSTLN*AQGIG\SSHLSSLNSLDYR APPLAVLLCCPGWPQNSWPQVILLSQP PKALGYRCEPPCPAPLLNFFFFFKNRL WFCCPGWSA
6332	20233	A	6386	2	188	FFKYICY/CINMYMCFYIFINIYSLIYL *IHIYKYIFAYIFINTYL*YICLYIYK YIFIYYR**YICLYIYKYIFIYYR
6333	20234	A	6387	2	241	WATKCR*G*RRGTGLTGG*WDCASGQL *KTFQQLISITY/PYGPALISLEIDPS ELKTYVHTKTRT*LFIAASFIITKN
6334	20235	A	6388	142	429	YCVCIYIYIFLVLFIFCTFFTYSSLHL

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						LIFSFFFFLERGVCFSPRGGGGKYLGL WRFFPPE*IKKNVYIYA\QQYYSIAKQN EILSFAATWMELEAIMLSEIRQAQNDKH YMISLICGIKR
6335	20236	A	6389	468	250	VHRRTPPCPIIFFFF/CKQ*VLPLPKL VSNWPOATLLPWPSLTVEFQALTPGWK NFKKMLVMWSWSIKKR
6336	20237	A	6390	616	1084	LCLCQYAGISVQCPDCVFQFFHNVDSTY EDYLRKLKTSLSFWRRSFALVQAQGVQ WCDLGSLLQALPPGFK*FSCGLGLSSWDY RHPPWHPANFVLLVEMGFIVHGQAGLEL LTSGDPPASASQSAWITGMSHRTQOE\Y FLNLKFSTSPGELLCLK
6337	20238	A	6391	415	200	SPPPRFFFFCPCPKNFFPPPRSKNFFF *RGPPFFFFFKTFFF/VFFFKPPFPPR /RFKNPPKIFFFFNRGPKNPGGGGKKK PPGPGGFSPLWGPFPFKPPPPKKNP PLFGKKKKKKKKRAAPR*NPRARGVF FFPPPLGFWAPG
6338	20239	A	6392	3	117	KLKPSH\DY*VGETYGDITSRGKDKP IACVCTFSPLS
6339	20240	A	6393	3	204	DRVSLCRPGWSAVA*S*LTATSNS*\VK QSVHLSIP*GSWDYSCVP\PLG*LVIL LRQPPKVLGLQA
6340	20241	A	6394	501	187	AGVKWYEHGLWQPPPPGLKRSSHLSLPS S*DHRHEYPCPANF*KIFF\VETRSHYV AQTSLFLDSSNPPTSASQNAGI*GMS HCAQPMQTFSLVKIGTNFLIF
6341	20242	A	6395	3	393	HACGAIMNSKPHAVTQYHTPLM*SVLI TT\VLLLLFVTILNDGITILLTDNRNT TLFYPSGGGDPILYQHL*FSGHAGG*I L/LLPFGTISHIVTYYSKGKEPFGYIG MV*AMISIGLLGIIV*AHHI
6342	20243	A	6396	101	135	FDSPTPGIVPGTWQTIRSLNVYLTRLTT SFSMLPS*FLFIFFCRDG/SLTILPRLV SNSWPQAILSPQPHKMLGLQA
6343	20244	A	6397	395	187	SSYLSLLGIWSYRHVPHPANFLFFCRD GVVYFIFFC/KMGAMLRLVLNSWAQVI LLL*PSKVLGLQA
6344	20245	A	6398	35	334	QNETLSKTKKIKNKKKKKKKRGGLPKK PLKGPKLTRACKKPFSLKG/WRKKNL GIFEKKPYFGGKKWNKPPTKIKSFKEK KKF*REKGEKQPNPGC
6345	20246	A	6399	464	146	HIQIREFQRTPTRMSPKSTLSHFKIKK QLVMNKRSEIKQWIS*QKPCQMARRD*H NIFTVQKGTNCQIR\ILCPAKLSFKNER EIKPFLGKVKLRBFITA*FIFKG
6346	20247	A	6400	723	632	FFN*DKILLCHPGWSAVARSQFTAASTF RVQ\QSACLGLPSSWDRHIPSCLATF* *KRGFAPLPRLLSNFWAQAILPPWPPDV \LGLQA
6347	20248	A	6401	522	46	FFPPFLSFFFSKIPKQSLGLVIFY*NK VWFCPGWRAIR*FPFPA/APPLGSKNS /SCLNLPSTWGYRISGMVPPKAH*IPPE IFFFFFF/CRQSLALSPRL/VVQWQVQA ILLPQPPE*LRLQVPGRVV
6348	20249	A	6402	103	261	NIPFTCLIKKKKKKKKKKKKKKKKKKK KKK/IK*KKKKNVGGVVKKLGDD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6349	20250	A	6403	146	384	GFLPSLSGSKELSLFELFETESHFVAQA \DLGSLKPLPPGFK*FSC\SLPRSWDYR RVPPCSVNFCVSPY*EG*SQTPDLR
6350	20251	A	6404	3	395	ETESHVAQAGVQWRNPGPLQPPFPKPK RFPYLSLPSSWDHRHMPPCPANSAPSV TGL/LHAGQAGLQLLTPGDPPT*TSQSA RTTGASHRRARSLKYFLISFVSSLLHG LFRSVLGSMYLRISQVFFCC
6351	20252	A	6405	30	205	CRLTRAEFRTRKTH\REKPYECKQCG KFFSCKSNLIVHEKTHKVETMGIQ*VMW LFL
6352	20253	A	6406	3	444	ARKITGY*ISKITIVFLYT/DELAKEIK KAIPFTIVPNK*DN*ELNLTQVKDPHK EDYKILMKETEQDTK/WKDI PSSWIRII NIVKVAVLSKAIYRPSAICIKIRVTFKT ECHWKKKIWIGKVAHACNPITLENQGR SLEARSLRLS
6353	20254	A	6407	480	307	QHDSPSAKKPPQKPKDS/HPSSRS/HPF PPPPPC*TPPPEF*YPPPKGEWGAPPP QG
6354	20255	A	6408	923	833	KAMKHFLIKTRAPFRHVTAHLIDQSIVK TELLYVTSFIAIFALLWYQKEPML/WP GAAHTCNPTSLGD*GGRTA*AQEFKTS LGS*NKTKP*CLSAV
6355	20256	A	6409	382	152	ECSGTLAHCNLCCLCSSDPF/SLFHN VSLSSNSSS*VAEIIIGLCHHVWLI FVS AKLFLGRVRNLFSPPTKNNMFSK
6356	20257	A	6410	553	173	CLLI IKNLTPAKKKKKKKKKKKKKKK AR/WFP*K*RAP*NPVKTGGSF
6357	20258	A	6411	38	562	FLRQGL/DSAAQAGVQWCHSSORAPPF GLGRSSH\PASLAGWSAVA*SRLAATST FRVQVILLSQPE*LGQSCSITQGVQ QWRDLGSLQPLPGFKRLSCLSLPSN*D YRRLPPRPDSSITFSRKFPQSPQARNLP PTPELKPQQVPVAPSPSELHLSWSSGNK CHFLWFLCP
6358	20259	A	6412	414	144	FFFETESHSAKLEK\ISAHCNLFPPGS SKSPASAS*VAGTTSVCYHAQLIFVFLA DTGFYHVQDGPDLMFCCPPRPVKVGLP RLPLICF
6359	20260	A	6413	3	455	AEAGGILEPRSSRLQ/CSQP*SHPCTPA WAT
6360	20261	A	6414	462	162	TGGPRLFPHPFGAPGGPVPLGWEVRPP APPKGPPFPKPKQ\NSPPWGGQPSIPPP LEG*ARKSP*PPEGLVPVTPKGPFPHP GQENPTFPKPKKKKKVN
6361	20262	A	6415	499	0	HFTSKHHFGFRAA\A*YHVFVDV*LF L YVSIY**GSH
6362	20263	A	6416	187	236	MCHINGIMQFFFFFFFENEVFFCPPARI GN*R/WPNLG*LKPFPGLTLFSLTPP RSWNKRPPPPARVIFLFFNKKGVFPLLP GRV*IPHTPEPLATNLLSVTIDLLILN VSYKWDHAVFFFFFFF
6363	20264	A	6417	158	412	SSDPSRRSCLFSF/CFFFLEREFFAPR VEWRGPNFCLLTTPPPPGKKHFFAPSLRG GGDYGHLPHPGVIFGTLRKAGFSPCGPG GS*PPPPGKHHFFAPSLRGGGDYGHLP HPVIFGTLRKAGFSPCGPGGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6364	20265	A	6418	457	11	HTGQSPYRCSECQK/AFTQKSAITNHQK PQKGRKSMQ*LRI*ESFFD*SHQLRHN RSSMNTMI VMGPFGTLVGEKPYRCNEYF KPSFLKISLVYRRDLTRRIIGQAHWPMP VISALWEAEAGRSLEVGSRRPWPNT
6365	20266	A	6419	103	376	SALSLILGITFFF*IFLETGSHFIAQAG VQW/PIHTCDHSILOPQTPLKPSCLS LLSSWDYRHHVPPVPTSACFECTILRSQ SVAHTVLWKAKAGGSLEVRSLKLACATQ GAPCLTKKKCDPQD
6366	20267	A	6420	463	6	FPPNPHKKONQQT/PKKAPQKKYTA DP/QDPPGNDPKAQAYKKSPAATYPAAS SSPSSPSS/RPPSTAHHVLRVPL*GSPP GLVGNRP PPPPGGAQHPQPPDTWQKRP HHGLQSLASPPGIS*EPQLAPRNSPHW TRDL
6367	20268	A	6421	1	479	RGFAVLFSAVEFPSSSKSHLDLETSPKA YKHGAPCSAPGSLQASLPKGRNQRNPF NFFVLF*DKISLCCQGSVAVQS*LTVA STSPGSDDPPTT PPPPHAPDTHDRHVP PHPAKFYIFYRDR/SFTMLPRLVNSWA QTVCLSSLFMLLPSLLWSLSP
6368	20269	A	6422	11	242	FEIIFSAVEFGWSDHGSLSQTQPPG\SSD PPTLDS*VAGTTGLHHHAQLMF*LFVEI GSPGLKWSVSAESEELYPA
6369	20270	A	6423	488	335	SCQLRPWNESIGQRSGIRWLTVPVIALR EA/EEAGG*LEPRSSRPAAWI
6370	20271	A	6424	454	229	RDPPASASQSAGITGVSHHARL/VSLFL IVM*AEGCYLSGIWRTLRKMNPPQ*RKE RQIQVKSTRSDIFFFYFLFL
6371	20272	A	6425	1575	1309	FESESHSVT\RTCSGTIS\AHCSRHL GSSDSPASASRVAGITGVHHHAQLIFLF LVELEFHHVGDGLELLT*VIHPPWPP KVLGLQA
6372	20273	A	6426	276	437	CFHEPEPNDQWGPPLGNF*IFWKKRG PPFVPOIILNPWPQKNFFAWPPKTLG
6373	20274	A	6427	445	240	RPRRADHL/RSKV*DPQGHGETLRRLK IQKISWVWHAGTLWPFWERDGSRLSA RTQMLGSWACSPGF
6374	20275	A	6428	114	450	LLLLLFESESCSVAQA/PSAVL/WILL GSL*PLLPGFKQFLSLLSIWEYRGLP PYPANFFKFLVEMGFHHVCOAGLELLTS GDLLASASQHSGITDVSHRAQPVTIFLK GLS
6375	20276	A	6429	380	224	LRHCLFTQAGIQROEHGSL*P*SPGLKQ SSHLSLPSSWNY\GVKLPKPNKFQH
6376	20277	A	6430	509	228	PHNKGSRVSPPPQNFPSRNLGGGWL PKIPPPKKRVFSKPPRGKKK/PPP*KK KKNFSPPPFFGPPPKI IKKPPPPFFFFF FFFFFFFFFFFF
6377	20278	A	6431	3	117	HSWESI*KRGACFNIFIAAQFTIADIWN *FMCLSGDE*IKKLGLIYT/MDCYWGK KRETMPLATTWIELKVNILSEIGQA*KD KYHVF*MNR
6378	20279	A	6432	417	271	LSKTKFPNSPQPPLPCSFL*NDRK\WP RVVVHTCNPSTLGGGRWIT
6379	20280	A	6433	385	145	TPGIKQSSCLHLEKCDWFSCEPPLANL NF/CKR*YIPIVNSKV*TFSQEVFSYT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WPHSSSFTGKEVIIILFPKBCPGMFK
6380	20281	A	6434	65	383	LFPNLLKKKKKKKKKKKKKKGGPIKK KP*GDKIKTRQKKKNFFPKRGGKKNQPG KFKKKNNFWGGKKMEKPP\KKKKTCKBK KKI*KKKGEKKPQIAPEKKKGS
6381	20282	A	6435	3	454	EIQRTPVRYTYK*TLPRHIVTRLKSKSTL K/EKKKKKKFLRAPTEKGQIPPKIP/I KLTVNF*KKS*RREKWG\PIFNILKKKK F*PKIFYPAKLTFIREGKKKFFPKQGL GKFVTTAPLKKILTGVNLKMKKGYLE PQNTILKYLAHNHP
6382	20283	A	6436	424	410	NFFFPFGGGGGGGFF*DKPPPGNPSSL FFFLGGGKKRGGPPPPKG/QTTPPGGL F*KWLGGKKETPKKFSPPPPFPGGGKI FF*KPPPPPGFFF*KSPGGGGPPSVKK KKEKKKKKKKKKKK*R
6383	20284	A	6437	3	214	EIDCCAAVWKQPKCPSADE*KKKMWLY TMEYCSATNKNEIQSF/VNNWKEVEIIM LS\KKSQAEEKKHGIF
6384	20285	A	6438	83	420	QSFP*ISCRKYS/WLGAAAHACDANTLG GRGGRAAWGQKPKTSLGNLEPGPKTADP RTSHGCELRRSSYTYALTHGFSSPTETA RPAPLLPPPPPTQREDYKEDLYDDL NK
6385	20286	A	6439	163	289	KMYCYYYY/C*DRVLLMLPRLVSNLWAO EILPPWPPKVLRLQA
6386	20287	A	6440	459	431	DKRIRTRITPLAIRKQIKTTV/RKQLQ SHYMVVVKETINNK/CGIFHSWWECKM VQLLWKTVSQVFKRLDLPYNLATLLIFI CQLQIKTLSSPKYLHMKVHSIIKIRKK YIKKNLKPSTDEWIIKI*C*SIHTMEN ERA*K
6387	20288	A	6441	478	36	VFGCRVILVEKLFLCEPLRVTFRLRGKQ LEKSL/WNFHDLNLSLHKNQPNRCVH QWRIG*RKRS*CSE**R/TMQFINSLT LIN*IPSCHTAMDIIIAQH/IHTVEY YSAIKNEIMCFPATWVELEAILGEIT QKQSQIWRSP
6388	20289	A	6442	464	206	LVQRSGIHLPSYSTVPL*GL/HQKNEAD VYRNTRMPTAALFLIVQNWK*HNYLQTG EKINKLPYIHTMEYFSVIKSNQHSIT
6389	20290	A	6443	414	216	CYIYTCPLTQOSRSWVAT*ASSKEWIN KLWHIHTMD*Y/SSNKNKLQINTTWIN LKSIMLTEISLT
6390	20291	A	6444	7	411	SFYCLHSFAFSRVSYCWNIOYIAFLDWL LSRSNSLHVFSW\WD/CKMV*PL/YETV WQFLTCLNILLHDSALTLLGIY*K/DM KSYVHTKMCTQIFIAALFIIAKTWKNL* CSSVGEWRNKLWYLQTMESYSSSVLKK\N ELSSHEKTWRELLRERSQSKAIYCIFIQ QYDTLEAKLWRQ
6391	20292	A	6445	257	419	KSLPFFF/CW*ETGSHSVTQVRVQWCNH IALQPQTGPKQPSCLSLQGSWDYKFFH TQACFY*RP
6392	20293	A	6446	20	417	HQYCFASFFFFNNFFKTESHVAREAGAQ WHDLGSLKPLPLRFK*FSCLSLSSWDY RCMPPHLDNF*FLVETGFHHVQAGLE LLTSDDPPALAS*SAGITGVSHRAPVE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LFLLRQGLRLLQNIIGIRQ
6393	20294	A	6447	371	3	VIGCQFL/RKTKRYLPYDLPIVLLCIYR/EKKNLCRH*TCSTSMFMTALFIITQH* KYPKCHSIGEWLNILWHIHTMEYYAEMK RNKLLIHEKTYMDLKDILFSGGQRVYLK SSILSIKCIIRQE
6394	20295	A	6448	46	332	LGEHLRQGPILKVCQVILTHQQYFESQ WSTIMALSNRKYNANCYLNKCPNSYIKK EML/WPGAAAHACNLSTLGGQGRHIA*A QEFKTIAPCLY
6395	20296	A	6449	2	381	LCSLVFTHICSIIFLFFFFFKDRALLP/H/PCWRAGP*SYLTAASNG/VKQSSNL SRGKPLCRANFGSF/CFWFWKGGPTMW PRLV*N\ILLPQPPKVRGL*AAAHAGGQ GHDHSLRPQTPGLKQSSNLSRGKPLCR ANFGSFWFLVLEKRGSHHVAQASLKQSS CLSLPKLGDYRHEPSHRANMFNFRSLPG LRKADCLYPY
6396	20297	A	6450	2	136	KSVGCWRGCG*IGAL/LHCWCECEMVQL LQNAVWQFLKNCKIVPHY*A/IPLHGIH PNALKTATQRNICAPMFIAALCATAKRC CK/PKCPSIDKT*YTHIMKYDSA*KKCW LLARVWINWSPVHCWCECEMVQLLQNAV WQFLKNCKIVPHY
6397	20298	A	6451	314	72	MLPLTNGSCRTKVS KDIEGLSNSINPLP LIGIYRTPFPKTAGTPFFFFFLV/PNGT FTKIDHILGHKTRNLNLRMI*ILKYIP
6398	20299	A	6452	54	350	LRSFCSALFCFETVLLCHLGWSAVA*PR LPAGSSNPPPS/CLPIPSWDHRLVPPH QVFLEAFFFFFFFF/CRKGVFFFLPGGV* NSGVKGTPRPNPPKALN
6399	20300	A	6453	368	172	WLTSVI\QRFGRPRREGHLRPGA*DQPG LR*STHLRLPKYWDYRRESQCPARPVIL KEANMFHLG
6400	20301	A	6454	1	365	NILKLNKLNNL\VKKEVAKETKK*LV LNKNTTYKOLWNEAKTVLHL*H*VKF IALSA*RIVSNQCSK*ASTLRNHKKSN LNPRLI*QOKSITLKREKSMKPKAGSLI RSIKLIIRLT
6401	20302	A	6455	364	1	PETRSVWPRLGQVQRDHGLPPLSP RLKQFSLSLPSS*NHRGMPPCPANLLP KFYLFIYL/FCLFVEMGSHHVSQAGLKF LSSRDPSALVSQSVATTGMSRRANQDII LQOKQAATAA
6402	20303	A	6456	91	300	GHAHFGRPRWGDCLGPEVRDQPGQHG ETLTLOK\KNKN*PAWWHTPAVPATQEAG ITGVSHRARPCCPN
6403	20304	A	6457	2	195	RFSCLSLPSSWDYRHEPPRLAIFFFF/C FWNFKKRGGFPLWARWVNS*PRGIGLL WPPKGWGLRA
6404	20305	A	6458	522	202	THNWRPSLQIFTAALFLAKKWKQPKCP STDEMIHKMWYVHKMKY*SVIKRNEVLI HSA\KWMNFENMLNEEACWERPHIV*FH LYEMSRVGKTGETKSRLVVV
6405	20306	A	6459	377	161	EMNIKCPSTDK*VKRY/LYIHTMEHCS ALKGNVLI IHAMTWMNLANIMLSEK SQNTTYSMITVVKCLE
6406	20307	A	6460	92	484	LLQACFLRTVLIDYKMWAEKGMVGMCVL

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						MRNMTVIIIFRDRVLL*HPGWHAVVRSQ LTSA/VKRSSCLKPPKC*DYRCEILCQV EIAFTHRSFLNSFLKRSMRVILLNLYWKD PSLGFCSYDSTGMALLRNFS
6407	20308	A	6461	483	192	MGLMLILRANFQSTKKKMICLLKSLTF LNCIVLSNWPCTFNMYIFVCVFAVYKLH VWAE\ PVAHACNPSTVGQGGERTIA* AQE FETSLGNIIRPCLY
6408	20309	A	6462	451	98	KQVWQLL* KQVWQLLESINMKLLYDLAV LNLGAYPREEKTHVHTKTCTQMTAAPP I\IKK*KNFSDMKYEERDKMWTIHVT QHYLIK*SID\YAPTWMNLENIMLSED SQTQKTTTHCIISFI
6409	20310	A	6463	395	67	FLRFWCTHHWSS/DILYFVCSLLSLNRS HSFPRVHKSPLYHSYALCPHSLAPTYE* AHKMF/RLVNFLFLVETGFRHAAQASPE LPSASNPPFSASQSAGTTDASHRAQTK
6410	20311	A	6464	485	220	FFETWSHVSQTQARVQWCNLSL/KPLP P/GSSDPPTSAS*VAGIAGMSHAPTHEI PSIQARQQHLQGEKKIRLLSLPTSASQV LRLLA
6411	20312	A	6465	1	371	ISIPPKKYLRINLTTYVQGLYEQNYKTD KRNQGRSSKWRDGPSCSRIGKLNIRMSVL SNLIYSFNVILVIVPASYFVSIT/RLIL KFT*KCSRPRIVPLFHLLPLLVPFVCS FILCRPGASLVK
6412	20313	A	6466	489	175	YKIEISRCIK/GLL*LWRTHLFSHPH WRRGMAYEKNADFRLGTVAHAFNPSTLG G*GR/WNQCFKTSANVVKPCLY
6413	20314	A	6467	2	367	FGTETLQAGIKGDPGEKSHWGEGLHQL REALKILAERVLIETMIGLYGS*LTEL PAAAGSAGAPGQTGHPPGSHLA/EPEL GSGAGPAGTGTPSLLRGKRGGHATNYRI VAPRSRDERG
6414	20315	A	6468	472	260	TTLGGAGNSGYRHIQPHVANYLFICRDR /SLILLPRLILNS*L*AILSRPPKVLV LQT
6415	20316	A	6469	88	435	RGVLLHMLSCLPLCKTCFCSSFTFHHH* TSFSFSFFFFLLGNKVSFYCQAEQGPN LG*LKPLPPGLKQFSCPT/LPEKWE*QT EPPGPVKRHFGLSYFPPLTRG
6416	20317	A	6470	34	106	EFAIPFLTITYPELNTHVHTKICI* MST AALSTR*KSPTCPSM\INKMWYIHFMEY YSAISKGRNHANVHQWIHKM*YIHTVEY YSAIKSNEALTYATTW/MNLENIMLSER SQS*KICI
6417	20318	A	6471	390	92	DFLIDAINHNKLVFFYS*PISMC/HPYN *SLSFSNIQKSLIKTMINVLSFKY*YL IYPS*KKTF*N*ROGLTMLPRLLSNSWA QAILLPWPPKVLELQV
6418	20319	A	6472	414	167	HIHIKTC*AIFSA*FIIAK*KPKCPT ADEWINKMWYVHTIEYYSAIK\NKLLI PWMNLENIMLSTGNQTKATYCMIPPI
6419	20320	A	6473	3	244	TTILLGTTYDALFPELYTTYFVTKLLL TSLFL*\IRTAYPRLRYDQLIHL*KNF LPLTLALLI*HVSIPITISSIPPQT
6420	20321	A	6474	12	224	IASGRFFFCYDVCV/VKRLCRHSYIIM *KKKKKKKKKKKKKKKKKKKKKKRGR

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						GGALKKKPGGEPPLFPH
6421	20322	A	6475	417	155	FQSFTENKMLSSSITCSSEIFGERKSQ LM*RPSSL/SY*BKLPLLASTTTVISQ RPSAL*VQPL/PTAKNL*LTAGSKGHYFLN SKVFSN
6422	20323	A	6476	1	131	RTREPTRTTRGRWLTPVFPALREA/BE AGG*LEPRSSRPANAI
6423	20324	A	6477	830	513	WNSVKESLPADTWLPLFLGLIDIFLL LIFALCLVNLVKFVSSRLQ*FHVKMLLA QGFPPIPSDDPEDKDILPLSLEQVS/G ILPLQC*AGSMPITSAGSSYRR
6424	20325	A	6478	399	196	SKQSSHLSTLSR*KYRCAPPWAWFF/SF FLINIFCRDE/SLTMLPRLLNS*PQVI LLPWPPKVFGLQA
6425	20326	A	6479	1	411	NTGIMPANTVSIILLIDQEVLVTKTCY LRNTFCGFSGSGHVS\QTFWIGSTILD AIKSL/R/DSREDGKISTLIGIRKK*IP ILMEDLVGFKTSQEEGTVDGLNLA*ELQ VEGPRDETELL*PDQOTCMDEKFLMDE
6426	20327	A	6480	381	162	AGFTHNFFFLP*DMVLLCHPGYSAVVQ SWLTVASNSW\VK*SSHLSPPKH*DYIQ AVHFRMASNSPGLYLQ
6427	20328	A	6481	379	85	SILFFLFHPINFFFFF*AWIFIIPPPH \RAFKVVRVVGFFLADSKVFIKRLPQY YFFFFPGFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFLSVC GG
6428	20329	A	6482	355	117	PKVKIFPPPLPRKWDRGPP*SPGTNF SIFFLVEKDFPHVAQAGLKLDDSSSTPS VAS\QSV*ITGMSPHAWLQVLLSL
6429	20330	A	6483	402	97	TAFHLLDIYHKS*KIMFTNQPLKCPLE IIAKN*K*LKCPRRADKQIVA/WCIHTI EYYSARKRNVLLKYTRLWMNLKSIMLCK RSQSQDVITYYVIPFICH
6430	20331	A	6484	714	365	NGFALVAQGV/QWCDLGSQRLPPTFK QVSCVTLLNS*DYRSMPPHPANFCIFSR DGV*SYWSEWSLTPDLGLPKCCDYMREP PCPANAKSFTVERTHTVYQAYETMLLSD HDESG
6431	20332	A	6485	408	146	LKTETQTETCPPMFIAALFTLV/RRWNQ PQCLSTDEWISQI*YICIMNINSIDIKRN EALKHAVICMNLKNMVPFISPTEKGKKK EKKK
6432	20333	A	6486	243	11	GMSQYQYYSKSNFFLSNRVLLCHPGWSA VAH/SRLTEALNRFK*SSCLGLPKLWDY RRVELLLAQNATR*NSL*SCPA
6433	20334	A	6487	403	161	DMVSPRPVWSONS\SLK*SAYLSLPRC WDYRREPSQASRNTSIGRGNRKNQNT CMYLLFILIPLLKKYMCNVRMEYFKT
6434	20335	A	6488	292	24	DWGRMAIPLKKGSKC*QGCRTGLLRY *W/MECEVAQPLQEMV*WFLQRLNKL S YDPDF/PLGIIYPKE*KAGT*TDICMPM LVATLFSG
6435	20336	A	6489	3	203	SSWDCRCIPPLANFLICCRDR/SLTML LRLVLNS*TOAVLLPWPPKGMPLLFVF YGGIVLSYVNIS
6436	20337	A	6490	413	30	RGP/YQPGFLGFSPPNGLGFG*KVFLPL PPPRKGP GKKGSPRARGFPQGAPPKKE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NQRGGGFWSRGRRLAKKKGFWFG*GPAKG KKFFFFFLGAGVWGLKVLIPIKKKKGFPF PPLFFFFFFLQTIHPIRG
6437	20338	A	6491	101	335	SSSFLGFPKYWDYRREPL/WPS/LWQFP RLNIHLLYNPSIPI LAVYPREMKTCDLI KSCMRMFTVAVF*ITQWKQPNVF
6438	20339	A	6492	532	127	STVFRARQLPCLHEPGRQSSP/PVPTSI LYT\PLPFPSSRYQNGPCLSSPKLSPS PELGTQSPFVHKSPSPCLPSPKPLTVPP ALPSTGPSQSL*QKHSLASLLHSHSTP PAPSCNPESWGLDATAISTCFYG
6439	20340	A	6493	399	1	LCPAPRGGVYRGR/ESSLSWDGLHSVQA SWPLCLPTPASAMVDAPPA\SLPSRSS ILDCCISSEQSGVMGPAEPGAG*NLIV CCLLRPLEKCSIWAGVSRFSWYSLSQLP LARKGKSPNPLSFPNEKMPRPVS
6440	20341	A	6494	319	75	KKIWGELKKKFGQLTRRPFKKWFKRPPF FFFFFFFFF/HVAIFLLPCDRDG/LA MLPRLILNSWP*RILQFWLPKVPGLQA
6441	20342	A	6495	333	190	LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL YSFRDGVLLCHPGWSAAMPS
6442	20343	A	6496	1	299	LPRLEYSGTITASNSWAPAILPPQLIK/ YNFFCCC*GRVLTVLPRVLNSRPQIVL PPPPPKSAEITGVNHVWPKKIIISNEKT THCSCSALLAKQIIS
6443	20344	A	6497	51	266	PVNVLPSWNLRHSPPCPARFFVLFCFL LFFGKN/RGLAMLLRLVSNWP*VILFP QPPE*LGLQVQATMLSS
6444	20345	A	6498	366	78	LLAHCHSSNNKSLILLDNFNIIHYGPSN TVTS*F*MSSLMILLSSP/C*GTSWSY LFYALKKIFCKD/RGLAVLPSLV*NSWP QVLLSWPPKELGLQV
6445	20346	A	6499	37	396	FPRPTRPKSSSPAKATQONTISFKKKK SKQKQONTVIIIRVKQNRKQKN*KLK Q*N*EQ*KINKISKPLAKLI/KKRVKT *IANIRNERSITT*STDIKRLWKYY* QL
6446	20347	A	6500	706	394	VPLLLPRLAVQWNLGSLQPLPPGFKRF SCLSLSS*DHRTTPCPA/NSFVFLVB TRLHHAGQVCLKLLTSG/DTSSASQSA GIKGMSHRTOPIEILFYSVFF
6447	20348	A	6501	403	216	ILNVLSFK/NMLY*HYTTVLRTVRPLSP R*ATVTCITYTSGWPEAAEDPQKMTFPHC DLFLPHPN
6448	20349	A	6502	377	116	LLPY*EN*FLMYLPPI CCLPFDGNSGF CHQKNFFFFFKTKSLVA\RLCOGGA PAHCKLCLLGSSDSMKNFLNEAEFPNLA FNGL
6449	20350	A	6503	3	401	CVQHLRASWSSRWAWANRAPHSEQPAGP AAPGNEGLSIRASGCGGCTGYPSASPP ALCSIS\PRP*LPSRRAGLATCSPPCLS LPPPPWAPVRPEPPRRVPPAPWRPVPS TTQGLRSASARHRTGRQLHLQ
6450	20351	A	6504	406	55	WPKGFTPPRFPKKEGSP\PPFPKVFILE TRQPGPQTKPPFPPIFKLITRGGRP* FPPPPQVRAGKPP*PQSFVRVGAIFPPP PPPLKGHPRPFGFKKKKKKRRKPRTRK RGGT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6451	20352	A	6505	3	281	FFFCDRVLLCHPGWSAMVVRVRSRLTATS /SFLGSSDSHACLSSSWDYRHLPPLLAN FCIFLKRQGFMTLPRPVSNP*AQAMRLP QPPKVLGLQA
6452	20353	A	6506	1	247	LGSLQPPPPG\SRHSPASASQAGIADM SHRTRQSIIVFLRTNNKPY*IENMMITIS CTTAYKYEILRHSFNKICARSLYEKL
6453	20354	A	6507	34	47	FDPNLTPRHIRTILWAVNKERMLTASRK KKQII*RSSNLSGDRLLNEEASWEP*CK KSMQETIQATEGWNDIFKVLKEKKNL\H SKILCPAKLSFKYEGEVKAFFPKPKWRE FTVTKPILOKC*RENQRTFDLTQI
6454	20355	A	6508	403	106	HYVPPPPSPS/YFFFSPPGKRGFFPNPF ILVSPGFFPSPLF*KPPPEFFFFAPLKK IFFSPPRELKFFFKGPPPPPPPP
6455	20356	A	6509	389	230	LSPFLFFRDKVSCLNPGWSAV/VTFELK RSSCPGLPK/SQSHCTKQPGF*KYIYF SFFIK\KR*SLTTLPRLVSSSWDQVIHS ALWHPKVLGL*AVAHAYNPSTLGCQSAE WIT
6456	20357	A	6510	101	419	ISFFFFFFFFFFLKKFFFFPPGWRGGGEF* LPQTPPFVWKIFFPPPKVGGFKNSPP PFFFFFKEKGFSPVCGFFKTNPKK/ SPPPPPPRGVGLGGWPPPPGWD
6457	20358	A	6511	41	376	EWWCETRGGAGQGRAHGAAGGATGRVLA IQARKRRPKREKHPKKVSCSVAQAGVQW RDLVLLQLPLPGLRVSLCHPS/WECGGV VSAH*NFCLPV/IKDGVLPCCAGWS*TP GL
6458	20359	A	6512	2	332	WEKVKIATLTGFWK*LI/SGSSRTLMGD FERFKTSVEKVIADVVEIARELELEVEP ENVTELLQSHYKTPGTLAFLSRLSPDVS LYSQLPETRSHEWQAASKTQPRKASTSQ
6459	20360	A	6513	3	294	FFFSEMESLSVTQVGWVWHNLGSLQPPP PEFKQFSCLSLPSWSDYRHAPHLA/NC FCIFNRDGVLPCL*LGWVSNSHLGFTGMS HCTQPLLLALSFLHG
6460	20361	A	6514	1	526	FRIGRKPR*GGVM*PVWSRGEPSVGAE AG/RS*SAPRRLLHHPAAGLATGLSASG RRSARWKMERASGLSPGGGLGATSRQMS PGTQLANPPDHGDKDCLGRISPGSGKQI QAAGQLPGPPTSLAPAQQLRLSLTPWGL QTPEHSEPEGIGHLQAATEAVLPHSTQN LITKRNLM
6461	20362	A	6515	747	451	QAGVQW*DLGSLQPPPPGFK*FSCLSLP SGWDYRYRPPNPANF*FLVEAGFHFG QAGFELLTSGGPPASASQSAGITGMSH TPLGVHALVGENIQ
6462	20363	A	6516	444	3	PGGGGPPPPPPWGGKPGKIS*/PPGGGG SNKPKLPCLPPGGPK/GNPPQKKKKK GFPGVVAHACNPIIPALWEAARGLP PDAGRYGPGGRREAVRREAGPQECQDPE GQV*GDPGCGAAHAPARGHPRKA*RGAE GSSPGLPTK
6463	20364	A	6517	257	575	ASSVTWAGVRWCHLGLSLQLPLGFK*FS CLSFPSGWDY/GHAPGPAPKFCIYSGDG VSLC*PGWSQTPHLR
6464	20365	A	6518	337	389	SQHFV*ISCLHDMPALASQSAGITGVSL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RARLIFIFR\MDSCYVPQAGLE/PPELK RSSHCGLPKPWDYRHEPQAQPVCRFIRA TKCAYVSTQALSPAPVQPGMTTPAKRGL PCQPPGSPCPSLCHHQLAGTTPPYE
6465	20366	A	6519	61	323	FMWDRVARKGSIEGASLELPLGGSVGGH GSCISMVVGALGHSS\THV*HTHTHTTET HTHTQTNTHTPSSDSKSSILDKEBAEG CMTPT
6466	20367	A	6520	399	101	KIQIKATMKY/HNIPIRMGFFFLSSQG /C**RCRK/IYTLKHQC*KCETVWPLWK SVW/RVFLKLNHPLHSPFIPLLGTYP /DMKT*TCM*MFTATLFTTYS
6467	20368	A	6521	1	276	RTRGFEGLRFFFLGFFGTVLLCCPGWSAV E\QSWLIAASASCLW\VK*SFCLSLLRG WDYRCIPPCLANF**R/CGSWAQVILPP QSPKALGLQT
6468	20369	A	6522	280	277	GDDPSCSMGGGHCLASRSE*GSVGVGPS KPGAG\YNLLVCYLLRPLEKRSIRVGV QFSRCHQSWLPFDRKGSPTCTYWVR
6469	20370	A	6523	2	327	SLFSS*D/YRHIPPHPGNFRIFCR/SAL TMLFRLVSYSWPQVILLPQPPSVGTTST SHCPQPCIMFLKADLNVPVRCQFRCALAP EPYIQDPFLRDDVAFPCLGASAPWHLA
6470	20371	A	6524	298	414	PGPQSETLTKKKKGGRLKGSNFTPAGM BGNIFF/CFFLSKSHSVAQARVQW/P*W LTAGSLQAPPPRFLFSSLL*VAIYASP TLSS*DYRCTPPRLANFCIFPRDGVSP CRSCKAAVFNLLDTRDWFHGRQSFRHLV AGDGFRM
6471	20372	A	6525	376	180	KCKKYPGGVAHACSPS*DYRHVFP/RPG YFLHF*QKHFGQAGLDLPTSGDEPPASAS QSAGITGVSHRTQPOLNYF
6472	20373	A	6526	415	86	LYLPYDLAIPFLGMYPRGKKKCAHTKIC TRIPTVVLFIARK*KRSKNPSTREW/I KMWNIYTVESHSVIKRKELLIHASMILV H*/WMIFENIILSDRSQMQKITYCMVPF T
6473	20374	A	6527	391	166	FFFFFRDWFSLSHPGWNAE\S*LTVISN SWSQARLIFKFLKLROGLNLLTRLVNS RLQGILSSWPAKVLGLQA
6474	20375	A	6528	544	176	TMRYLLTPVGMATIKKAK\NT*C**GGR E/IGTL/LQCR*ECKLVPLWRTVWRFL KKLAIELPYAPPFLFSLFGLFSLGSTN CAQLRSVYRKAVQNHQGVSGECAGFQDS SHSAPVAIPTAQ
6475	20376	A	6529	392	139	TYVKMHCK/WLGMVAHAWNPTLGGRRG QIT*GQASTKLSHWSLSRESRFWLECY SRSCSFCSCRLPADCTSLTDSQ
6476	20377	A	6530	362	87	NGPPFFFFGEIDKLILLLWKCK/RPK IAKTVFKKKNKVGGLI*HYFKAYYKGT IKLVQFWHKVRKTDQ*SRRESPETELHI YVLVNARDSA
6477	20378	A	6531	1	346	APTRPRLKKTLSKLTNTNLQLPYDPAPS FLSVYPREMKT*R\PAKICV*MFMASLF MIVTQ/NVPRCPLMGEWLNKWR*FIT *YHTGMKNT\VMHKTWMSQRIMLNEK SQLTY
6478	20379	A	6532	3	294	FFFFRDRVFLYHFGWSAVV*S*LTAALS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PWLKRHSHLSLPGS*GHRMH/PPHLGNF FV\FCLFL* RQCLAMLPRQVLSRWPQVI FLPWP PPKAVLGLOV
6479	20380	A	6533	2	280	PRYLVRNPPTTLGSCVTVDK*LSLWASV LYIYIYTHHTDIYRKIYAP/IPVCVYI YIFI*KHIYYKEQAHAINDAEKFQDLPS ASWRPGKLV
6480	20381	A	6534	96	183	DQLNVFHRKLRDYDTYTFVALLARHGG SC/LSLGSS*D*RYTPPLQTN*K*FFL* ISL PMLDWLVSNWPQAILLPLPPKSSG LEA
6481	20382	A	6535	2	241	GPKRIDSNFESSVGKVPTN/TIFCERKS LSMHQI/SLLSYFKKLQPLQCSAATTL /IS*QPYTLKQDPPPTRLQPAEDSDGY
6482	20383	A	6536	485	97	PTTRPILLGFFYTK*LKS\NKSDSCPPM FIATLF/ILKCPSTDKWLKMWYKHTTD YYSALKKGNHA/YM*QQMNLGIMLSEV SQSHEGQLLHSTVRYLK
6483	20384	A	6537	411	57	LFPSHIKFLVSWQSCFAKTSGPQTPSFF FF*LFFF/RDRVSLCHLSWSAV/VSWLT VASTSQAQACLSLSSWDYRCPPPPAN FSRRGFTILPRLVSNRAQEICPPWPSK VLGLQRRGI
6484	20385	A	6538	438	201	IYPKEMKT*VHTKTCI*MLIATLFTLAR KWKQTKCSSTDEWINKMWHIQ\TMEYYL AIKRNEAQLHGEIIMLSERGQSQ
6485	20386	A	6539	466	131	SFPKKGGRAPPPPPPPPPPPPPPPVEA VLSLCCPGGSQTLGLKRSALVLPKC*D HRHKPPCLASN/SFNRHRMMTNCLMC IKSWCLCIINPFYHLDSSLLWMLSLIYR
6486	20387	A	6540	419	50	PLPFFKPGPRIF/CLGAPKKKI*VPT/L REIKLFPPLKGPPLFFFLNKGPLCFPGRK GRGVLFLLATPKSWGQKIFPPSKEGASF PPFFPFFSW*RWDLTMLPRLVSNWPHV ILPSQPPRVLGLOV
6487	20388	A	6541	1	341	SIITAREKCLVY*GTSIRLTGDF*KY I/SAKILQVRRQ*NDIFKVIK/EKNCQP RIQYPKLSFINERKIKSFNPKQLREF ITARPDLOEMIKGILYLETKE*YLPK*K HMKV
6488	20389	A	6542	409	290	NCKQPTCPSTNEW/IKL*YICITEYISA IKRNKLQLHTTT
6489	20390	A	6543	32	397	AMIVPLQASLGNRSRKTLSLKKRKKKKG EKETLPGGST*KEKVRKKQNNLLV*KTH IKPG\AGAHGPNPNIWGGGGRQITRSGN KNHPG*HGKTPFLQKKKRGALLKGTNL TARGQSKTF
6490	20391	A	6544	402	0	LSWTQ*CKPIAPATGEGGTGGSLEPRES RLWCAMIAPVNA/NCTPAWVT
6491	20392	A	6545	1	365	RKVTSLPSTSRCLSLPHFSDGPRPVKP LQ**LRCSICSASLPTLHTARAAGLLP \LASSTAVNQ*N*SRELGACVWEHSGIK YGLF*RD/RGLTMLPRLVLSNWPQAILP GQPPKLLGLQA
6492	20393	A	6546	1	331	ISTFKSYLRNIFSKAIAAVDSNSTEGSG QG*LKTFWGYTIIDAKNIYDLWEBGK TSLTPGVWK\LDDFEG\FQTSVEVTAH VVQIAKELELEMDPEDVTWKWLQSHDTN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6493	20394	A	6547	1	417	TRPKINKTKNLLFERINKIKP*VKLT NKNKNTPHITKIRNESEFTIEKLKSI LRE\YMNVCVYNLLYANRKPQMDKFL RYKQLKLTQEETETLTD\YITSKEIKFV I*NFSTK*S*GPNGFENSEFGRVLWFTPV
6494	20395	A	6548	410	288	AHFLPFCINK\SLTMLPRLV*NMWP*VI FPPQLPKTLGLQV
6495	20396	A	6549	1	216	IDRGFTMLPQLVSNLS\LRSSHLSLPK CWDRCPEPPCPACFHLSECNTCIKNQL HVTLPFPNT*GLTSEG
6496	20397	A	6550	479	146	VPGFKQFSCSLSPNS*KYQRAPPCPANG FAFSVETGFFPHVGOAGF*FPTSGDPPAS ASQSAGITGLSLHAWP\ENL*KLRHAT GLRLHDHVLKVPNYLKVCSFKFEIADV
6497	20398	A	6551	42	484	SMRWNSMNVTIMPANTTSIPQPTDQEVI SVFNS/YYYYRYCKATAAIDSNLSGGS RQSKLKTFWKGLTIIYAIKNICDSWEV KIST*TI*KKVIPTFMGDFGGVKNSIK\ EITADVAEIAAR*L*LEVEPRVGNLTPI PALRKAEVG
6498	20399	A	6552	304	74	HTGKAAKKKEC/WRGTVAHAYNPNTLGG *NGWIT*GQ*FETSLINMVKPRFYSCIC ISGYTHKVIHRIIICKGKKLE
6499	20400	A	6553	432	62	FWAGNSRMQQWCTDT/VAHCSLDLLGS SNPPASAS*VARTTGARHARLMITMN EKPLGARYCARIFENKLGITYPNESVPT KTNANVVSKRSCPSHDDPDGHWIYLM SGLIVNKIGKVK
6500	20401	A	6554	2	174	YCNLCPLPGPSDLPTSAS*VAGTTCMCHY TWLIFFCI\LVETGFYHVAQAALFIYS I
6501	20402	A	6555	3	268	DAWADNIKCR*GYGAI*TLIHCWWECK\ W*ATWWFLIILNMLLPYNPVIW\PRTC IQIFMSTLFIINTKTWKQPRCHLVGEWIN CGTCR
6502	20403	A	6556	3	402	DAWTDNIQCR*RYGAI*TLIHCWROC\K W*ATWWFLIILNMLLPYNPIIMDHK\TC LQIFMSTLFIIDKTWQPPKCHLVGEW/I KLWSMPAKEYHSLARTEL/IVP*NT*R RLSCT*LWEKSQYEKATYCVVPTV
6503	20404	A	6557	396	2	KKQNAFQSPSFLPRL*TPKITILISFHN IYIYTHTYIYIHVCIFTYIHTHIYIFF/ RDRFLLCPLGWRVAVVQSQTAASTSOAQ GIPG*FFFK/SIPCRDW/SITMLPELVS NSWAQAIPPPWPVKVLWDYRCGS
6504	20405	A	6558	393	175	FKSQGLVLLPRLPFGMLIAHCSLKLPG FSDSLNSA\SQ*LGL*GCTATPGPYLLI IYAGELGLNKRISISK
6505	20406	A	6559	401	188	SPPEFFILGGPRVFPPPPFLKPPPRI*F WGPKKKKNF/CPPPGPKNFFF*KGPPLE FFFFFFFFFFFFHRS
6506	20407	A	6560	37	343	YEPVVLLDIYPRKELKT*AHKRTCTRI IASFFKTKVMWQPD/CP*ADE/WDK*T ACLQTVB*CSARKRSELSTM/IEMWRKL KCVALSERGOSEQAACVVIPTL
6507	20408	A	6561	792	141	LFPPPP/YLSTSPNAGA*TTSPLPQFL YHSPPRRQSGTKPPFFSKK/PBPPSP/S PNKFYPGPWWGVSPFKPPPPQKS*GPK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KSPLEPEAF/PAPPLTQDCPPFVSNPGG KKKTTP/SAKKKKDPTPS/PSPPPRH*I GGPPGFSPPPLFKTPPKLILGPPKKKK IFPPPGGKNFFFLKGPPPPPPPPPPPP FSLFPVGVWSRWLRSEADLCGECYSS
6508	20409	A	6562	1	356	FFNFIFIYLF/NFLRWSLALSPRLNGV QWSDLGSLQAPRPRMLPFSCLSLPSRD HRRPPRLANFLYF**RWGFTMLARMVS IS*PQ/CDPPASASQ\STGITGICHGTR LIPRNPMA
6509	20410	A	6563	416	84	LSLPSSW/DYRRPPPCLANFLYF**RRG FTMVSI*PHDRPTSASQAGITGVSHH TQPIISFLKSFFFTLNRFNRVCIDSEL LLQCKDFYLQKFNHLHAFQEYTHCHGVH Y
6510	20411	A	6564	2	51	FVVREMQIKTVLRYFSLKLVKIKK*DST FFWKG/C/GETGNLIHKAHW/R/SI*QYL KKLYVHFLFVPVIPPPEIYLNKKILST K*LFAVFIVTEKC*KKKRCG*T
6511	20412	A	6565	2	511	VRW/SCAGL/LHTAV*IPGRIITSEKCA QQVDETHRN/LQRLQPALINRKGFIILH NNTCLYTAKPMLQKLNELGCEVLPHLSY SPDLSPTNYFFNHLNDVLQGHSHTOQN AENAF*EFVKF*SMDFYATGINKLIS/H WQKCIACNGSYFD
6512	20413	A	6566	3	248	GDICT\SMIVPALFTVPK/TWNPVSIS K*TDKMWYIYPVEYLAIKTKFC/SFS ATWMILEDIMLSKPGTER*ILHVLVLCG R
6513	20414	A	6567	3	258	WRDHSSLHS*PFGKWFSLSPLSNWDY RDVPACPANFEKVL*K*GLIMLPRL/LL SSPPEW*ILSSRLPASSFQSVGITHMNH CS
6514	20415	A	6568	392	166	GGGGPPRGGGLEPPGPPPPFLKNKK*/R PPGPGPPLFPFGGGRREEKFFYLGGKNF H*TRVGPPPLSGGKKKKIRG
6515	20416	A	6569	234	411	PGAVWHAYNENTLGGQGHRI*GQEFKT S/LGNIVRPHLY
6516	20417	A	6570	1	175	FLQHV*NKFTMSDQIIGKIDDMNTLID LEKNVKDL\LITQTEVERLEGENKIPIL PG
6517	20418	A	6571	392	140	LPSSWDYRHVPPCPANFVLLVETRFLHV SQAGLELPTSASQAGITGVSHQARP/E **NSIRKGATTIQRDIGPVLQVRYLVRC
6518	20419	A	6572	2	228	RTCTQMSVATLFLIAKNWKQPRCPSTIGE WINKL*YILTMYYLVIKK\NDPSSHKK TRGNPKCILLSKRSQSEKA
6519	20420	A	6573	412	100	ALHSHPLGGPGQGVPKSRIPNPPCQGG TPFFPKNPKLTRPGFARLFPPLKCLKP EKFPNPG/MPGVPLN*IPPPVSHPGVQP NFFSKKKKARGFCLVLNPSSS
6520	20421	A	6574	406	257	NKREKTRKMLDSIVIRKRHIKSMRCY SAPIQMAKV\SNRQSPKFWVRCRQTISL *HC**ECKIVQSMW*TLQKFLPAIVFLC IYHTEKLRFQTP/CT*IFLAALLMIV/ RTV/KRLVCPSMGWLSKLW*VNLSFSV
6521	20422	A	6575	370	68	EQGSVMGRPSEPFGPYNLVCR*LRPLE KRTIWAGVS*FSRCSLSRLPLARKGKSP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6522	20423	A	6576	1	259	NP\CTS*VRFSNGLS IDLIDVLRPSLTVT*AVVQWCNLGS*P *PPG\SGDPSASASRVAGTIGQHHRWL IFVIFVEIWRHILVYFHTAIKNYLRIG NL
6523	20424	A	6577	418	218	KGKTRLGRVPPCNPSTLG\GQGGWIT* GQAFRTSLANIVFPLM
6524	20425	A	6578	1	401	EKAGCSGSYL*P*HFGRPRQEDHLTLGI *DQPGQCSNLSLQKNF/TNISW*WPG IVAHACNPSTLGSGRRIT
6525	20426	A	6579	3	356	HWDIRHEPPFPV*MHFFIWLPGCHSLLA SPNLTGCFISITISLSSLFYILETRV *DLQCSYFWERRG\SLCCPCWSRAPGLK RSCCLRLPSSWDYSRLTPPHLANYCILG GEGESS
6526	20427	A	6580	411	158	IGSVAQARVQWRDLSSSDPSAN*APPGL KQSSC\PASLPSRWY\NKCTPPDLANF YIFFVETGFPYVARLADCFPPPL*KMT GSY*VFTMCQIPH*AFYKF*FI*FRVGE DKNSLPAWQHRETL*SLQKKYKN
6527	20428	A	6581	399	218	GGAEKLVPK*GGGPGSPPLPPLOKPRP KGPLWPGG*GPPRPGEAPSPLKNKN*/ PLPG/AGPPPVPPNWGGGFYPRG*GFG* LPLGP*TLARGKQRPVFKKKKN*NVN KKKAKL*KS*QFFFFLKTGSRCPFRAK VQGPNGSYPKPQPRG
6528	20429	A	6582	392	214	GSSDPPNSTSRVAGTTDEVLPSPGWS* NSW/VSK*SACLGLPKCDYTRPQHLLA RSNF
6529	20430	A	6583	390	257	PKRPPPPAFC*PK\SLGMLPRMISNSW AQAI I*RWPPKVLEKQA
6530	20431	A	6584	65	251	HYFNSFNFFLMGSSNHPTKNPG*FFFFL TFYKNK/SLTILPRLVLNSWAQGILLPW PPKGLGL*AQGILLPWPPKGLGL
6531	20432	A	6585	2	143	RHMPPCLSSF/SYFL*RRGFVLPRLFS KSWQVILMPWPPKVLGLQA
6532	20433	A	6586	142	334	GRWLSQLLILNFTTSVLKQMSW/MACV SETWPA/STLGGRGRIT*GLKEFKTSL QNMRPYLYK
6533	20434	A	6587	485	377	RTRLSCRFILSLIFRFGNFYCTLKF/ H**VFLLSFVFC*GHP/FBFIKVFPI IFFHFKVFCVFKYLLFFFIETFYF FVNIFSKKFSVMFVLLIEMFYGRFT IPLR*F
6534	20435	A	6588	241	251	NSLFTKKKKKKGGALLKEPILRAGGGEG IIFKGPQKSI PGPGFKAGREKPGPSP *NWFF*KGPPFFFFFCKE/RSFTMLPR PASNSWAQAICLPQPPKVVL
6535	20436	A	6589	429	54	YFLFLPSLPTFFPSFSSFLPSVLSFFLP SI/SSFLPSLLFYLLSSPSSPSSLF LSFFLSRVSFCHPG*SAVAQSRLTATSI SWAQAILP/CR/NRDTMLSRALNS*P QVIRPPRPKVVLGLQA
6536	20437	A	6590	411	137	KCIGTITTHCSLHLGSPDEPTASRVV GLQAHHHIQLAC\F*LID*LID*LNVM ESRHVAQAGLELLGSSDPPTLASQNAEI TEMHCIP
6537	20438	A	6591	412	196	QPQPPGAKTSGGGFPPIR/WGHQPPPPG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AKKYNFFFFFFFFW* RQALAMLP RVVPNCQ T*AIILPWPPKVL*LQA
6538	20439	A	6592	28	400	IMPNCFPKWL YITFFFFF* RQSL/DSV AQAGVQ*HSLGSTATSAFLGFK*FSCPP AFLE*LDYRHVPTHTNFCVFNKD/MGF TMLARLVSNS*PQ/CNPPASASQAGIT GMSHRAQPHLFVLKMEKPPPNFLFILLM NQSIHLYLLNFYRF
6539	20440	A	6593	414	23	QTHLFWFPFGFSPPPFFKNRPRIFFLGA LKKNFFPPPRHKNLFFLKAPPPFFFK RSFFPPGWCAIGLFSLQPPPPRFK*FFC PSLPKKWGYRPLPPRPGKF/CFFFFVI LVENGFFHHVQDGLDLLIS
6540	20441	A	6594	91	274	ILHWS*PLGNYHL/WLGUVAHARDLSTL GGRGGRIAGQGDFKTSLSGSKQSISARK KKKKK
6541	20442	A	6595	391	251	HLKRCSTSSVIREVQIKTTTCHPSE*K R/SEINMCW*BCGQTELSALLIRC*\WD SEMVQLWERKEYLKQISTESSWAPAIP LLDI*P*ERCASLSLRKGWGYRPEPPBL ASFLGSIYI
6542	20443	A	6596	465	268	YLLCHLGCSAVAQD/LTLCSLKRSSH LT SPSSWDSRRGPSHLTKFF/C**RGLNTL PSLV*NFWAQL
6543	20444	A	6597	3	229	CHGSPQCP PGLK*SSHLNLPTPK*L\ D YRGMPPRSANFLFL*RWGRCAQAGLBL PDSSSLPASASCP RPVL YF
6544	20445	A	6598	122	418	IIIVNELCHIMCFFFFFKQNLGTOAG GQGGKNG*LKP KPPRLKGS PWLTLP GG WNYGGFPF/HPS*FFFFLKGKGPYFCP PAGGKFFNLKGPPFFA
6545	20446	A	6599	1238	930	FETDSCSFA*AGVQWRNLSSLQTPPP\G SNNSCASAS/RIAGITGTHHARVIFAL LVETGFHHIGQGWSRTPGQAIRPPQPP KVLGITGVTSRARAIKHFV
6546	20447	A	6600	398	78	PSSPFYLFIFRQSPFFFAVVEKGGHPG FPNPPPSGLKFFYAPAPPGSKAPGQGP PA/RFYLFIFRQSPFF/CCPGGGRGPS GFPPQPPFVGKIFLCPSPPRK*GPRAG PPRPRKIFFFFSSLFFFFVFWGFTML PRLVNSGAQAICPPQPPKVLGLQV
6547	20448	A	6601	3	473	FPGKKGKGP PPGG/QLKNPSKPKNRK PGAPPRGPRGPKGGGLGSPQSPQGG EKWTLKGGPNLPPPRGGLGARPPPKIG GGPLFPKGGGPKGGTPPPPLFFFLRRS PALSPRLCSGAI*AQTSS/SPPARVGC PSPAPTRPTGLTVSPGSN
6548	20449	A	6602	398	156	NGRKHTDVKEELPSWVPTRDLTPTGTA GAF/Q/RGYGYNYKYVTVKKS IAGVS TVLAA*VLFSYCLSYREIKHEQLLRAH
6549	20450	A	6603	380	77	PPPKSPPL*NFFPFF*KKKVPPPPGK LPLSFLFFPFF/RDRVLLCRGWSAMV HGHGLSPVNFCISTNRAL/SLNRPIS NTWTQAIRPS*PPKVLGLQM
6550	20451	A	6604	352	204	KRGPKI*NFFFG* RQSLHMLPRVVPNSW AQMILPPWPP\KVQGLQA
6551	20452	A	6605	631	357	FFF\DRVLLYHFGWSAAR\SLTTTSA SWV\KQFSCSLPSS*DYRCAPP CPASF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CIFSRDRGFTMLARMVSNS*PQVIRPPG PPKVLGLQA
6552	20453	A	6606	3	397	VLHKLQRCSAVPLRAPTAFLIEGTQTP KRVWKR*P/RETQNNLLDKEQDFKTYQ KATVTKAVWCQHEDTIEQWDGIESTEKK FHTQRAAGGRDHSVSRKRRKESLFFF LKRGILILFPNLBGRGGISTP
6553	20454	A	6607	323	35	YLKTKIGKPGGLAALQFLGFRPSKNTQL GNRPMCTHTHTHTHTHVHPHTSQYLPH RSISFCSYLD SI /SP*VLTESSNSNPTP LKCC*HFPSFCL
6554	20455	A	6608	439	252	LVPPLFFPRSFLLFSPPKKRGGPKPV*F GPPRAFYP PPF /V*RGPPPPFFGAPKKK IFFSPPPG*KCFF*SPPPG
6555	20456	A	6609	3243	2602	FFFGRDGVLLCCPGWSQTPRLKQSSLS L/PKC*DDWH/RATSSGLQVFLSICCSI ISIFFMPSICDKSTKQFSN/PORAYILV G*R*VIYLGVLAFLEFVLRQHL/NTVA QAGVQWCNLSLL*PPPARFKRFSCLILP RSWDHRRLLPFRPANFFVFLVETGF\TIL ARLVSNS*PRDPPASASLSAGIMGVNHR TWPILVFLHPSVFFKVLQLEFYL
6556	20457	A	6610	81	395	TWAALKLYSTCIFSSSETEPDVSQSQT DTTACIMEPGLFW/YRSIIWTL*FHFH WRDGLTLTLRLVWNSWAQVISLPGPPK VLGLQASATAPNSFILIREGIS
6557	20458	A	6611	1	126	GRLRQENHLNPGGRCSEPRLHHCSPAW AIERDSVSKK/NKNGLKRCFHLRKKTLK GEKRIVV*PGGRCSEPRLHHCSPAWAI ERDSVSKKKMD
6558	20459	A	6612	389	67	YLFMYLF*/DRVLLCHPGWSAVAQS*LT AASNSWPQVILLNRFKSWTVLLSSKI PVVQGSTPCPRCYSWHPKCLQLQGLLGL DCSSPKYPRGPSLAARSLPKWHV
6559	20460	A	6613	1	384	RCFKVKDLKMRPFWN IQVDFKSNKDCPC KRLKRRGHASLPPEKRRRPGDKGGRGW NSAVTSQGT/VEATRSWKSQGSVLP*SL *RERSPV\ELAHF*QRLAMLPRLVLNSW PQDISPPWPPKALGLQEP
6560	20461	A	6614	385	174	CLRLSALKPKLNSWY*K*LYIMEY*SA LKT\NGKILSFAITWMNLD DILLNEISQ TQDKYHMNSLICEI
6561	20462	A	6615	1	370	MNPAHLSFLLRRKERRILWLKALGHIM /FTV*GLTGIALANSSLYIVLHDTYYGV SHFHYVLSIGAGFAIIGGFH*PPLFSG YTKKKKKNIRGGGTKNFLLCPALVQREK VNPPFALTNLWG
6562	20463	A	6616	3	342	YRHEPPHSAIFAQLYKL*K*LIYALKTG KVVYKLYLNKAISQ\SYNRASLSLT* *PRVKRRS*PGTGAHTCNPSTLGSQDG LIA*VQEFETNLGNIAKPLHQKKKGA PV
6563	20464	A	6617	1179	915	FFETESCLVTQAGVQWRDLGSLQSPPS G\SSDFQLIFVLLVHGQAGLELLIS*SF ALASQTARITGVSHHAQLVWSDFIKSIN LFCCL
6564	20465	A	6618	3	390	HASVKMELPYDAATPLPSIYPKELKARF *DLCIPM/FITALFTIAKRWRQLNCPSV

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						VIRSWGREGVKESCLMGMEFHSAR*KSS GDTFHNTENCY*TVHLKIVSGKF*L*C VLNYVGGFFYHNKNIKRLS
6565	20466	A	6619	392	49	QFLFERLFSSYSYGVSGVKMLGSTEVQL FPRKCEMKSCSVMPRLCSCGGISAHCNL CLPGSRDCPASAS*VAGLIFY/IFLVEM GFHHDG/RELVLNS*PQVIRPHQPPKVL VLHV
6566	20467	A	6620	193	282	TPGLK*SSCLSLQNSWDICIWYRRLPLY PVNCFCC*FVCFVC/IFVEPGSCIAQYC LELLASSNSPMSASQSTGIIGMSHGACL ILT
6567	20468	A	6621	383	8	LNDTVSTFFF*DRISL/CPSWSAVARSQ LKAASWSWQAILPPQPKTNLLGSSDSS TSA*DQSPGFK*SFCFRLPGSWDYGCVP PFSANF*IFCRDKLSL/WAQAILSPWPP KVLGLQALWEAEEGG
6568	20469	A	6622	395	42	HVSSTSFQGDHLRLVALPLP\PLHNL PLPLSPRSL*C/HSRGWTVLPSPRLTAT SLPD/SSCLSLLSAWDCRRAPPHLSGFC WSAVA*SW\SLQPPPPSRLPWPKVRRRL QPLPSRHPV
6569	20470	A	6623	3	327	PSPPSRWNP KDVPNPQENLGIFFFFL*T RDLATLPLRLVPS* TQVI/WPPKVLGLQ A
6570	20471	A	6624	395	47	KNRALFFFFPPPKRGFFPKPLIWGTFRF FPPPPF*NPPPYFFFGAPKKKFFS/SP PGGKIGSKRPPPPFFFPKQNFPPVPPG GGPRGDFGSLQHPPPRVKGFSC LAP IIF FSSF
6571	20472	A	6625	100	267	LSLSKKANISKFWLGT\VAHAV\DPSTL GA*GRWIT*VQGFETSLGKIVRCLYFC
6572	20473	A	6626	409	126	PSSSFSSSSSSSSPSSSSSSP/PFFFFFF FFFSFW*KWGVSLCGPGWSQTLGLKQSS CLSLPKCWDYRNKPLHLAFLASLILFTF QEVVDITD
6573	20474	A	6627	506	323	REAPGTLPWCQKYDMIAQLVWQFLRK PNIYLPYNPAIPL*HTCPRKINTQYT/C FITKTCTRMFIAALFIIPQNWKOPT*PF CPFTIISHSCSPRDNWF
6574	20475	A	6628	330	117	DVCPRKIYTLVLQQLCI\RMFTAILFSI AL*FCKPMCTSILEWIKL*SIRTEYH LVMRRNKPLLYSMPQM
6575	20476	A	6629	396	139	FFSPPEKKGVFPSP*NLGTPGFPPPPPF KKRPP*FIFGAPKKK/HISPPPAEKFF FFKRPPPLFFFFFFFLLFFFFSAFKL KV
6576	20477	A	6630	79	405	VSGRMTALESYLLASSA\RNKCSSNCKI KKMTARLDVLAHRCNPSTFGG*GGRIC* AHKFETSGHHIRPCLYKKKKGRPPFKR TQFSPARWQGNFFWGT LKNSRAGF
6577	20478	A	6631	2	417	SFIFPCKFLNQFISFYKNVCHDFDCNCV ESKDQLG/WPDAVHTCNHNTLGSQGGW IA*AQELKTNLNDNMAKPCLY
6578	20479	A	6632	74	417	KTVFRYNGWAL*ASENRISLADLLPSF HVLLCLPKAG/PNFPPLSSIKKFFDLDP LIRSHKTHISEGVLPFP/RRKEPRTER PRRI*TDRCWVSSLSLIVLDHAPFVQS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QFYM
6579	20480	A	6633	740	776	CSFFLLKKQTRSRRAAVQAGVQWCHYSSLQ PSPDLKQPPASASQTV/KD*GAYFWCC FFLFLKRWGL/NSVVQAGVALLPDLFVV RRLVIPLSLWAVEPALWAAQL*LL/SP CPLASQSPRHQTGQSPHQKCFDILGLH LALRSSFSPLERPTLRLPPGLASFHT* ATWLSWPLPYK/PPKRVNMYLVKADRPE PFL*GTRGRKSVQMTHAKTLQETLYSG PEAQAAASVTDEF
6580	20481	A	6634	2	296	FFFLRQSFALVVQAGVQWHDLSLQPPP PRFK*FSCSLSPSGWD*RHAPPAIFV FLVEMGF\TMLATMV*IS*PGDLPTSA CQSAGITGLSYRRAP
6581	20482	A	6635	407	212	GRPR*TPPPLGKKKKGAPPKTKKKKNF LGGDSYSQKKPPFF*RNKTRPGGGGPP GIPPLKG*AKKKGLPRGPKFPVT*/NK PPPPPPGGNNQNPFPKKKKRKRSTR*I*K IRISRFILYFFFFFLLERGFSGSPRGGG GGAFLSYGKLWPPG
6582	20483	A	6636	20	223	PCKKLQPLQPSAT\TLISQPLTLRKD LLPGKRL*LAEGSDSYQLVAKYFKIK GLSPGRNLANI
6583	20484	A	6637	866	647	FFLDRVL/LCHLGWSAVMRSLTAALTS GLKQSSCLSLPKLRDYPHQHANNIS *SSWSDSNMQPRLKTTL
6584	20485	A	6638	398	26	KGAPPPNIFFFFLFNIFFFFFFFFF FFPINFLQCLLYYRALHFNKVKVINNF/ PLNFCAYYHPL*NM*FSYISFQNLKFF LI/FGVFNLSGIYFNVL*IANF**G*LI LPGTIYLKLCYFTTN
6585	20486	A	6639	1	341	NWDYRHALPCSANFFILVETGFCQLPRL VLNSCPQVSHHA\KFLPIFFFLFLEEG GFVGPPRLEYREGSLQ*LPKLGSTCL TLPKG*N*RGEPLPPARSSFFFIKFFI ET
6586	20487	A	6640	391	118	NANFEKSFSMGKIL*NSLAWYKKILCD/ RKNRSMQKTPLD**YYFKKLQPL*PSA NTTLIGRPALTSRQGLPPAKTL*FAEGF DPMILSLF
6587	20488	A	6641	352	285	KKKKKGGGGGAYSGIPTF/CFFFLNGVF LGPAGVQWQNRSLQPPPGVKLEFFFLS LPSH*GPRHGPPRPGMFIYKNF/CFF/V RDGVLLHCPGWSQTPGLE
6588	20489	A	6642	433	64	TGNFFLDSLFYFNPGLGGGILKGFFS FFFFLETKFFFPAGGQWRYFSSSL*PP PPKFKQFFFLSM/WPRPGKFFFFFGIL VEAGFHRVAQAGLKLSSGNLPTSASQS ARITAKSHRTVP
6589	20490	A	6643	424	11	PPSIFLAPPSRGGGPPPPPKKK/QSP KKKKKGGGGPKNPPPKKKGPPKTTGF KKNPPQKKKKKNSPPKKKGPPANK*KP PPRPQPFYFLTIFYKIPIYIFLLKFLLF YILFFFFLSSKQGRPLAI
6590	20491	A	6644	411	2	PPLRIWLASPPSKIF*PQPLHI/YFSPF PP*KFFFLKPLIFLGGFFPKFPPPKKS FFPKNPQGVF*NPP*KKKIYFSSPP*NF APPKIFLKTTPPPFFFFFVFVEMGSRY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IAQARTRETRGRTRGRTRG
6591	20492	A	6645	34	381	AKLGTRGAAGQKEIKVTRI*WKEIELS QFTEYTTQKNL/NVTDKLL*LVYMFSKIT GYKVNLLKNINCIFHKHTNQOQKILKMPF IIA*K/TIK*L*INLTQDQDLYAEIYQ TLKAEI
6592	20493	A	6646	17	448	HFYAKLGTRASLSCSGLHPV*ASQPLVYL PTQASAMADAPFPARLPNLSISYCCTS NEQGSVGVGPAEPGAGYNLV*HLLRPLE KHSI*VAVSRFSHYLSRLPLARKG\NP QTPCASWVRQCPTLLRLALHGLHPLSNQ SQGD
6593	20494	A	6647	462	336	SLRLPGSNDSPASAS*VA/GITGFCCHHA RLVFVFLVEMEGLS
6594	20495	A	6648	447	62	KDDIWIATHMNRWSISLAKRKM*IKIT MKYPYTSIKMA/IKQTNKN*KKSSSIKC W*ECRTMRTLHCW**HITG*PLNKTWV KFIIKLNLYLPYDPA\TCTQMFTA/ALF IIIKY*KQSKYPSSGYCVPA
6595	20496	A	6649	3	1492	LAYARAFLLDDTNTKRYPDNKVKLLKEVP RQFVEACGQALAVNERLIKEDQLEYQEE MKANYREMAKELSEIMHEQI/CPPGGED ERLTFFPSHLQRHQWDSNKHNGSRDDQL VFGRVITSHGPCVGTCTFVICKLRMLSKA NHWGDRAQ/ERTKGKGRERK*RTTLFLN R/RFYRSWKKVHIF
6596	20497	A	6650	495	170	GAAEFPASQSAGIAGVSHHARLEEFFSL DSGRVMRGTEVLKYLGGYTTI*SIFFP FSFF\WPLGSLQPLLPQFK\LSLLSRW DYRCFAPHLISL
6597	20498	A	6651	9	222	QTTRPERNRSGDPTHL*SSWDYGHVC HHAWLIF*K/CFSGGLALLPRLV*NSWA QAVLPPWPLKVLGLQV
6598	20499	A	6652	241	833	KKTPLAMWNPWPQPPQIPHPLTKLVQMA G/QENGCLSGHDLSEIRPAGLHNSARGE VLGLSSSLGKELVFLQEBDLSEIHIPE AQEVEMASGHFAFLHVPVFDGRAPYCKA SLSASSSLEPTPPEDTAISSLRPPSAPE MLTQHGAEQVEDHPG/Q*QPSPHSQSR PSPQKDPQALVIASLRSTRERKQASHGG TRPG
6599	20500	A	6653	1	398	FFFDIGSHSLTQAAVQ*HDHGHGSLHPR LPGFK*SSHLSFPES*DYSRHTPPRPAN F/EVETEFLLHVPQAGLMRCNLLPAT/AT SKSARITSVSHHVQPEVSIK*NNISNL IKCFLLFYKYKCI FINTKFVFTV
6600	20501	A	6654	489	282	PAS/WDY/RHMPPLANACAPLC*RDPS MLPGLVSNWVARVICLPWPFRVLRIOAR ATTPG
6601	20502	A	6655	953	908	SQSCSVS\RLCSGASADCNLCILGSS YSSTSAS*VAGTTGARHHTQLIFVFLVE MGFHHVGPQGLELLT/*VIHLSRSPKVL GL*APSSARGQNSVSQ
6602	20503	A	6656	412	44	RISERRKSLGAVHTKDKYSSSRVRTSN PNCARSASSKQSFLLFGKKRAPHGPKIS F\KDALLVVDGITGVHHA*QIFVRSRE R*IRPVIPALWEAEAGGSRAQKIETILA NTVKPRPSLLRA

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6603	20504	A	6657	3	241	FFIFLEARSHSVIQVGMQWCDHSSL* TPGLKES\PASSFHRAGITGVSHHTYLF L*GH*SHSQGPHPHDLITSKRPCS
6604	20505	A	6658	467	42	FFFFFKQGFGLPQLEGKEGIPGPCNP CPPGANDSPFSTPLGNGGPGPPPNP FGIFGI*GGEGGF*TPGSGKPSGPGSPK \IPFCWVIRERPHGPPPPRFFFLRQSL CFAQAGVQWCDLGLPQPPPPRFKQFCLR NS
6605	20506	A	6659	2	286	KNLKINWT*WLMPVVSAT/WGGSCLKPGR LRLQ*AVIAPLHSSLGDRAPYLSVSQY LYFSLSLSLSLSLTHTHTHTHTHKIE LLGCVAEIIHFF
6606	20507	A	6660	3	249	LSPRP*CGDTISAHCNHLGSSSSPAS VSQVAGITGACHAWLIWFVSVMGFFH AGQDCLHL/NLVIHPPQPPKVLGLQA
6607	20508	A	6661	3	1507	PEAPVPFLDSNQENDLLWEEKFPERTTV TELPQTSVSHVSEPDIPSSKSTELPVDW SIKTRLLFTSSQPFTWADHLKAQEEAQG LVQHCRAKVTLPKSIQDPKLSSELRC FQQSLIYWLHPALSWLPLPRIGADRM AGKTS PWSNDATLQHVMSDWSVSFTSL YNLLKTKLCPYFYVCTYQFTVLFRAAGL AGSDLITALISPTTRGLREARNNEGIBF SLPLIKESGHKKETASGTS LGYGEYVIK ITL/SSSTDLTWTHEIDLHNSL*NRDSN CSNF/LREQAISEDEEESFWSLEEMGV QDKIKKPDILSIKLRKEKHEVQMDHRPE SVVLVKGINTFTLLNFLINSKSLVATSG PQAGLPPTLLSPVAFRGATMQLKARSV NVKTQALSGYRDQFSLEITGPIMPVSLH SLTMLLKSSQSGSFSAVLYPHEPTAVFN ICLQMDKVLDMVHVHKELTNCGLHPNTL EQLSQIPLLGKSSLRNVVLRDVIYNWRS
6608	20509	A	6662	326	1	IMIFLFFQTGSRFVA\RLCSGTITTHC SLNLPSSNP\PTSAS*VTHCRTRVIL NPSVDPGSRHVVKGGLELLDAILKPWPP KVLTRGSTPEFRSGGSGVIRIRGFN
6609	20510	A	6663	414	105	QGVGFVKVGLNPLSRLHFFKQKLFVLS *KGQVKKLSLKI PFPFGGFFSPPI*NPP P*NKPQRFPKNPFMGFT/IRKKILFLAPK STKSGG*NPPSK/HKKI*FSF/CFWETE SRSVTQAGVQWHYLSLQPLPPRFK*PS FCKPHKRVFKPLGLVLWGGISNRRRKK SGGKRNPKA
6610	20511	A	6664	1	407	GCVPVPAAREARAG*IA*TRET/RLRW AGIVPLHSSVGNKSETLSQKKGAPSKK SLQGVALFSLQGLPPLQKRRPQRG GGRGQLAPGYNPPAGKTLVGPGLHSLFC SKKAWKELRPWKPRGFWFLINST
6611	20512	A	6665	1	280	FFFF*HRVSLCCPGWSTDHLHLLPP*LAR FKRSSHLSLPSSWDYRHTPT/HPGFFVC LPVFCRDRVSFVLPRLVSNFWAQAILLC GDRKVMGLQA
6612	20513	A	6666	408	89	WLPNSLILPN*NYFVSYSLSRVVSLCRP GSTAVAQ*ELTA\A*TLGLKRSASFHS HSCSLPSSWDYRCTSSHLANFFFKRWGF TILPRLILNSWPQVILLPOSQRH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6613	20514	A	6667	484	208	ITTVSAAGLIHYSFLNPGEPMTEKYAQ EIDDIH*NLQHLQPALVDRKGPIFLHDH A*PHAAQPK\LQKLNKLGCRVLPPLPYS PDLLPLT
6614	20515	A	6668	495	227	PAFVKVPPEKDQRQNSTHAGRNHLPMEY LLL*KKKLIETESHVTLRLECSGVITA HCNKLKLGSSDPPTSADYRLKPWHLP SSFSMS
6615	20516	A	6669	2	65	DGVLLTSLRLARLV\NSWPQVINLPWP PKVLG*QAGLGTPLK
6616	20517	A	6670	403	224	ILL*P*PPGLK*/FLPSSWDWRRLCL ANFLFFVEMGYPRVARAGLKLGSDDPSA SQSAGVTGVSRRPGRFLIRTVL
6617	20518	A	6671	406	162	RSVAQAGTQWLDFFSLQP*PPGLIKQSS HFSFSQSASH/RHPDNYCIPCRNRVYVG QASLELLGSCDLPASASQSAGITGSCCL
6618	20519	A	6672	453	32	VVSATLHTSVVVCACATRCVGMCMTLGV CGCECVVV*GCVCTSVN*HTSTGWSEK V*LCVCGCV*LCVAECMAFVSRCVCDP VCCLEPEKMRSLPISVA*VCAPMKVSPCP PQLSELHLLSLNIYINKCVSLSQNAWLF L
6619	20520	A	6673	378	180	NEVIRSYKVSFLSPRIEKWINK/I/HWY IYPMEYDSAIAKRNEVLHATT*RKLENI TLNERIFDIIPFI
6620	20521	A	6674	378	94	PVKNRRTKELHIKDVTCPMLIVILFMI K/S*KQPKCP*IDWMMNMWYTHMVEYC SVSKKEGSPFICYNEDITLNEISHKKTN IYNSTYIRYLE
6621	20522	A	6675	1	380	VCSL*VLCRHMSCFQNCSL*FSFSFWFF WRQCLPLSPRLECGGPMASAHNLRPGS SDSCASASLVAGIRGACHHARVIFVFFV EMG\FHCVGQAGLELLT*VICPPWPPK VLGLQVLATVPGQPHIF
6622	20523	A	6676	424	135	SHRWGVKCFKYNIFFFRD/RV*LCCTGW S*TPELK*SSCLGLPKQDYRHETLRVS Y*F*NSI*QIGVLAMVSKVLNS*AQAI LLPWPPRVLGLQI
6623	20524	A	6677	408	91	HTHFVWPPVLIP**PMR*VLLLTPTNTF FLRDRVSPCHPGWSVEAQSQITAASN\Y GLKQFSHPSPKCDYRRELPCMVSLLII FIYVHLHMYVHARKEKPEYPL
6624	20525	A	6678	1231	217	PPYFNNPLTFPQKRFFKGDKTLKKWL*I REIILQNRGIG*KTDSIR*MGKTEAPLK EKFLLGTAQPSFLPYMLGHFKEE*GBE FPGTHSWPFPSFPVWGLGLSVNHRGIEG PRVSLQTWGPGQREAMECEGNHGTEDTG \GAVLQPG*VT*GFHTPTSEPLVAPPC TCSGLKAEA\GFLKLPGKQG\SEGALPP *SPLPSACFPGLRLRGSSPGLMIHFG WGLFTSPLGLKILGPRHPAGPALPQIAQ RPSLKFR*RRLGWGPPELLPAQTCGAQSL GPSTAPLLGQGPWGLG*HASRWGTLGLA VAPGNEVPSLSPR*PRGAGPLHRHRVPV RSWG
6625	20526	A	6679	1	178	RGWDYRRPLP/RPG*CFVFLVEMGFHRV GQDGLYLLTL*SSQSAGITGVSHRARLQ PPIF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6626	20527	A	6680	3	135	KSEHLEREPTIEQLSTMFF/TAKYGWHL RGH*HRCQKKPEPPEDR
6627	20528	A	6681	425	107	KGPPTPS/PPPPSPVFFTEKILVPPPPF PPPPFKKPPQNIWGPCK/IKNFSPPR GEKNFFF*TPPKYFLGAKKKNFSPPR GEKNFFF
6628	20529	A	6682	424	284	CFLQPGP/PGSKGASPPSFQDNWGLRQA LPPP/RESFFLFLFLFFPIVQTGFHHVA RAGLELLTSSDLPASASQSAEITGVSH* A*PPF
6629	20530	A	6683	1290	449	PLSAPPPGDPSP*KSSPRAPNLPAP*PP NLSPPWPKCPRPRR*PASS/PP*LPVPP KSPSPPV/PVVATEASRGHPQIT*ELG SLVLRMTEKGTWG*GIPDSIMPLPRRS EPRTCRE*GDRWRWRRRRSTGAVSTF SPGFACGGGSGA/PAHPGEQKLGAARP DE/PVCPAAWVLLPSARVVASPAAPP LPSQPVH*RFKP\SPPY*PP\ALPPLSP FEPSAPPHGTGSPVY*QGVPP/SEGCPS SKPLISVRPPVTINGCLPQSQPPKHTV SRLYEEN
6630	20531	A	6684	425	40	EWASLKN*HPP/GANQAVEAVEAPTHCW *GCKSIEPLWKTWQCLDKLNICLLYDS TPE*MSEHVYQAACKKSFTAVLFMIPP *KQSPCSTGWLQAWWLTIVIPAPWEA KVGGSLEPRSLRPAWATG
6631	20532	A	6685	2	107	SWLTAASTSQ/VKRSSRLSLPSSGDHRC MPANFFFLKDDVSLPRLISNSWTOAIL LSLPTKGLEL*AHCSLNLPGSSDPPASA YQVVGTTGACQLIFFF
6632	20533	A	6686	12	224	TPPGSTHASGAPPLANIKFNYL*RLP RLFWSNPQVILLPWPSKVLGLQVWATV PSPFLIFDRDIDREI
6633	20534	A	6687	404	2	TAARGTIYGGPIKLLPRKPADVK/SGS FKTAAPFFFFLGTRTLTEFLFIION*K QPKRPST/DRINKLWYISTIEYISAMKR NKLLIHTTAWMNYKGIMVSKRGQSQSI FSRTKTGFRNHISGCFLYPLPLRL
6634	20535	A	6688	410	163	PRGNTPPGFSPPPEKENQKVFNPFPNIV *KKGPPPPQGAQKGPY*GPPLSFLPP KKKKKKGPPPPPPKKNPPKNS/SFSP KKKKKFFPPPPKKKG*GGPPLKTLFFW GGGKKFFFFFWGKKEPLGGFFFGGGGG GGPFFFFFG
6635	20536	A	6689	205	405	KSPSPGGPPLIGKLEIGGAPKPNWPF PLGPKGENPPLALGGGAKNHPNPQF ILLFLGGKNP*KSPSPGGPP/ANRKIG NRRGPKTKLAPPLGAKGKPPPCPRGR GGGQKPPQSPVYSPFFGGKKPL
6636	20537	A	6690	3	199	HGSLQH*PPGFKSSSLSLPSSWDHGHV QPRPAIF/CFFLILEKRGVSPGFPGGPE TPGLKGLDLL
6637	20538	A	6691	8	350	SVCLGLP/RCWDYRYEPHPLA*LAFLOQ IIFHMDWIYHVSILVVDGYLGCIFYFLA IINN\G*AGLELLTSGDPPTSASQSAS ITGVSHCTHFCYCTFLTREITTPKEVKI GLCM
6638	20539	A	6692	373	197	LPSSWDYRFMP*HMLFFK\FLELLFCRD

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						E/SLTMLSRLVSNWAQATLPPQSPKVLGLQV
6639	20540	A	6693	369	100	PMLARMVIS*PRDPPASASQSAGITGV SHRARPIYFFK*R*SHAGYSAVPVHRHD PTTDKHSFLFCFLQTGSCFVVQVGMQW HDHISL*PRTPGFKQYSHPSLPRH*DYK PTPE/HPS*FVVQVGMQWHDHISL
6640	20541	A	6694	12	182	FLSSWNYRCVPPHLAN*KKNFFFYTDOR/ SLAVLPLGLVSN*TOAVLPLQPKVLGLQA
6641	20542	A	6695	402	248	SSWDYRCAPPCCANFYKIL*TGS/LLC* PRFVSNWDQVILPPWSPKVLRGV
6642	20543	A	6696	301	309	VQEF*DRILLSRCHPGWRAVA*SRLLTA ISASRLKARPSHLSLLSSWDYR*VPPGP ANFLHFFCR/DRGFAMLRRLVSN*SWTQV ICLLRPPSVGITGVGHRARSILLD
6643	20544	A	6697	3	387	PCLANFF/VFFVETGTHYAA*CGLRLLG SSALPV*TS*SAGIIGMSHCTC/LQITL LKTSHS\VAQAGVQWHDLSLQPLPPG FM*FFCLSIQSSWDYRRTSPRANFCIF SRDEVLPWCWPGWS*TPDLR
6644	20545	A	6698	1	287	LWFLYQGNAGITGISHRAQPN*SVFFKD RVLLCCPGNSAVA\HSLTVALTSOQV IFLPQPPG*LGNFCIFSRD/RGFAMMPR LISNSWAQVIRPP
6645	20546	A	6699	412	3	FEMESCSVARLECSGTILAHCNLHLLSS SSSPVSASRVAGTTGACCHTWLFFFFFP V/FLVETGFYHVAQMGMLNNAKAILPQP P*VLGLQARITTSPPNSSTREHTSGSG VGYPKAFHSIVLLLLLFLHLLCGVF
6646	20547	A	6700	393	88	QKLYPYLTPYAKV*QWIKNLSVTAKNI *FLGENTGVNLHSFRFIKGFLLDM/TPKS ISTKRK*KIKWSSSKL\KNFYALKNNIK KMKRQPTKYEKIHLTLNNWV
6647	20548	A	6701	494	239	KAGSHS\VSRLCSCGMISAHCTFCLLS* NNPLTSASLAAGTTGVHHHAWLIFVFSV QMGFCHVTQAWVLI*FDCGFSPINIKYN LL
6648	20549	A	6702	2	379	RPTWVTWQNPA*TKKKINFFFKTKSPT VPQAGGQGNLG*RKFLPPGLKRFSGLK RPEAPKGQSCSLMGGGLCPLLPP/WSGT PPQR
6649	20550	A	6703	220	47	TGFSGSQIN*EK/IWLGTVAHTCDPSTL GGAGGQVT*QGEFKTSRHEPLHLTVLCS LF
6650	20551	A	6704	80	414	ICYFYFVFAIYLNQPFNSCYRSFTFFFC PFETESRSAAQAGGYNPTLTLHPPPLG IKQFSCLTLPSS\WARS*KPPCPTWNGS VFVGIYKNKLGCGGAIRRVQTCNQTYSG
6651	20552	A	6705	69	416	NVEKRNNIHNKKT*PVYFKGFLLYCCKA EVFYVLDNPFIFYFLFYFFETHCVAQAG VQWHNLRSLQPSHP\SSSDYRCAPPHLA NFCRDGVSPCWPSW/S*APGLKLIHPFW SPKVL
6652	20553	A	6706	373	75	HAQLTFKFFYFRNTFC*AVASTKSNSSD RSE*SKLKT*FWKGLTILDAIRNISDSL/ REVNMTSTFRGV*KKLTPIIMDDFEGPDF TRESNHRGARHGG SRL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6653	20554	A	6707	331	379	K*KINKN*KGLTILDAIKNICDSWEEVN IST/LTGVWKKL/ITLIDGSEGFKISVE EGNAGVVEIARELEIEV/EPEYVTKLLQ SHKKT
6654	20555	A	6708	578	152	LQQHNPGLSLQPLSP\GFKRFSCLSLPSS WDFRHAPPCSANFFVFLVERGYHHVG*A GLKLLASSDSPTSASQSAGITGVSHRAQ PLIGFKVNSVKKSVPTRILKGNMSM YEQL
6655	20556	A	6709	392	146	FFETESLSPGLECSGTVSAHCNLGSSDS PALPS/RLLGSSDSAPAVVLYSPKL*I Y/FHKTCNYVLKINILLHVAIPYSPSWS C
6656	20557	A	6710	9	393	KSKPCN*DKSQSYRL*LFAQLFTF/SNF FYFLETF*ESHCVIQAGIHSGTIMAHT LKLQSSNPPASAPPSSWDHRCGPPPLA TFLKIFL*RQWAHYVSQARDNGLIMFPR LVFELLGLKRFLLPQPS
6657	20558	A	6711	34	387	QDFGFLSFFLLFFFEKGLGGPTCRAGPE SNLME\GGPGLKQFSGLTLPRTGNNGR ASRSRAKFWN*KGKGGPPGPPVELETFT LRGPPHLSPPKGKNNGGPKPDFFKKVG KKAPNP
6658	20559	A	6712	1	188	IQAWWYTPVVPATWEA*AGGLR\EPRRS RLQ*AVIVVLHSLGDRVRPCLNNKKG SPPQPLW
6659	20560	A	6713	377	98	SLGLKQSSHLNLPSSWDYRVPVPCPRNW FVPVPPFF\RE*GLAMLPRLVNS*QV ILPPQPSKVLGLQARTTAPGFFSHLLKT LVPNNVNLNI
6660	20561	A	6714	353	229	SSCLGLPKSWDYRHEPPHLYFY**RQ ALV/MLPRL*Y*FLDVNM*LPLPFHVAP SHLLNSVGMV
6661	20562	A	6715	371	64	ENHGDCPTAWATRAKLRFKKKT/CYQMF ITTLFTIAKRK*LKCPSSDK*INKMWYI HMMEY/YAIKRNWTLVKLNQNPYAL*KV LLRE*KQNP*SVRNIFKTHI
6662	20563	A	6716	462	232	HFNLITIKIIPFF/C*DGGLTMLPRLVP NSWAHAILLQPPPK*LGLQARACKL
6663	20564	A	6717	425	48	GFGGPPFFKKARFGFLHFF*TFPVLRFRP FPVFPFGGFKASPPKKKTPK/PPGGGGPP PYFHPFFLSFFPIFFEKEPPFFFWRG LGPPPPPPKNPFFFFFWVBGGKFLPQKK KKKFFQSISTRSVIHK
6664	20565	A	6718	3	413	GTFLTKTSLOGTLLY*VISYMCV*FIS* \SYLVYIIYFKDICV/LLYMYIFYIYTC VHISVCMYMYCMYVCMYKA*PANLKT CTQKHLAWGWVQWLISVISALWEAEARE SPEVETNLAQLGPTLSLPRKKKKKKKK
6665	20566	A	6719	408	71	SSWDYRC/LPPGPANFCIFSRDGVSPYW PGWSRTPD*RSLPGGDVMPALVIRHVPE LLKKQHSSVRSSRPANPIW
6666	20567	A	6720	375	57	SVIREMQIKTTMKYFFIPTGLIVIKKTE NN/RGWQRCEIKACIY*WWGCKMTQLL QKTIW*FLKKNLIEL/PYDPAIPLGM* LRELKTCPLRLGVVAHACNPSTLRG
6667	20568	A	6721	391	164	RISETCT*MEPAALFIV/DQNNPDKWTN LMWSYTHTMDYSIAIKRNEVLLHSSTWM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						\ENLENLMLSKRGQSPKTPFG
6668	20569	A	6722	381	278	SSLQPQTPGLKQSSCLSLNS\PPRFID *SISLYRQGLTILRLLSNSWSQAIVLP GPPKALGL*ASKKFLYSNI
6669	20570	A	6723	2	363	QRSLEHRPCKKC/CGLVV*VS*KVQYLV YKSSSFKNLLRRIHCNLFSGIVFHF* KLLRTPRSFCLCGLHIPINFTIF*IKIE KFKKC*PGTMAHPYNPSTLGGGLGWIT* GQDGLDLLTS
6670	20571	A	6724	352	58	HGGAIGARPFKVFNLI*FNLVCKDE/SF SLLARAVINSWPRVILPWPVPK\VGFG AKTLPRLKGFLESLPSLKKKNLAYAR TITAQIGLLVCFIDQQ
6671	20572	A	6725	383	54	KSSFFFFFEQGLLCCPGWSAVVSPLOPK CPRLKQFSPSL/LPSN*EYSCTPTTFSL HVCVSIHKYI*YIDQYIFKFF/CR/DRT LAMLRLVSNWSQAILPP*PPKVLGFG V
6672	20573	A	6726	3	343	LEV*ARATRQE*KINGT*I IKYKKVKQY SQNDMILYIQNPKDSAKKLPELVNKFSS FKVNRQNSVVF*NSNKS/EKEIKKRL /PFTIAS*RIKYLGINLTKEVKNLGRAQ WVTA
6673	20574	A	6727	3	615	HTSQGNL*IQYHTPWHPPSSERVERMNQ TLKSHLTKLVKTRLSWTKCLPIALLKV RTVPQKEVGLSPCEMLYRLPYSHFTVDI PTFETKSQFVKS YVLGLSSTFSSLKAK/ ELFSTDATLGSSPGTSAFSLGDDVLIRS WEEGKLKPAWEGPYLVLLTTKTAVQT/D NKKMQTHHTPVKKASPSKSCAIVPRPI PTKLKIKKKA
6674	20575	A	6728	2	228	SGAI/SVHCNLHFGP/SSSDSSASAS*V AGTTGVHTMA*LIPVFLVETGFHPISQA GLELL/NHMCPPWPPKVLGLQL
6675	20576	A	6729	98	359	KVEYTVLLP*GPKGKPTLPYLSPSSSF LKNHLISNFFLNRLVLLCPDWSVVG*FT AHCNLNLSCLSLPSTW\DSRCVPTGAWL RFI
6676	20577	A	6730	10	428	RSTRDYAALREVLDPDRRCRPRTGAW NGRRDRPGAGHSGPKAEARETLEKGL LFCCPGWSAVA*PRPTATFASRAQSLTV SPRLECGGVSAH*NF\SFHFQWGLAV LRTLVLNSWSLALLLLWPRKVLGLYALA
6677	20578	A	6731	425	158	SQTHDLR*STCLGPKCWDHRCAPFPAL FLF/FNKCPSIRKIENQA*LPGI*KKN FCRDDHLPLLSRLILNSWAQGL*CRPL KVLGL
6678	20579	A	6732	431	22	RDRVLLCHPE*SAVV*S*LTTVQNSWAQ GILSSI*DYSCVP\LPVNF*TFKSVYY YFIIFIFIYFCNSKALGL/LGVSHRAR PPRLVLNSWPPQVILPSQPPE*LGLEAL ATAPAI PRNSNLVWHQYSFKSIPDDL
6679	20580	A	6733	44	414	AIYDLPLLLIDLYPMELRASIRAHTCT* RFVATLFTVTKRLNQPTCPSTDE*QNK WSL/YIMNYPAIKRNEILIHENIMLCK RSQSOKAHE*FHCISIRISKAETED ELVVATRWGKGRE
6680	20581	A	6734	375	49	QRLTYHCRFSYNTASNKRLS*TMHQK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SACSMCPGRL*GVHAMRPKVLMRLSRSH /VARPIAATCAQ*VCDRIK/R/SLLEE QKIVVKVLKAQTQSQTAKFKNETFFRNK N
6681	20582	A	6735	381	88	SLFPRLETPGLRPSFFFFLFLSLH\PGW SVVV*SRLTTALNS*ARFILLSWCVPLH QAHHF\FFCRDR/SLTMLPRLVLKSWAQ AIPPEPLKRSGLQV
6682	20583	A	6736	384	293	AHLSLLSGWDCRCMPCLDNCVCLC/RV FVCR*GOAMLERLVNSNSWTQVILLPWHF KVLGL*AQDQEPWGRSGPGLPQAASG
6683	20584	A	6737	24	300	NILSAFLCLS*P*H*YGLVIL*NVQFR FLPLFFPMQMYTHIFPKIRIRPGVVSHA YNPSTLVGGQGR\SHEFKTSLDNIARPR LYQVQNKIR
6684	20585	A	6738	2	353	IHCW*KCKITYTLEKTVWQFPIQLNIVL PYIPA/IPLGIHTREMKTTHIYK/T/C MQMFGVVLFIIAKIVFQVNR*IKL*SI HKVDYHSE/IRNKQLYBAT*LNLRCTVL SE*S*TQKTT
6685	20586	A	6739	2	336	IHTYTNP*HRH\VHTPTHVHT/HVYTH NGTHHTARAWTPAPPTSLILPSPTESP PALQIPNLFPGLSSSPHAGSSSQGEPEE GGCQRRAKNRVGHRAEKWETELCAGDMN L
6686	20587	A	6740	3	385	KKQATLLWIHLATTSVEI*QSKIEVH DIFKVLKEKKK*TFYPKITNPGKIAFI HEGKIKLY/IVK*QLRDFINSGVLKAM LKRVL*SKRKGH*QIRNLRVQNSLVTA NTQPNTEYCNIVIVGN
6687	20588	A	6741	406	155	TGSCSVTQA*/CWSAVIVHCSLDLPSS NPPASASWIAGTTGMCYHAQLPSFNLCL QFYCMGCVFSRFLRFTFGLQSYTRKQK
6688	20589	A	6742	1	215	LFVSPDLSPDT/Y/HFSKHLDNFLKGKR FHNQQDAENAF*KFIESQSIDFYAVRIN KLISHWQKRVDCCNGSYFD
6689	20590	A	6743	376	109	YHMEVWNLYSLKGSYLRPLSSWDYWCP PP*QANF*K\FFCRDKDLAMLPRVVLNS *LQAILLLRPPKAEPLQLLQGFQFRRES GVVN
6690	20591	A	6744	382	148	NIPQFMFDILFQ*LITLSCPAS*SKFP LSSLYFIQ*GR/WLGTVAHACNPSTLGG RGQR*A*DOELETSLAHKARPHL
6691	20592	A	6745	403	209	HIVINRIIRKYCA*HYANKFNLDKLDT FLE\NTTCKNLQTEETENLNSPVSVKEI EQGKLCSDRN
6692	20593	A	6746	366	40	QGSVLSILNVKIVFWFKTGCVHFLFPLN FLSLFQNYVCSHTS/YPLSLIPHESLWS FPPSFNHSS*Y*HFLKTN*MPDAMAHAC NPSTLGS*GRWIT*DEEFETSLANI
6693	20594	A	6747	392	57	APKKKGGGVYPLYPKKSGRKKKPEG/PP PKPKKKLKTGPKNDADIKPGGAKFFF SPKKKRGAPPGVPPRLF*KPPQATI*GG PKKKKKPPQEGGKKGAPPKAPPLFFFL YF
6694	20595	A	6748	376	140	LEDNI/GYSNQAGAGRV*INTPKIKV S\QSKIADWLIKPKRLCAAKVSMNRVN RQPPWDRIFFALASAD/RGFLNKILG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN '09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6695	20596	A	6749	540	172	FFLRQSL/DSVAQAGVQWRHLGSLQAPP HRFMPFSCSLTLPSS*NCRCPLPPCANVL YF*QRWGFVTLARMVIS*PRDPPASAS QSAGITGMSHCAQVNTLSLHAFSCDKV PQNDLL/WPSKSCGTLSHEKACKDNVF TTWAQWLMFVIPALWEABAGGSRGQIE TILANTVKEHLC
6696	20597	A	6750	1	353	WFLERESTRSENSVNIVEMTT*DLEYV SKAVAGFEKIDSNIKRSPVGMSTSL H/CYREIFHERKSQSMCQTSLLSYFKKL PQPPQPSASATLIVNIKAKISAKRIKLT ECSDDC
6697	20598	A	6751	404	231	SPS/PFPFYPFGGPPGFPPFVF*TPPPE YFFGAPKKKKNFPPPGGKNFFFKGPPP
6698	20599	A	6752	77	371	ITCEVLYLTSRNTKTKKYLDCCCFWP* WNNRDQTYLHLFFF/CFIKNFFFPQKR GARGGFCINETPLGGKNPPPPPPGRG EKRAPPKTLCFFFFF
6699	20600	A	6753	354	169	ETESHVTHAGVQWHLGSLQPPPPGFK RFSCSLSPKK/WPSVKLN/PNT*SFCYH ILKALII
6700	20601	A	6754	1	442	CICRTAFELTGRATRSEKEERKKMYD *KKERKKEKEGILLKKDQEEBEGRKEE RKEGRRQTQDEFGGQNRSLTVKQGS*PK KRK*GIQ\QTGAPTQERDKETSONKNEE KARHDS*QQA*RTQSRLOQEGRKLWKR GLVSRRK
6701	20602	A	6755	366	262	FF*RWGLTMPRKLVLNSWAQVILPPPL E*LG*QA
6702	20603	A	6756	3	223	GLKQSSCFCLSNEDCKHVPP\HRLFFL FVCLFCFVLFV*RYGGGLAVLPRVLKS WP*VIPQPWPPQMLRLQA
6703	20604	A	6757	418	244	FSLSSWDHRYMPRMATF/SFVLFCLR EGCLTRFLRPV*NSWTQAIFPQSPKLLG LQV
6704	20605	A	6758	46	256	KLKNKTEARHSSSACL*/LPGSWDHYL PPRLANF*TFWRDRVSLLPKGVSNLWAP TILLPWPPQVLGLQV
6705	20606	A	6759	391	55	FIFFFPHSSHGVSPCCPGWSRTP\GSS GSPASASQHAGITGRNHHTRLQDIY*LE /TGQTVTLQFSLADTTLTKRLSWSILC CYNKIPETG
6706	20607	A	6760	377	2	FGEPPGFSEPPVLKTRPRNLFGLPHKKN INFPPP/WELNLVPLKGPPFFFLR*G LAMLPRLVSTSWAQVILPQHPKLELQ VHAMVLSSRTSHSPRSRLSPRFSORLL PVSCNPAQSPMA
6707	20608	A	6761	2	259	LTIA*KNFIFLGL*QGICQIPKDYQTSI R*IKDNLNK/WDTPCSWIGGLNIVEMSV LSKLMYRFRAIQMKTSGFPPFFFWKKG IFF
6708	20609	A	6762	1	169	FFETEFRSFA*AGV*WHDGLSLQPPQSG \SSDSPASAALPFFFFFLKKKIFFFPPG
6709	20610	A	6763	1	496	MATCTPKHINTQICVSLSLKLEFEQ MSIFKKGENELALGTGNIRPYDSCPGNR P/APFATSPAPRHPSGSPWRPPTSGGVP ARAECPASPNPLPPGFCQSPSRGRKEE *LRGESTTLAIF*APNRYHSF*LPRQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						P*PHGDCPARKKKKKPNDPRLQPTVT
6710	20611	A	6764	1	229	VLLLCFFFFVL*DRVLVGHGPGWSSRLYL KTKTKQKKQNNIFVCRVGG\LTTLRLVS NSWPQMVLSPQPLNALGLQV
6711	20612	A	6765	580	273	WRQSLTHSVAQPGVQWHDLSLQPPPPG FKRFSCLSLPSSWDYRRAPPRPTNF*Y LVQTEFHHVGQAGLELPTSDDLTSVSQ SAGITSVSHHAQLDMIFLR
6712	20613	A	6766	220	239	AQEFKAAASTTALQTETLCLKKKKKKG GVSLGGVSSNFRITGGASVTSPIF/CF FFFF*DRVSLSGVQWCSLQ*TPGLKRS SSLSLPSWERYRHVPLHPA
6713	20614	A	6767	89	387	FLSPSGSQEHLQTLRSTFSFFFFKR EPRFGRVGGQCPNLG*WKPPPPG*RFPS GLTLT/SNWERWATPPPTNFWIFKKKG NSPWWKRGAKIFGPWDP
6714	20615	A	6768	397	223	IREVGVVINWQHKDECD/KWNCVY*L* *WIHKPTHDKT\HRNTHTHTHTHGMHS HTQK
6715	20616	A	6769	3	367	SWKVCSKRPIPSPLFF*KHPRVLLRAD GT**VSLATL*HMQLS*AGSVKEAPRS NAPPHKATFLFLFFCTD/SSLTMLRLV LNTWPAILEPCCPKVLGLPARANSSSL SVFKLTSFCC
6716	20617	A	6770	490	260	FFETESCSVV*AGVQW\LELLTSSDPPA SASQSAWITGMSHCARRCGTHYHLGERF LVSFVTALLSOLLELGLAHSRC
6717	20618	A	6771	418	130	PSPRDLNLFPLNGPPLFFFF*DRVLLC CLGWSAVASN\FDLK*STRGLPKCLDY RHEPLCPAMWDTLSSL*EIFGLFCHRP LPAPRTGPGSQ
6718	20619	A	6772	311	314	FAVGELFLLHHVGHACLPFCHDCKFPE ASPAMLPY/QPVEL*AT*TGIEVLTGPG RFQAVFGLKVGFFHQGPTPVYLG
6719	20620	A	6773	465	283	CPSLPSWDYRHPPPRPAF/*YF*YHV GQPGLELPTSSAPPASASQAGITGMSH RAWPK
6720	20621	A	6774	410	91	RDHSLQPTQFRLKQSSCLSLPSN*DYS HMLPCLAGWLAGWACQTDRTQTDRTDR QTDRTDR*TDR*IDSRDR/SLAILPRM FSDSWPQVNLQPQ\WPPKVRRLWA
6721	20622	A	6775	409	253	LIFAFF\CRDGLAILLRIVSNS*PQAI LPPWPPKVLGLQARAPGVRPDL
6722	20623	A	6776	3	278	FFFFSLHLWAPLAFFFGAIHAYNLPI PG\SSDSPASASQVAGTIGACHVQLP\ VFLVEMGFHHVGQAGLELLT*VIHLQP PPKALELQI
6723	20624	A	6777	79	442	RDEDRGLERRVCASCTPQLGNASTT*G CPGVSDPSLHILF/CFKCN/SCFAPQA EGGHNLG*LEFGPPGLKQFSLTPQRI WNNGAPPPLYFFFLKKRGSPWPWG A*TS*PRS
6724	20625	A	6778	77	417	HRGLHLSFFLF/SFLFFFLKRAALLWPR EQGRGIWVNCTLSLRGGISKALPS*E AGTKGGRPHPTLFLVF*KKTSFSQVDQG GIDLWARGNPPGNLKWFLQKETLCPG HIF
6725	20626	A	6779	62	235	IQLRIREGKCLAYEHTARNGKSQDLHA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
						GLSCLCCCCCCC\CNCWP*STRKFPTKPR
6726	20627	A	6780	908	566	SKMEFRSCCPGWSDLGSPQPL\PLGPKQL\SCLSLP\RAWYYRHAPTHPANF*FLVBTGFFHVSQAGLELPTSGDLPTSASQSGAGIIGVRHHAHPECVFOKQLSEANLRRINWQED
6727	20628	A	6781	11	483	TTALLKAVRH/G*HLSLQRLLSL\VCCLCPAPRGAYRGRQAS*SCGGLHPVRASRLCLLPNQAWAMAGAPPTSLPPCSLISDCCASNQORDSVGVGPSEPHAGYNLPVCRFLSPLEKRSIRVGVTRFSRCLSPSLTRKGNLTPCASRVSSASPCS
6728	20629	A	6782	225	589	SRSEPGNFRSCLGVGVTCCMCLSLSLPSRSFLRPLFLSLSVCFVCLGTRVPCAPEGGFLARRPFFWSASPRVSAWVLPVGNRPPGGSGGLGVCEGLGNVGI\WSEPQGFSPPHPEQPLC*AGSRRALPNQQR\LPGAHRLPAGGCPQSFKKVVVTPVALCPHREM*PQLDAGTEKEAGKGMGQACLKLGWPSWPSHPFDTPPRMPVVVAVNPRIPLPLWPLL*PPAGRNARRKKPETDRRGRSAGSQPQACADGVRVSLPKSGALVMSRTGLPVC PWAALSPVARSRGDONPATSGAAGWVLPVAVCSLSLSLLALSFAFSFLCPSVCS CALGHVCPVRRRVGFLHVLSSGQPLPASLPGCCGRLAIVFPAVPAWGSVKAWATWASASEPQGFSPPHPEQPLC
6729	20630	A	6783	458	170	PCIVTASASQAGITGVSHRTRLNVNFSKVGSVTISLG*EVGLRHWP/NI/GRLDK TGPGEKQHFILHAPQSAPSVYHCLGNTQELPPLSTAMISQPKR
6730	20631	A	6784	1	192	FFFFG*ILPLSPRAGVQWHDLSLQPPHPGFKQFSCLSLP\RG*DYRACATRDGLIFCNFRLGD
6731	20632	A	6785	3	246	SLCVCQYYCRCACV*VPKQVSG*VTMGI/CATGFVLIYLCG*QCLCG/C/C*EDPFYCEQLCVHVCSCVLGRGWSVCVCISRL
6732	20633	A	6786	408	128	GPVPYKARG*SPFWPPGEKPSFPKNPKTPPGGGGAVLPFPWPWRGRPNSPPPGKKRC/QPN*IFFLPPHPGHKTQGPPIPKKKKKISAEFLSVV
6733	20634	A	6787	1	418	LTILGVMKNICDSWKEVKISAFGAWKKLIPTLTD/EY*GPKASVEBGTANVLETA RELEVEAEAVTEL/LQSHDQT
6734	20635	A	6788	3	237	FFFLT*VLTIV/PG*SAEVQS*LTAASTS*\VK*SSHLSLPSWDYRRMPPHPANF FFFGKKSLILHPGRGGPSLPTP
6735	20636	A	6789	282	3	PHPDNF\RFLV*TGCLHVQNGLLALLSPGYPTLASPSAGITGVSHCTRPKRYF*MVLSNKSILNRFLCTVLPTCLQAPRRTGPPATVLGRGT
6736	20637	A	6790	62	328	FFRDRILFCHPRWSAVIQ\SWLTEASKSW\IK*SSRLGLPKWCDCRHEPLCLDNITY*CRQNTLPTILIGCFRVSLLPYAKYTGKFWGAEG
6737	20638	A	6791	67	353	TNKHITYFLELNKREKPQLTVFFFF*RELRGLILANGNFRLRG*SNSPA*PSKVAGI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TGPPHQAGLILVFLEKTGFNYVG/RRGP PPPPKELALQA
6738	20639	A	6792	744	382	MTFKKTAHIYFYLYLYLRQSL/DSVA QAGVQWHNLSSLQAPPPGFMPPFSCLSLL SSWDYRRPQPRPA/NFFYF**RRGFTVL ARMVSI SRCPDPPASASQAGITGMSPR AWPKLHIFKL
6739	20640	A	6793	372	129	RVLPCHSQWTAVVQS*LIAVSTSQ\KR SPHLSIRHVPPHPA/NFKQFFCRDGLIM LPRSVSNFWAQAILPPQPKVLGLQA
6740	20641	A	6794	395	25	QPGLFCFTPRKKPDSFSKVFAVLSF/FP PSL*FS/PLSL*VQEMVICCPGWSAV\ TPGLK*SSCLSLPKRGYRCAPHSANL KFFL*R*VLFMLPRGLH\SWVQVVLCO WPPKGSRLACTSKI
6741	20642	A	6795	412	176	KKS*/CLATPRSENWVL*NGPPLFFFPL *RRDLAMLPRLVSNWAQVMLPPWPPK\ VLGLQAGATMDHSCVQYSHSFAPE
6742	20643	A	6796	444	95	NFVRNCSFLQSGCTFLHSYQQFLL/PC PCQH*IMSVFQILTTVIGVYMLV*ICS ALMTFDLFMCHVLI\CHLHIFFGVSVQH FSLLLFLFESGSIYVVQAGLHLFFSSNP PASAS
6743	20644	A	6797	378	732	FFFWLNLGSSQPPP\PAFTR\FSHLGLL NSRDYRHLPERLANF*FLVETGFRHV QAGLKLTLTSGDLPALASQTGTGVTAS PSLDEGVFKALPPVGTTLCLPPWTGG PFLGPAL
6744	20645	A	6798	444	1	PLCFPPGGGGFLSSHQGFPPPPPKRKS VGAKKKNIPPGPPFFFFPKNFF*GPY PF/SEPKKARWGPPPPGPGFSPPRSLVS PLGEKKKKKI\PPPETQPPSFGA*WGKK RAPPPGPRAGGRNSFLEGGRGQRTGGS VREFRAGR
6745	20646	A	6799	462	83	IEFLRPALCLS*SNPASI*KPHFLFF/ CLPFLSFFFS/SFPFSFPLFPFPFSPF FLIPFLSYSLCCSGWSTVA*GLTIAS\ TYGLKQSSHL/SLPASWFPCLTN*KKIF FRDGGTLMLIRLAYLFLNF
6746	20647	A	6800	433	185	PPPGGRLLVEKTRGEGQLKPGQPGROAG LGMRGNPGKAQPRPASGAPEMQLPARPP SGGHLYGCGAKNNEGGANLLCGGTGSG SVAAAGEVSKSAPDSGLMNSMLVKKE/ AGGGGEPQANQETEN*EG*PMSPEGAL LLTSPAAATLPLPVPPQRRGFAPPSLFL APQP
6747	20648	A	6801	395	60	IEFLFLPLSVDGRLWSHQLLPVMNEAT /MSIP*HAFATC/SSFLRGGLGA*ST LLYGGYMFYLRNKQTI\FOSSCCIVNGE QPRMRNRLFS*FIQHLVFSVFLIRAILB GI
6748	20649	A	6802	423	98	RGVPY*PGGLQPPPV/REFFFFFTIGRVS VLQAGAAAPT CRAQSILPGSWDYRHLHA NMSS*FLYFV*RQVFSMLPRLVNSWDQ AIHPSQHPALFFTCVVSVKPLATL
6749	20650	A	6803	396	194	SLMKLAHV*VLHTDGGFMHPDSAISCHD IFDSLHLTGEGSAKICRALYELIMQLME EHP\GEKQTTIA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6750	20651	A	6804	373	192	PALNPWAQANLPHQTALSSNFFYF/CVEMGLTVLPRLV*NSWPEAILLLPWHPKVLGLQA
6751	20652	A	6805	370	242	KKGTSKFLFFPSYSFFSKFWYQKKVKIAFFFF*DRVSLCHPEWSAVW*S*LSAALT/CPGLQGSWGYRHVLPCLANFS\FFC*DGVSMLSRLENWPFCLF*PVFQPGQHGENSISTKK
6752	20653	A	6806	464	182	DGPHRFEPPISS*FLPPWPPQKLEIKG*APLAKQIFFFFFFL*RDIVLLCC*GWGTVYSVYSWSSRLTAAS\TAVLKQSSHLGLLSSWDYKHHH
6753	20654	A	6807	3	228	YTCAGFFRRQSLCHLGGAVARSQLTVALTL/VPPGLK*SSNLGLPKCWDYRCEPPHLACVNFNTVKDVCFCILS
6754	20655	A	6808	506	173	NLHLPGLKQFSCLSPPPSRDYRRAPPC TANF*FLVEMGSRHVQAQGLELLNSGDS PASASQSAGTTGVSHHGQISLFKQILTSTRISEVIFLTLLLRILHDLPLCLKLPSL
6755	20656	A	6809	676	397	VSSCPRDQPGHHGETLSVLKIQKLARHGGCL*SQLLRSRL*QTRLNSGVGDHSEPRLSHCAP/AWATEQVSVRKCKKRQLHQKERIPEWVRS
6756	20657	A	6810	367	31	QVFQELYSQDLFIYLETSLCHPG*SAVARSA*VVTASDSW/VKQSSRLSLPSSWDIR*VPPYSAHFDVNSSFLTYCTSPGLTQKIEDSWLGTVAHACNLSTLGGHSGQIT
6757	20658	A	6811	469	251	LLSSWK/YQVPPPHLVFIKIL/CRIGRETASCCI*PRLVNSWPQVILRPQPPKMLGLLSATMPGPISVFCFCFCF
6758	20659	A	6812	16	462	EIISYCGFNLHFSNDYKKKERERERK KRKKENIGE/HI*DIGVSDILDLPKAWTKLNIDKWHYIKL/QKLLS*RVAKTNKLSFCTAEEIITRVKRQPMWEKTPASQTSKGLISNTYKELQQLNSTETNKQKNNFDLLSADKG
6759	20660	A	6813	492	243	SSWDTGCTPSRPD\IFVFLVETGFPMLARMVLIS*PRDPPASASQSTLVDTSRYSKYQNIHQVNMNF*NYGWCFDIFASVGD
6760	20661	A	6814	32	308	EYTLPHPYLITGPPVPKPEYSHS*YFLSPNTQCIQ/PAPRTLNTASSCLSRRTARFVPIYQDPSLEPLQLPPNSLTLPTRLHSPCWV
6761	20662	A	6815	97	274	GRFLELKVKGSLGLGMVVHAYNLSTLGG*GGRIP\QGFKASLGNIAKSLYKKNKGAA
6762	20663	A	6816	74	376	DDFIVYSVFTHLVNIKVDKDVLYKSLKYFFAIYRMGENIYKLYILGGINIQNISMYYTA/IKKD*ILLFAATWM/REDIILSEISHEQKS\KRCMFSLICGS
6763	20664	A	6817	1	1127	MRVTAPRTVLLLLSGALALTETWAGSHSMRYFYTAMSRPGRGEPRFIAVGIVDDTQFVRFDSDAASPRMAPRAPWIEQEGPEYWDRETRNMK\ASAQTYRENRLIALRYYNQSEAGSHTLQRMYGCDVGPDRLLRGRYHQDAYDGKDYIALNEDLSSWTAADTAAQTQRKWEAAREAEQLRAYLEGLCEWELRRYLENGKETLQRA\DPKTHVTHHPISDHE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
						ATLRCWALGFYPAEITLT\WORDGEDQT QDTELVEVTRPAGDRTFQKWAADVVPSSGE EQRYTCHVQHEGLPKPLTPERWEAILPS PTSPIVGHCWAGAVLASWSSGAVVAT VDV*EGRSSGGKGG\SYSGWRPSRPVP QGFWMCLSTALKKP
6764	20665	A	6818	34	382	STAGAIHVCMCVHVSTCVCACMKCVRV KF*IWDIETGAQLSCCVLVAQTEIIYL QERNSSLSERECVCAK\CVMCMCVHVS TCVCVCVCV*V*KRHNWPGMVAHVCSNS TLGG
6765	20666	A	6819	1061	305	FFLRWSL/DSVAQAGVQWRDLGSLQAPP RGFTPFSCSLSPSSWDYRRPLPRPANFF YF**RRGFTMLARMVIS*PRDLPASAS QSAGITGVSHRARRRNTILY*HLNFVIK SHKPPDIVFRDL*GPRHLLENPVL*GAK SHSSCPWLNLSPPPHAGSHCLSSSSPR MGARQDLLFNASSHTGLFPFLQLNQTAS RPTSQVPSKSLCFPLPWPQFFALPWPVRQD EGRASVNSPDPPRVPSCAGFTHSCNLS
6766	20667	A	6820	610	248	ERRSHVA*AVVKWCHLGSLOPLPP\GS SDPP\T*AS*VAGTTGVRHARLIFVFF IETVSHHVAQPTGF*TPGAQAIRLPQPP ENARITDVKPLCLAHFCYSKHFIMVPAP CISHQKVPH
6767	20668	A	6821	3636	3332	TCLGSHATPHCGHSFSSCKILLF*FFVF EM*SHPVAQAGVQCRDLRLSPPL*FK RFSCLSLPSSWDSRRPPRLANF\CIFS RDGILSCWPGWSRTPDLR
6768	20669	A	6822	563	146	APGLSFNCYIPPAFAFMGELTLFEVD/ NRSIFPTEY/TIHLISSEDILHS*TIP LLGLKTDALPRCLNQTTLTGRPLYG QCSEICES/N/HSFIPVLELILLKYFK T*STSTLYKCHKAQHLEFKLIDGVYT SLQ
6769	20670	A	6823	399	201	KAEPFPAKSWSKGGYVLPRS/IRLDHVK WALEPDDIAVLNFMKRRHPQSKS*TILQ KWIQPFSPVQR
6770	20671	A	6824	323	323	LPTVIVILSFYNFFFSMRLIRTLSPF CMYVCICIYVCIVCIYVCVYIIYVCYI /IYINISF*NDRISFFMLB*YVCVYIH EWIKKI
6771	20672	A	6825	396	122	LPPGGHRPAVPGGREGMGPGRNPGNPGR F*KKGPPSPGGGPAPGGPPSPG*ARKM G*PRGPSLP*TQIPPPGSP/WGPPGVT PETLVGFKKRGHPRGGGPPPGVPLPRR AKPEKWVNPQGQAFHEPKSPPRGPPRGA KPETLSPKKKKV
6772	20673	A	6826	414	64	RGVEGGAACIFKGLSVAGKPG/YLSAMR SCFRMLLFKS*G/QVIATKMLPTVLR MVGDPVANVRFNVAKSLQKIGPILDNST WQSEVKPILEKLTQAQDQDVVKCFAQEAL TVLSLA
6773	20674	A	6827	2	519	KTKTCLVEEIS*ITGRFLERINKIDKPL VNL*KK\VOVLNIRNEKVDVTTDRT*K \IIKEHYGQLYANKFN/IDEMDKFLKRD KLAKLTQEEIENLNIPVSI*KFLI*NIP KMKTP/GPDGISREL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6774	20675	A	6828	413	114	GKKRGPGPTPHPPARGPQ*GPGHFAVQV PEPPGLSFPFRGGFPSSGGCQRGEGRK ERRPSWTGFSWMAQEGRTPAARLEGAVL PG/APGPEAPGTGTTMSAPTWPPEP/G/ GRQVDVPAFPEG SARQAR*HEE*LHWK EILL
6775	20676	A	6829	479	261	PCFSFLSNEDCRHAPP/RPV*F/LVERG FRHVARAGLEFLT*SCLPASASQAGIA GVSHCAWPLQVGI EASLQY
6776	20677	A	6830	492	313	HPIGWPVNWGRASAVGEFRDWKLPYPEC EIRTMGGREHGQSPGAQRTFFQLLLSFX VESK
6777	20678	A	6831	378	1	SNGICLQASSASPNKIVPSTSLKVCNS\ VRVDGSRNPSVAFPLTPNLFVAVAPSIS SGMGIETIPIQGYRVDEKTKKCYIPF/V *ANRHPSPGVYNINVHALVSGPPLSDDS GVNKPOMKHQHC SA
6778	20679	A	6832	374	76	QLVEKWTGNVKSMTDRVLTMRCELRLRL *ALRTPGTWNLINDQIGMF/KFSGLSPK QVECLVNEKHIYLMPSGRINVSGLTAKT LGYVAASIQEAVTIIQ
6779	20680	A	6833	369	56	LKYLGTSVENRYADQAKWLSPVISALW* FE/CGWIARSED RDHPG*QSEIPS/PAN FLFLVEMGEFYHVDQAGLDLMTSGNPPAC NTGMSHCTRPGRTDVLAILCSDP
6780	20681	A	6834	457	142	DCLALSSRLDLQWCDLGSQAPPPGFKQ FLCLSLPSSWDYRCLPPRANF/*FLVE TGFFHVGOAGLKLTLSSDLPASASQSAG ITGLSHRAWPDSSFE GSSSS
6781	20682	A	6835	407	35	TAPAIRGVHLRGRGWTVYGAV*AVPPAS IPAYPGVVYQYGFYADLYG\DMQHSDM RGLMVSQHSMPHT\LOQS\SVTVMAGC TQPSHTMPLPLPLVY\ELALWRVYAEVA TSYLPPAEVMLAPCK
6782	20683	A	6836	1	428	GKTLNPPSLGKSFGLIGLEPPENDWPPDV SVPRAAFPLRGRPSVQSVVREMEQSV AQ LLL*MLTFTPHKRISAFRAL/QHSYLHK DEGDPE
6783	20684	A	6837	3	612	FKGSGVFNRRKKLEEHPLWQDVALGTAL CPQLPSLPGWGVIEWPRAACLPNPNL CPHCCGPQEAQYPL*AGGQ*GQHQEKPG A\GPHPPSGFQVPSAPGEAMTAMEGRKL SPAQAONPPQRKNLPRGFLPRGAPTTT P*SLRPR*TPVGAGLAAPIRSHHPGCSG QEALALCPDRPHKDRGVRRGAGGPRGRR VQLGGIPP
6784	20685	A	6838	3	412	YRWGFTMLTRLVLSS*PR/CDPPASASQ SVGITGVNHRVRLFFFFGTGPHS\MAQ AEGQGHNLG*LQPQPPGAKGTLPRTGNF KGGPHTPPNF/CIFFGKNGVSPYCPGWD FGAKAILPPGPPKELEBGSPPAPGKVF
6785	20686	A	6839	419	26	EETSRLWSIGQCPLLIQTAQVLSFTSGH GRHREHRKPTDSPLSACPAP/RLTPPP SMCPASHSLPSSQCMGP TLTPPTACAR PDTHSPPPSVCPAPLP/CRPVCPPPRSL PTPA*TKPRTQLPSSMYCGRSS
6786	20687	A	6840	365	66	LLERQIGRSVYGPSKSSIFDVPSLPHR GIKLVFCLCHTSSWDTGVHYAPPA*SWH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TVVHPRPRQVGQ/AGFELLTSCHPSPLT SQTARIAGVSHRARP KFM
6787	20688	A	6841	445	188	GFQ*FSCFGLLGWDTRHVPRLADFCI F/M*RWGFAMSARLSSNS*SAPSASQA GITGMSHCARPATLNSPICGTSPLGSGF FF
6788	20689	A	6842	3	412	PQQSPQLTTVTAPRPRALLMGTMTANLQ TRVSTSHLQGPRLTSALTYQMAQVAVAT PPVSVLAVVVLARVTVLP/LN/VNGI SVVIRQLQKAAGROPSPHQTRNNSLE* VASNLSKFLILEVAELFCHVLTFFSYQ
6789	20690	A	6843	113	410	NHCKNVNFYNGPRSLKRLITLFLHYF LNFILCKSSYLTLNLKQLTNLFCK/YE M/ESHFVTQAGVQWHDLSLHPKQSSYL SLSS*DYRGMPPHLAN
6790	20691	A	6844	2	357	FCPLARILQSGRFAVLWNGLVRGRQ EGPHGAFTRHT/SLRAPQPRSENER/ RIACALRAAHQASGWRLTPRAPRSPSGC HCPPAEPTSR*EAWGARRKGHGCCPAPH QPAEQDIS
6791	20692	A	6845	392	279	HFFFPCRD/KSLAMLTRLILNSWA*VIL LPQPSKVLGLQV
6792	20693	A	6846	3	275	VNLVDKAAAGFERMDSNF\ETSSTVGKM LSSSIARYREIIFYERKSPSMQQTFLSH FRKLP*PF*PLATTTLIY*QPSTRQDP LPKRAR
6793	20694	A	6847	1	454	FFFFETQPHSLPRLECSGAISAHCNFCL LGSSSSPASASQVVGITGMHHAIIIF/ VLFLVETGFHHVGHAGFELLTCGPPTL ASIMCILVYLLVFQHLVSLKNLKGQNAS FYFSPFGQHLSGFVKCSIWCCGSLSGLE GHFLPPHSPPLH
6794	20695	A	6848	13	148	GSAWRHTPAG\ELLKLRHRYGLNPEGG GCTEPIWCYRTPPWTTD
6795	20696	A	6850	204	30	TIFSRQVLRIONVLSKLRVSTVYANNG S\VLQGTLWASVYHGKILIGTVFHKTLY CEL
6796	20697	A	6851	2	429	EVWASGITGKAIMAMPIVIQPKNPSSYP CRRQFPLQLEAKRGFQLLTEKFKHGLL IPYN/TPILPVKKSNEYRLVQDLRIIN EAVVP IHPMIPNSYVILPQPPDAQWFPV LDLKDSFFCISP/VDPSQFLFAFE
6797	20698	A	6852	3	160	SGWDHRRHTQLIFMYSPLFFCRDR/SLP MLPKLVLSWAQVILLQPPKVLGL
6798	20699	A	6853	2	243	ACMILAAATILRVV\PLRYILIWGIN KFTKLRNPYSIDNNELDLFSLRVPDVS QKVQYAEKLCSSHSPLRKKRSAL
6799	20700	A	6854	24	458	SRAARRAGTTRSSHTGCRPRPADPGA RCLPRGSPHPRMDPPESP/PSETSPGPP PMGPPPPSSKAPRSPVVGSGPASGVEPT SPFVESEAVMEDVLRPLEQALEDRCRGT RKQVCDDISRRLALLQEQWAGGKLSIPC KEENG
6800	20701	A	6855	3	183	CCDFPVSASQAGITSVTY/Q/WPSLGS LQPPSPFVKRFSCLSLSSWDHRRHPLR PACKVFC
6801	20702	A	6856	2	242	GNHPYARKLA\AQRRASTVSSVTQVEVD ENAYRCGSGMQMAKDSKSLKTHQTQPGI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RRARDKAL\LVANGKRLWCIEGSVC
6802	20703	A	6857	54	401	EGERLQKFMHVLKTHTH/ANTHERAH THHTTRHTPRSGMHRNNRNLAKNLFFK IFFFLSSSPSLFFLIIPFLLSLSSLSL SLSLYKHTPLCILSLRTEHLHRMGALLG GHILE
6803	20704	A	6858	1374	579	CENPSRSTRPGQGPLLLPHQLPFH/RPA PSQSSPPEQPQSMEMRSLRKAGSPRKA RRARLNPLVLLLDAAITGELEVVOQAVK EMNDPSQPNEEGITALHNAICGANYSIV DFLITAGANVNSPDSHGWTPLHCAASCN DTVICMALVQHGAIFATTLSDGATAFE KCDPYREGYADCATYLDVQSMGLMNS GAVYALWDYSARFGDELSFREGESVTVL RRDGPEETDWWAALHGQEGYVPRNYFG LFPRVKPQRSKV
6804	20705	A	6859	36	269	IALGSMVDLTILMFNEHSEKNEIKRTIPL KIATR/IKYLGINLT\RGKKDLDTENYT TLIEEIEDDTNKWKDIPCSWTGV
6805	20706	A	6860	47	888	TLRARALQARPRTGSSCTAATWTS/SGA SQHSLRALSWRRLYLSRAKLKASSRTSA LLSGFAMVAMVEVQLESDEHYPPGLLVA FSACTTVLVAVHLFALMVSTCLLPHIEA VSNHNLNSVHQSPHQRLHRYVELAWGF STALGTFLFLAEVVLVGWVKFVPIGAPL DTPTPMVPTSRVPGTLAPVATSLSPASN LPRSSASAAPSQAEPACPPROACGGGGA HGPGWQAAMASTAIMVPVGLVFVAFALH FYRSLVAHKTDYKQELNELNRIQGELO AV
6806	20707	A	6861	3	391	NKISFFCRDWGLPMLPRLVLNSWAQVIL /LISTCQPFKVLGLOA
6807	20708	A	6862	322	175	GCRCVPPPRASFRI FGRV/RGLDILPKL VNSWPOAILPPWPLESVLQOA
6808	20709	A	6863	700	294	YVLRQGLTLPLRL/ECSSAIIAHCSLKL LGLRNPPTSASRVAGTIGACHTRVIFI VFVVIESCLLAQAGPKLGGSDPPALAS QSAGIAGISHHAWPPYFYWLSSTIPS VLSLHSHLILATILRGGDVTSQTDK
6809	20710	A	6864	371	77	RSMFAN\NLVYDTSDDYHLLKVL EEG IQTLMGRLVSGSRRTGQILKQTYSKFDT NSLNHVALLKNYGLLYCFRKMDKVFET LRMVQCRSVEGSCGF
6810	20711	A	6865	273	34	DYLEPTYLKLFRLLFF/CLIIETESHYVA QAILELLSSNSPTSASRSAGITGISHH TQPNFSNNTLLKPYLRLSYALLFA
6811	20712	A	6866	1	190	GAKGMHHTWLVRYF/CCVEMRSHYVTW VGLE/PPALKHSSCLSLPKCRDYRHEPP HLALFCFSF
6812	20713	A	6867	506	293	EKPSNGHKKPYTWISIAILFIIAKTWKQ S\PRCPSAGEWINC/WYTQTM EYYSMLK RNELSNEKT
6813	20714	A	6868	2	116	LFPFCRDR/SLTMLPRLISNSRAQGILL PWPPKLLGLQT
6814	20715	A	6869	10	141	GSAWLFFIFCR/DRGLALLPQLVSNPWL QAILLWPPRVLLQQA
6815	20716	A	6870	2	603	APTFFINFPAGKPKRGDTYHLQVRGFS EQIARWIADRTDNIIRVIRPPNYAGPLM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LGLLLAVIGGLVYLRRSNMEFLNKTGW AFAALCF\VLAMTSGQMWDHIRG\PPYG PKDPKHGHVNYIHGSSQAQFVAETHIVL LFNGGVTLGMVLLCEAATSDMDIGKRKI MCVAGIGLVVLFFSWMLSIFRSKYHGYP YSFLMS
6816	20717	A	6871	375	1	GFPFPVPKFGIPAPVAPQNPPPPPSF/ PQGPSPGPGPNPNGKNPFPKTPFFLK NSPQKKKI\FLKKFKRGPP\GPNQKPPFK DFKKRGLKPKKGGPLKKKKKKKRSN YSLKKIYSPFGFHFF
6817	20718	A	6872	255	23	GRVDPSTSTQNAGITGVSHR/GVQWRDL GSL/QFLSPGFKRFSCLSLSSSRDYRLV /PFCIFSRDRILPFWPGWSQTPHLK
6818	20719	A	6873	5	157	YLLFTSYTHAHTHTHTHTQFLLWTS GLS\SCCYIFSLSGPNTKCMIF
6819	20720	A	6874	351	132	SPRRC SAYVA/TYLFYFLINLLSLYS IFYGFAPNSFLCEVQEPSLG\SGWEPLS GNHFSSIKMKIAHREVN
6820	20721	A	6875	99	337	AGSFPQKKGKKKISRVRNQPIQLEKIFM NCASDKGLVPERIYKELESAR\KYQSIPS KVG
6821	20722	A	6876	69	306	YVSHLSFFF/CFGGGEKALFFCPRTG IKWPQFGLLEPSPSGLKQFFGLNPPETL EYRVFFPPPGKFFFFFFFFFFF
6822	20723	A	6877	335	169	WHDLLGLQPPPPG\SSDCASASQVAGI TGMHHSFNFYILFCYFEKVFLTFDLD
6823	20724	A	6878	2	237	ELGVKVLPHPPYSDLSPTDYHPLKHLN NFL\FHNQQCAENAFQVFIESQSTDLYA TGINKLISHWQKCVDSNCSYLN
6824	20725	A	6879	2	199	RGRVGRQFQKEIEELKKLEEGEE/VAP SSSSSSDPLISEPDISGEEDDDEBGE VGEDGEEKKKK
6825	20726	A	6880	1	206	FFFPETESCYVAQAGLELLGLGDFPASA SQVVGTTGARHHAQLIF/VFVFLVEMGF HHVSQDGFDLLTS
6826	20727	A	6881	1	123	WYIHTMEYYSALKRRKFLSFATWMNLE \EIMLSKISRRRG
6827	20728	A	6882	15	105	SQLL/WRLRQKNRLNRGGGCSFPLWCH CTL
6828	20729	A	6883	223	1	AASTFLPPLKNSLRG\SLRTFSSVTNV RKTALTWLSQDIQFFFSRSLTLVARL ECVVRSWPAASRLGCL
6829	20730	A	6884	193	3	OGEQDFLPCLPNFNF\FFCRDVSML PRLISNSWPQAVILPEPHKVLQARAT TPSHVFIF
6830	20731	A	6885	2	355	RLLTSSDLPASASQSAGVTGMSHRARPR NF/CILPNLSPCNTHSPSLPQPLAPT LLSLWICL/SLDIS/WDYRHPRLAKV FFFGDGVSQ\YRPGWSAVVPFAASTSGV EAILPPQPPK
6831	20732	A	6886	1	151	HSVAQAGVQWWDHGSRLRPGTPGLKQ/FL PPLKQSSCLSLSSWDHRCATLY
6832	20733	A	6887	314	203	FLFFCGDKVLLCP\RLVSNSWTQVILQP WPPKVLGLQE
6833	20734	A	6888	334	86	QNRSTFKRGM/MGAWWLMFVIPATWRA EVAAKIAPLHYSGLDRARLSKGMKCTS IFCSKSAKDCQTLFVKKKISLPTLPSI

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6834	20735	A	6889	345	152	QHARIMSVFIVETGFHHIGQSGLELMT/S/GNMHASASQSARITGVSPHARPSLPY YKCSKKQLCNE
6835	20736	A	6890	2	169	ARECSGATTAHCSLDLMSGSDTFTSASQ VAGTVGVTIMPRYIFK\FFVEMESHCLIA
6836	20737	A	6891	361	184	NQSSCFSLSSWEHRLMPHLANE/SFF DRDE/SLTVLSRLVSNWSWQAILEPRIF FENS
6837	20738	A	6892	3	330	HESAAITGVSHCTQTFFFF/CETGPRFV PQVKGQGHDLSSGEFGPPRLRNWPGTLT QNAGNTGTLPPhRTNFGDFRRGSFSPCG PGGFGRDLGGFPHLTGKRDTGLDPP
6838	20739	A	6893	2	348	ARAFFFWNFFCK/NRGLSMLPRLALNSG AQGILPPWPPKKLGLRALPTWPKTGSSG LEGHSSLYPHHSLIFPHHCSKFCFIKQW RLFILRITENQGLTPLNAKPAEPVMNE ARTQA
6839	20740	A	6894	340	240	CRD/RSLRMLLTVLNSWIQAILLSWPP KVLGLQA
6840	20741	A	6895	155	1	HLCFWAG\PVAHSCHPGTLGGRGRITR GQEFETSLGPGTQDVLAKCSRA
6841	20742	A	6896	454	294	PSSWDYRHA/PPMHNVDFFCRDE/SL PMLPRLVWNFWAQLILLPTWPKALQLQA
6842	20743	A	6897	49	333	IYICLSFYQSIITYLYDRQHDVLETVSHS VSLDLPGLRFSHLSLWDHRLILPWLASS NNPF\CRNRGLLVLPRLVSNWSWQAILE PWLPIVLGLPA
6843	20744	A	6898	434	324	FFFFCRD/RSPAVLPRLVLHSWTQAIRP PWLKVGLQA
6844	20745	A	6899	127	365	LPERRRYVVISGYRYHLQSLFFYAHQ ATFNNELW\LGVIACHACNPSTLGGDRGR MALGQEFEGLDISIVRLHLCNKIK
6845	20746	A	6900	208	1	FFFFFWILVETRFHHVA/RAGLELLSAG NPPTSPSQSARITGIWFFVWFSSNLSQF CYAHSFFTCWYSRA
6846	20747	A	6901	1	162	GTSGTRLFTIGKRWQPKCPMAELINK MW\YTMHYSVLKRKEIFCTNLTLQLL
6847	20748	A	6902	120	313	DKVL/WRLRQENPLNPGGGGCSEPRSHH CTPAWATRAKLYLKKKNFKGTLNSWYS FRRVANTNLQMQSGSNYMQI
6848	20749	A	6903	340	234	IFFCRER\SILPRLVSTWPAQLLPRP PKVLGLQV
6849	20750	A	6904	1	327	GTSGTSRILPWGPGCIRTPELKQSAHLS LPKCWDWCWNYRHEPPVYSFAMLIKLPF ELHLSVILWFLLLANPQTQTESKTFSTK /PRLVLNSWPOAVLPWSLKALASQA
6850	20751	A	6905	532	359	RDG/DLVVWPRMVSMGPKQSSHLGHFK CWDYRCEPLCQDFSYSIITVVPSPSREL RR
6851	20752	A	6906	270	3	GGTTVYPRKTKT/WPGAVAHACNPNI LG GRGGWITRSGLPVSTKNTKISRANCCAA VVLATPEAEQENRLKPGDGRDHGHQHG ETPSLSC
6852	20753	A	6907	1	312	GTSWKKMLPTLMDDFRG\KTLVEELIPD VVEIAREVELE\MEHEVDVTELLQPHDKT WTDEBLLLTDEQRVVFLEVGSVPVEDAV NIVEMKTKOLEYYISLLIKY
6853	20754	A	6908	331	61	FRHVGQAG/LQKLLTSSDLPAPASQSAG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ITGMSHHIRPKLILRKKSMRAKLDNRQT RLQPPVVEQGLLEQHEVYNVMAHVSX SSSRKLS
6854	20755	A	6909	419	199	SAVQDGV\SWCDLGS\QFPLSRKQFP CLSPFSTWDYKCAPHPATFCIFIRDGV SPCWSDSQTPGLK
6855	20756	A	6910	341	69	EAEVGGLLKARSLRPAWAIQDDPISILK KSFILGGQGGWITRSGDRDLRASASQSA GTTGVSHRAQ\LIFAFLVERRFHAGQG GLDILLTL
6856	20757	A	6911	174	356	KTYLMPLRSSLRPGMVAHACNPSTLGGQ GGWITRSG/ESRPSVLNRLTRCQANT VKPCLY
6857	20758	A	6912	391	3	SPPPPPPPSPPPPPPPQNFPPPGASSF FGPPPP/YFPKKSPPPNPPPPPPPP PPLGKQFFSPPPPPPPPPGPPPPPP FFFFFFFFFFFFFFFFCDKKYFIC LMICMLFFCKYILNFCRYS
6858	20759	A	6913	43	331	IRDTYSFSLAPALAPMLGTGKGVLLAVA SLGSRGASLCVFCVCLCVRIH\IGVQA SGCVCVCAC/CVCVCVRVCVCVHPWA SLLTKDLQCLPFTV
6859	20760	A	6914	250	11	TPNLWGLFLVFCFEM/EVHYIAQAGLE/ PPGLKPPSSSLSSSWDYRHVMPHAQI CISVFSLAQKGVPPSNWILITHYSIKS
6860	20761	A	6915	532	53	SQMALHEGFLLLFLKEKELHGKFSHPP SAPNSSMSKVVFFSETESHVAQAGVQ WCNLSLQPPPPGFKQPSRLSLTSSWDY TYLPPHLANFLFLVEMGFLHVGQAGLKL PTSGDLPALGSQSVGITGVSHTR\PRF LFKIGPLFLFSKMSQDEARI
6861	20762	A	6916	2	373	WHTPVVLATHEAEAGGSLEPRRAKLQA MIVA/NCTPAWVT
6862	20763	A	6917	1	270	GTRQSPRLSLLSSSCDHRRVSPHADF/ SFFYFFFCR/DRGFTMLPRQVLIWAQV MLLSQPPKLLGLQVGVSHGARPPHCLG YSWVYNKP
6863	20764	A	6918	2	367	RCAPHCNDNSSFFK/RVKTGLTIFPRQT SNSWPQVILLPWPP/KVLGLQA
6864	20765	A	6919	3	354	HEVNIVETTAKDLEYSINLVDKTFEKI DSSFKRRSTVSKMPDSITCYREIFCER KSQSMQLTSLLSYFKKLPQPPQPSA/TT TVISQQPSTLRQPPPAKRLRCAGLND FQHFWL
6865	20766	A	6920	366	41	STSGEDAVHIVEMTTKGLP/YTAVPGF HPSSERRSVVGNMLSNSVTCYRGIFGER KSQC/RQTSLLPYFN/KPQPPQPSATIT LI\SOQPSTSRDPLPPKRLQLTESND H
6866	20767	A	6921	3	368	QLLMGLHLEPATLDDLQKT\TIQGGSH SHHITAIP\PS\FTRENTLMFIHLSPI LLSLNPDIIITGFFLLKKKPKKHNKRG PSYKRTPEGPLLLLVVAQKTLPPKGGLY KIAPLRLFGEDS
6867	20768	A	6922	3	91	FSVLPRLV\QNSWPQVICLPWHPKVLGL QV
6868	20769	A	6923	334	91	ERCGKCAHISEIFLSSLDYIYIFVY\F FLLFFFFFFFFFFFFFFFFFFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						QKFNTKSKKMFNKTMMKVQVTF
6869	20770	A	6924	375	37	TKAGVQWHDHGSLOPQPRLKPSCSFSL PSSWDYRHAPP/RP/ALFLFLFGLVWFG LVFLVEIGSCYIAQAGLKLGLSSDPPTL VSQSARIIGPTHAWPTLTTSIQCTIRG PG
6870	20771	A	6925	647	1054	CFWKAHIQAGETNNIQEGSERFHFCPAD EVYVHSGPAVEDQPPRRSFAL/SAQAGV QWCNLSLLQPLPPRFKQFSCL/SLPSSW D/HRHVPACLAFCIFSRDEVCHVGQAR LELLTSGDPPFASASQSAGITGMNHHV
6871	20772	A	6926	3	204	DAWETTGFMIYDSLIDYAKKNPKHR/L ARHGLYEKKKTSRKQRKERKNRMKKVRG TAKANVGAGKKK
6872	20773	A	6927	1	112	PTPRTRGVASVLYFTTILILIPT/ISL IENKILKWA
6873	20774	A	6928	1811	478	DRARSPRSEAR/RRSSSRLRQDPSSLGR RRLRREIRPGLPESEPRPPPAALTAD QPPPRLESERGGGGMSE/AGE/ATTTT TTTTPOAPTEAAAAAPQDPAPKSPVGS APQAAAPAPAAHVAGNPGGDAAPAATGT AAAASLATAAGS/EDAEEKVLATKVLGT VKWFNVRNGYGFINRNDTKEDVFVHOTA IKKNPRKYLRSVGDGETVEFDVVEGEK GAEAAVNTGPDGVPVEGSRYAADRRRYR RGYYGRRRGPPRNYAGEEEEGSGSSEG FDPPATDRQFSGARNQLRRPQYRPOYRQ RRFPYPYHVGQTFDRRSRVLPHPNRIQAG EIGEMKDGVEGAQLQGFVHRNPTYRPR YRSRGPPRPPAPAVGEAEDKENQQATS GPNQPSVRRGYRRPYNYRRRPPPNAPS QDGBAKAGEAPTENPAPPTQSSAE
6874	20775	A	6929	324	203	LIFVFLVETGFHHVGDGLDLL/NLVIR PPRPPKVLKLENP
6875	20776	A	6930	3	364	HEASLTQTRTTMTHCSRTTGCSTASGRT WTRSRHSCAWCSAALWRAAVASRCPS/ IPVTPPQCCLSWP/WKVPLQCPPALS
6876	20777	A	6931	2	165	GRVGFCSVAQAGLQWHDLSLKLPLPP/G SSDCPASASRIVGITSALAFHFLNNVF
6877	20778	A	6932	1	370	TELSYSYSPNGAISQCNLCFLGSGYS/ RSSTSQVAGITGA/R/HHTQLIFVFLVE TEFHHV/AKAGLELLTSGDPPASASQSV GIAGVSHCAWPHVYILKEIMLGNLVRL MSICHHHTESICLFL
6878	20779	A	6933	1	441	RRANTPNNPEAPPN/QKKKKKKKKKKG KNPPGGPPPPFKTPPPFKNGGSGPPGKK KGGEKKRGGKIFFPPPGGKKPPPKKKG GGGKKKIFFFLFGPGGGGNFFKKKKGPP PPPPRKKKKIFFTGGGPKKKKKKKAPPK KPRGFYFP
6879	20780	A	6934	518	340	PKPKNFPS/PSPPKIPPPKKKVFSSKKPP GGFNPPPHKRRKKNFPPPEKLGPPKEFL KRPPPL
6880	20781	A	6935	396	299	VVEVC/GVCVCVCVCVCVCIHSLCKSTL HRTGV
6881	20782	A	6936	486	272	PTRAPTRPAPPHLADFLIFCSDR/SLIM LPRLVLNSQPQMILPLWHPKVUGLQA
6882	20783	A	6937	1	264	YSNLRDRARSCLSLPSSWDYTCSDYKC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ASLRLANF/SNFCRERGLAMLLRLVSN WAQVILLPQPSPKVLRLCLAVSVFPGEKQ GQCS
6883	20784	A	6938	2	407	TTGTCSRVSULTFVFLVVTGFHHVQAGL ELL/RPPQPPKVLGLQA
6884	20785	A	6939	422	65	LKGPPPSFFFFFFFFFFFFFSP/LP YILYFDCASNACLFKKNTWRYIKRIFF SPTPPIPFHEVENVTLSYVMVFQYCFL FF
6885	20786	A	6940	462	209	LSEFWDYRREPPLPAKFAIFMLCRDRGL DTLPSLVSS/SWHQAILAPQPPIMLGLQ VHSAYKGFCLPVLTFEEVIGNRPLGLLP P
6886	20787	A	6941	491	299	CAEYSPESGPTHASAHAS/SNVQMVYSR ISCHEELLLGRTSPSKNYMMTVSG
6887	20788	A	6942	429	256	FSHLSLPSSWDYKHLSSCPANFCIFVQT GFHHVQA\GDPPASASQSVGVGTGMSH S
6888	20789	A	6943	932	661	FKTGSYSV\TRLEGSGEISAHCNLRFLS SSDFPHLSSQVARTGSSQYARLIFVFF VEMGFAMLPVRVGLKFLGFKPLHPP\RTP RVLGLQE
6889	20790	A	6944	381	55	PASLPCCSLISDCCASNQRDSVGVGPSE PGVGYSLVRRFLSRSEKRNIRVGVTRF SRCV/LSPSLTQKGNLTPCASQVRQC LALLRLAHGACTHWPAPTVWHSVR
6890	20791	A	6945	816	513	FFIFIYFFEMESLLPRLECSRMISAHC VCLPRSSSY/PASASQVAKITGA/TRHS RLIFCVCLVERRFHHLAQAGLELL/NL VIHPSRPPKVLRLQGVTRTA
6891	20792	A	6946	383	234	LIPSLMDNSEGLKTSVEEVTADVVKIVR ELELKVKE/NVTDLLQS\YDKT
6892	20793	A	6947	423	60	LNPPPPPF\YKPPPKKKKFFSPPLKFG PPTKFFKRPPPPPPPPPPPPFWHGT PLNSLVGPPKVEGWVSWAQLPRAVGPP PNPKWGLNKPAGGLNKPPIHFPPLNGSG EATPPLIPWC
6893	20794	A	6948	1	327	MRLAAALLLLLLALYTRVDGSKCKC\ SRKEPKIRYSDVKL\EMKPK\YPHCBE KMVIITTKSVSRYRGQEHCLHPKLQSTK RFIKWYNWNEKRRVYEEAAGLRRRIG
6894	20795	A	6949	952	796	FFLHFLVEMG\FLLVGQAGLELPTSGDP PALASQSAGITGMSHRARPSVSS
6895	20796	A	6950	364	6	ITTHKNYFLSRTATPPKEGLPQRKKIFL FFTPIFIFVGFIFWGGGRGFLVFFV FFFFFFFFFFFFFFFFFFFFF\RVK TFIGFKVLFFKINVFFFLIRAVPLDYM NHALTIFQW
6896	20797	A	6951	418	266	ISFFXXXXXFFXXFFLLFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFN
6897	20798	A	6952	459	7	PSYLYKPGSQPNRRRHSVP/HIRSNKD PPPEVMKKWGPPTPQKKYFPKRKKL GGGGGPIYPPKKKVVFFKKPGGPKKPK KKKKIFFSPPEKRGPPPSILKNPPHPPI FFFFFFFFFFFFFFFFFFFFFLIGKA MLLDMGA
6898	20799	A	6953	325	143	LPSSWDYRRVPPHSAHFKFFCRN/RGLA MLPRLAKPRFSPSIFLNHPQVSEILGA

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						TRLAR
6899	20800	A	6954	585	306	KTESHSAIRSQCS\GEISAHCNRLRPGS SNSPASASRVAGIKGTHHQVQLIFVFLV EMGFHRAGQDGLRSPALVICPPWPFPKVL GLEAWPALHC
6900	20801	A	6955	2	155	FLVETGFHHAGQAGLELLISGDPPTLAK S\DSQDVIRITGLSHRAWPFLDIY
6901	20802	A	6956	3	346	DAWPDAGWK\RNWPPHQAIFYTFVE/TG FT/HVGQAGLELLGLSDVPTSSSLDAGI TGMSHCSRPRPEISSRDVHTIPGALQET WHTPDCLASSIRSLRCRLDCPHNHCFPLDK DGVTL
6902	20803	A	6957	1	224	QCGIRSRKDKARKGNVQIIPREGRRRTS PRYLFVPTGQETDGWG\MGLPAWLLKTR STSPPRSPRLHRRRGATSW
6903	20804	A	6958	102	344	GLLKPKSLKLQCTIITPVN\NHCTAAWA T
6904	20805	A	6959	3	296	KEEEEGEGEGGGGGG\EEEEEEEEEEEE EEEEEEEEEEHAEFTGHVESITQCKLLL CHLSLRVEAGITHLLCFTVRAVTRSQR LTKRRNGSVGHTSE
6905	20806	A	6960	3	172	RLGLPKCWDYKREPP/RPGLELLTSSDL PALVSQSDGIDVGHDTPEQDFYTLGQD P
6906	20807	A	6961	2	224	LALLPRLARSGTIIAHCSL\NRSRLRGL SDPPASASESTGTTGMSHCSQPAKLLST CIRNSVAETKYLLMPKCK
6907	20808	A	6962	2	330	KGTLRRQVTKGTLIR\LVADTLAETFH ARKEWDDIFKVLKKHCQPRILYLAKPSF KNEGESFSQRKCITTRVARSKMARGVLH LEVKDISTIIKQMKIRSSSLVEQIHKW
6908	20809	A	6963	1242	929	ETGSCSVQAVVQWCGHGYLKPQPSHAH /DDPPTASSIAGTTAHHYHAQLIFKKPF NSLCCPGWSQVSWRILGSSDPPASASQN AGITGMSHGAWPQLSIYRKGN
6909	20810	A	6964	1	378	KFFLQLFLHSFIYEHFLFFSFLFFFFFL RPSFAFVAQAGVQWRDLGSPQPLPPRFK QFSCLSLLSRWDYRHAPPQSANF\EFLV ETGFLHVGQAGLELPTSGDPPTSASQSA GITGVSHRTRLAFY
6910	20811	A	6965	393	43	VSPFPLKNFYFSFTPKTFVGGGPGSGPP PQKRFFHTNSPFFPPPPF/YKSGPRP GFFFTPPPEKGKNFF\PLRLGPPPVFF TRPPPPPPFFFFFERQRTCSFLHFLVVR PLFRFYL
6911	20812	A	6966	225	2	TRVECHGVFFGSCNPLLPGLKEFSAPAP RGSGNSGPPFPPR/RNSFFFFSVVLL MGFHHGQADLEILTSSDPP
6912	20813	A	6967	8	341	FVSVPILHYLFKIFFFFLRRSLCLPPR LECRGTISAHGSLGLPGSSDSPS/STKN TKLPLRGGTCGLPQLGLLRHEKTWTLG GGSGSYPKSGKRAMALQGGVQNKTCVPH
6913	20814	A	6968	29	362	DYTCKHPSSELKKKKKKKKKKKKKKK KKKGGPPKKKP/HGGPQFPGRQKKIF PFGGFKKPPRGFEKNPFFGGGNLGGP PPPKNKPGEKKNFLGGRGQKNSFLSAW
6914	20815	A	6969	391	17	VFFFFLKKFFPPDPKKLFFPPFLKIF F/SPNPFFFLGGFSQISPPPKGFFPK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IPPGV/YFSPPPFKKNFFPPPLNFGDP RVFFKGGPPPPPPPPPPPPPPPPPP RGNAGDCNGYGDVSYK
6915	20816	A	6970	374	268	IMLPRLVLNSWPQVILLWP/PKVFRLQ VRAPVPG
6916	20817	A	6971	614	315	FFFGDALSPGLECGGAVLARLQA/CLLG SHRSPASASRVAGTCKRPPPRPSGFFVF LVEAGLHRVGDGLNLL/NLVIRPSRPP IVLGQGMSSHARLFYFL
6917	20818	A	6972	861	528	FETESRSVTQAVVQWCNLSLQ/P/PPG FKRFFCLSLPSSWDYRRTPPCANFCIF SRDGVLPWWPGWSRTSDLVIRLPRPPQC WDYKREPLRLAKSRHPWNHLPQEVKHF K
6918	20819	A	6973	274	119	PPN\FVFLVETGFLQGGVKLSTPGDPPP PASRRAGITGVSHPACPGKEYIFKN
6919	20820	A	6974	370	194	KITNFAKLFYILPYSHYFWCLEKNRNR /SLTLLPRLVSNWSAQAFLLWPVKVLR LQA
6920	20821	A	6975	2	239	ARGPCSSI/SDCCASGEQSVGVGPAEP G/MGYNLLACCLLRPLEKCSIKAGVSRF SWYSLSRLELT/RKGNPPTPCISQVR
6921	20822	A	6976	361	270	PQWLVPVIPA/LLETEVGGSLERSSRP AWAR
6922	20823	A	6977	363	48	GPPKEMCPYPN\PRPYECNLFGRVFPAD VIKFKILRW/IILDYTDQDPKSNDECPY KKQKRRGHRQIKRSQADQGGRDWSGAT ARNAKMITSVGEDVRKRKPLAYC
6923	20824	A	6978	9	163	AGYNFLVCC/LPRLLEKCSIRMGVSRFS RYHLSWLPFARKGNSPTCTSWVR
6924	20825	A	6979	408	212	IETGFCHVAQDG/LELLASDDPPASASQ SAETIDVSHRAQPHSAFLPWFSKIFAY GSVWLVPFHS
6925	20826	A	6980	395	254	LIFVPLVETRFHRVQAGLELLTSSDLF SLASG/ITGVSHSRPSSAF
6926	20827	A	6981	408	2	KVSFFFFPKGPRGKKNGAGGSPFFPPF LGGGTKNFFYPPIFSQGGKK/QKPPPP EKKKNPPNPAFWGPPLVLKNWGGP LDPKVSNFMGAPPFLFGAKKKTFFSPP PKKKKPQKKGGGRSRRTSRTRG
6927	20828	A	6982	2	302	RKHLPPH\PVIFVLEQATLRHVQAGL ELLTSSDHRASASQSAGITGVSHCSLPA TSFSTPPFSVAKMLRGTKMKVPLIGPL PQIRLVAGHYFIYIT
6928	20829	A	6983	2	375	RGRVGGPVGGPVGRITFIFFQAGSDSARI LVLPFYCTLPHPLPGLFFFFFTGIKSW VLNPSRFRVIFLEKKIFLPQPPFF/HI LSPFHPGGAGGNPTARKIKGLSYRDPK EGHKRGVVAHTTP
6929	20830	A	6984	1	146	PRANFC/DPLVETRFHRHAGQAGLKLST SSDLPTLVQSAGTTGMSHRA
6930	20831	A	6985	2	95	LTMLPRLCNDTIPAHCSINS/SGSSHS LTSTSKVAGTTGVHHHFWLWF/PLFIQ
6931	20832	A	6986	340	169	VCSSGLSSPLLEQHKTNLIFYASGDICT /ANGKSGFNQPPFLKTFCTHRIMCT YL
6932	20833	A	6987	346	218	PCLTNF/SIFCRDE/SLTML/PRLVLNS WAQAILLPRPPRLRLQA

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6933	20834	A	6988	345	141	NRPKCPMTIEWIKMWHIDTMEYYAAIK KDKFMSF\ETITLGEVTQEWKTKHRLLS LIRGS
6934	20835	A	6989	154	236	ELISFSRSVERCISSEFIKVLVETDLFT LSLSPFFSVLFFFC/RRWGFTMLPTLV NSWPQVILLPWLKVLRLPT
6935	20836	A	6990	2	156	FLVE/TGFVHVGVQGLELLTSGDLPASA SQSVGIIGVSHRVRPCFLFVCICLV
6936	20837	A	6991	310	96	KNFFFLVKKSP/LNVAQGGKLKLGSDND PPASVSQSGGITGVSPRARPLNFYKEAT DPNTSVLKGLNKKKK
6937	20838	A	6992	15	279	NLLCFPSISPLIGIFFFERGFHHVGOA GLKLLTSGD/LRASPSQARITAMTRHP HPLVCGLLNSTHCDWRGRIPHWFDLRF REGPS
6938	20839	A	6993	127	352	KLADTPQSRFVLVCV/LIETKYLCCPG GLQLLASSNPPTSVSQSATITDVNHAE SQVFLNLVVPKSSKPTNTGL
6939	20840	A	6994	323	119	SSSEDHKHVPPHSAMFCFF/CLRQSLTM LPRLVLNSWAQVILPPSPKPLDALKK KSSKWMSSLLIT
6940	20841	A	6995	230	1	FFFETESCSVTQAGVQWCDLGLSLOPLFP GFKQFSCLS/LPNSWDYRHALPCPANFC IFSRDGVSPGWSGWSRIIDL
6941	20842	A	6996	346	121	RDICTPMFVTALLIAKIRSPHKCPSVDT WIRKMW\IYTMEYYKAIKNKILGMSH HASLPVFNHMKLKYLS
6942	20843	A	6997	2	198	SNNTVVAFREPGITGMCHHAQLIVLLYM QFHHVDQDGLDVR/NLVICPPWPKKLG IQALNQSPDI
6943	20844	A	6998	183	31	MRHLKSSQIQQGTGVGHACNPSTLGDHGE RITQGGFEKT\GNIVRPCLYKD
6944	20845	A	6999	3	471	LALSCSGTILAHCNLHLLGPSLPPTSAP RAAGTTGVHHHAWLIFVFFGKDGVAQPG LKLSFK/VIRPPQLPKVLGLOA
6945	20846	A	7000	483	239	GNNILFLFLFFIETGSHFVT\RLCQW VQSSAHSQPSAPRAQVLIFFVLLQTGFH YVG\QAGLQLLTSSDPPHSALLKVRD
6946	20847	A	7001	132	353	YAKLGTRGFARGPVVPGGFLTAVVWMSF AQAGINPFCIFSNRELRCFSTTL/PL LQKIQVTKGTLLCYMREHL
6947	20848	A	7002	2	399	EDAQVELQEGKVHSESDKAITPHSQBE FQKQERESAE\SELTES
6948	20849	A	7003	2	135	IFQFLVMGFHHVGOAGLELL/NLMIHP PRPSKVLGLQAYWHSTRP
6949	20850	A	7004	2	114	IFQFLVMGFHHVGOAGLELL/NLMIHP PRPSKVLGLQA
6950	20851	A	7005	455	1	ALFFAWLWLPSSSKGGLKLSHGTTTLTF LLPSSTLKDLPQEQWL/GTCNSQHFG PRKADRLAPGVQNRPGORGETPSRKGG EGNWGGGELHIYTYTHTYVHTYIHA NWTWVCVPVLAFAQETEVEGGPLEPEVAP AWTVRRCPLKKK
6951	20852	A	7006	371	172	QVILCLSLPGSWDHRHTPPHPA/NFLVE TRFQHVDELLASNDPPASASQSVGITG VSHCARPCYDL
6952	20853	A	7007	486	252	PQTVFFFFFFFQALFSTFYILHVF FFFFFFFPKQFFFP/LSLIKQKQFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFFFCYLCNSLFIVVTQYFFVNE
6953	20854	A	7008	1	113	KNFCR/DRSLDTLPRLISNSWPQVTLTP QPPKVLGLQA
6954	20855	A	7009	105	383	SLHRPAHPGLLKFGKKAHSFIHLCDK GDLAAILPRLVSNWPQVILLPWST/NVL RLQA
6955	20856	A	7010	609	348	ESHSVTQAGVQWYDLSLQPLPPGS\SD SPASASHVAGITGMRHHTQL\IFVLLVE TRSHHVSQTKFVLFDTTKFVVIIFYSGKR TRIEL
6956	20857	A	7011	382	233	DLEIFRGKTFLLHHIFPPFFFFFC/RRRG LAMLPKLVLSNPQVILPKCWD
6957	20858	A	7012	359	199	DLLPSLPPLPSFL\FFLPETESHSSPR LECSGAI PAHCSLGDRAHRLKINK
6958	20859	A	7014	3	274	CFFFFFETGSHSVTQAGVQWRHLSLQPPPGCKRFSCLS/LPSSNDYRHV/PSSP LLVRNSSICLLSCFEMTPELFDGVLAIY CCVTNDLKA
6959	20860	A	7015	372	54	LPSAWEAEMRGPLEPKGLRSQRAETAP\CTPAWVTEQAYVSNKINTERPPQKIEHV EGLSCTTQKPFSSND
6960	20861	A	7016	548	158	KFDT/GATLFDGPAVFDPA/DFFSVAV YLTGAEYTGELSDTWQAEHLIEVFLP AQVPDSELDAMESRIYVMSDIPALSD LITSMVASGYDYRRDDAGLWSSADLTY VITYEM
6961	20862	A	7018	396	34	QKNEIKPTMQLHLTPARMAI IKKILKNG GWHGCGE/METLLHCWQCKLVQPLWKT MWRELKEPKVELPFDPAIPVLGIQQSQH WESSNPSTGDPALPPLGIQQSQPRRKVI KCRYLHTRL
6962	20863	A	7020	2	241	FPGPTAARRRQKEDRYEYDKVLSDKLK EABTRAEFAERSLTRLEKSIDDLQDEL\YAHKLKYQAISEELDHALNDMTSI
6963	20864	A	7021	347	3	NDLKSLSLTHSVAQARVQWQ\NISSLQRP PPQKRFSCFSLPSSWDYSLNCKFYHLH FADEIEITLTSQRAQLECKSNMYKDIHN TVRSYKLYKVPQKLESRNRKTSSTRE VRS
6964	20865	A	7022	2	160	LRDDRRGRGFHFGQAGLELLTSSD/L PTSASQSAGITGVTHRAPDWSFCQF
6965	20866	A	7023	3	248	DRVSSVAQSSLELLSSSNPHLGFPKCWD YRNPPLPFSSRSLFLPSFLIFCRDRV SMLEKLASSFW\VRPPWPSKVLGLQA
6966	20867	A	7024	483	143	PLNPLKFFFFPKAFKFWGGVGPICSPPK RRVLSSQKSVGFYFPQKEKGYTFPSPG KFGPPKEILKRAPPFFFFFFFLRRDK/SLTMLPGLVLNPWPQAVLPLQPPKALGL QA
6967	20868	A	7025	414	81	PHPLKFFFFPETFYFWGVFSPFSPFGR KVPPQKSPGGFLAPPKGKSPFPKCFK IGPPRGIFKRAPPYFFFFFFFNRRDK/SLTMLPGLVLNPWPQAVLPLQPPKALGLQ A
6968	20869	A	7026	16	218	KFAPRCRNSARENTQNQPRKHSPTPLK K/HKINNKNKLAGRGTHLWSQLLGRLRW EDHLSPRQSRLQ
6969	20870	A	7027	28	272	EFVGVGPSEPGAGYNLL\CAFLSPSEKC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SIRVGVTFRSRCHLSPLTLTKKGNLTPCASVRVQCCTLLRLAHGALHPLSSTP
6970	20871	A	7028	277	480	LGIFHMLSDSFLLLLFCLFVFKIFFGI FCRD\RSCEVWAMPLRVLNSWAQVIL PPWPLKVLGLQA
6971	20872	A	7029	24	153	SVVWNSP/RSSGEFRKTVGHDADFRAHI IDMLAKASKIEVYRGN
6972	20873	A	7030	2	470	IETPRPLWHSAYRGRQASLSCGGLHPV R/ASWLLCLPNQAWAMAGAPPPASLLPC SLISDCCASNQRDSVGVGPSEPGVGYNL LVRRFLSQSEKRNIRVGVTFRSCV/LL PLSLTRKGNLTPWASQVWQCLALLRFA HGARTHWPAPTVMHSLVR
6973	20874	A	7031	487	107	SPPAPGVADPPPPTRVFSKKKKKFFFF FLKKIFFFKPGGDPGGIFFPGGPPPGP KKFSPPLFPKGGYRVFPFPGKISIFF FFFFFFFF/CRDR/SLAMLPRLVLNF WAQVILLPWSPKVLGLQA
6974	20875	A	7032	576	36	GYTSQMGRPGRGAPHPFDRAAGQRRSSL PRWGGWAEALLTSQMGRPGRGAPHIPD DGQPRGAPHLPDDEQLGRGAPHLPDDE RPRGAPHPFDGAAGQRCASHPTRGGRA EVLPTSQTQPPRGAPHLPDGGRPRGT PHLPDG/GPRGAPHIPDGAARQRHLS PRRGNCTTRIVDQ
6975	20876	A	7033	2	129	YGPTHASGAMLRSCAARLRTLGALCLPP VGRRLP/EASRDPS
6976	20877	A	7034	1	287	RLSLALVARDGVQWCDLGSPPPTGPK RFSCLSLPSSWDYRHVSRRPANFVFLVD TGFLHFGQAGLELPTSGDPPALASQSAG I\TGVSHRAWPK
6977	20878	A	7035	3	315	HASAHASALFYFIFFEETRSRVQAQEVQ WRKLGSLQPPRFKQFSLSHPYRHAPH FANLVFLVETGFA/HVQAGLELPTSSN LASQSGGITGVSRARPGINF
6978	20879	A	7036	430	304	VIFYLIFFCKDGV/LTMLPRLVLNSWLH AILEPPQPPKVLGLQA
6979	20880	A	7037	3	256	FFFFNRQKDLFGNFQTCQKWHSPSPRPT /APHQAPKNTSPPSLPITLTLASTCTY PIPQAMLENWSVPSPAQAAGEAALWHP R
6980	20881	A	7038	13	481	FARLHEFGTSRVIIYLLARLVSNWPQVI CLFWPPKL/LGLQA
6981	20882	A	7039	455	255	SCLSLPSSWDYRRAPRHPANF\FLVET GFRHVALAGLKYPPALASQNAGITGVSH HARPEQFILTN
6982	20883	A	7040	490	172	KCWQG/C/GETGLVHC/WIGNCTMMR PQWQAWQVFKLHRELPSDPAMPLGV QPGGLKIDTQT/RMYMALLTVKRWKQP ECPPVDK/LDKLWYIHTTEYRVTIKK
6983	20884	A	7041	438	37	IFPNLPPKLHYFPQFSPEKLPKPLLIK MAKRQSQGVFETPKK/SRAGPPPKFT TGFSABKNGGPKGGYISQVQKKKNNC HSRILHSAKLSFKNRSEIKTFLNKQKLK /DFTASRALQKILQEAFFHRTD
6984	20885	A	7042	292	463	IEAISFLPFFFGDSLTAQWRDLGSLQF LPPGLKRFSCSLSPSELPC/CSGRQCS
6985	20886	A	7043	59	257	LASLVSSQSWMKMWWIYTMKYAATK\G

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NEIMSSAGTWMKLEATILSKVTQEQRTK HHMLSLRSGS
6986	20887	A	7044	279	14	RTADTEIGRGSSLCWRVGLQIQVSKSH NFFPETGSHSATQYGVQWHNLGSPQPQT YGLQSSSHCGLPKCWDYRE/LPPSMECS GTISAHLCLKMGSSNPLTVASQSAGIT GNSSRLHDINYGLQ
6987	20888	A	7045	578	253	AAASTFSCFFVFPFETEPNSVA/RLECSG ATSAHKLCLPGSSNSPVSAPQVAGITD AHNHIQLIFVLVETGFHHVQAGLELQ/ NLVISLPPWPKVLGLQAWSHHAQPFV
6988	20889	A	7046	3	229	FFKTGSLSVSOAGVQW/PNLSSLQLPP RFKQFSCLSFPSSWDYRHPPHPANFCS FSRDRVPPCWSGWSQTPDLR
6989	20890	A	7047	367	151	LSLLSSWHYGHVPTSPANFFYY/CVDTG PRCVSNSTQAVCLPQLPRVLGLQA
6990	20891	A	7048	370	141	CQPPHPANFCIFVEIVFCHVGQTGFKLL TSNDLPANASQSAGIWD/TGVSHHAWPS RFNSEVQFDYVSNKNVDFSL
6991	20892	A	7049	104	361	VTAPGLEAAFKERVWPGAVARTCGPSTL GGRGRRI/RGQBIKTILANTLKPCLY
6992	20893	A	7050	2	325	RFSCLSLPSSWDYRHEPPRLAIFFFFF GIIRKGGFTH/VGRGGFKPWTSGNMPAL PSQGVGFPLGFSPPRPVRGFFYPPLPKWG GLFLQNGVKFKKGGSGDLFKMEKK
6993	20894	A	7051	14	208	AHEILSEIENPLEPGWDHRCVSSCPAHF FVF/CYRDGGLPMLPKRVLNSWAQAILP WAPKVLGLQV
6994	20895	A	7052	103	368	GNRVHTYMLTALFMTAKKWNKPKC/PVS DEQIRQINSVHAMEYYSAIKRNEALICV TTWVNLNIMLSESSQKTMGCMRLRSIY MKGPE
6995	20896	A	7053	421	2	LFLPPEVARGFPKGRGRASPSGGFFFG PRGGPIFPPP/SFFPTRPWSKGEVFPSP TPGKGFRRGFFFFPPPKGGGVPLFFKK YLGEGAPQNKGGPVFLWPPHSGGPPGP PKNFFFFFFFETESCYVYPGCSAVVQS Q
6996	20897	A	7054	489	40	IPEAPGGPGFKREDSPGANKSGPKALYP PKTFHPPWEGRFRSFQKGAPPPVFFFP FFPLPFFFLRQSHSIPQAGVQWRDLGSL QPPPPPGFKQFSCVSLPCFP/RQMGFRH VGQAGLELLTSGHPPDSASQSTGITGVS HCAEFHRTD
6997	20898	A	7055	3	261	TGSGSVTQAEVQAEVMAHCSLNLGSSD LSALASRAAGAAGTCHHAWLIIFVFFIEM GFHYVPR/LGLELWARVIHPPQPPRVLG LQV
6998	20899	A	7056	1198	1040	FLWKIALLFYFKLPQSLQPLVATTLS QQPSTSRQDPLPAKRL/RLAEGSDDR
6999	20900	A	7057	271	33	LFFFFKMESRSVARLECSGAILAQCNLA RLFLVE/QGFHHVGQDGLGLLIHPPWPP EVLGLQAQATPPSPKITIYAATVM
7000	20901	A	7058	2	194	CYRRQPPHLMNPFYLLNFFCLFFC/KA LSLLARLLNSQLQASLPQPPKVLGLQ ACGTTPCP
7001	20902	A	7059	3	272	NMWKLNILLNNQWVNGEIKMKIFKNCK E/NGNTTYQNLRAAEFLKGFIAVNT

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						YIKKDYRKTCRLPYSYHFFNKEKEYTLKIMIKV
7002	20903	A	7060	397	129	FWGPHKKNFPLPARGRKLSGFKTA/LPL FFFFFSFSLSLFFFSGSCSV8\RLKCSG TITAYCSLEFLGSSNPASFSQAAGTTF TFFLFIG
7003	20904	A	7061	3	351	SCFRLCLPKAWAMAGAPPASLPCCS LISDCCASNQCDS/VGVGPSEPGAGYNL VVRFLSGSEKRNIRVGVTFRSRRPSP LSLTRKGNLTPCASSQVRQCLALLRLAH GARTH
7004	20905	A	7062	60	324	DDFVSVVQTVHWCGRGSLKPQPPRLSS TSRLSSPSSWDYGRVPF\NIFCRDRVSL CFPGWPRTPDLRGSSCPSPKVVKLHTRV TAPGQ
7005	20906	A	7063	481	160	RPGAPG/PDDFARMGPRPKGAFTLVHP MPSGAAPPGLLSEP\PHRGPRSFARSP TLRYPGRAPSKGSGEDPARPPATGPGPN LIQDGLVMSLTENVC
7006	20907	A	7064	65	481	CLCPAPRGAYRGRQASLSCGGLHPVRA SRLCLPKQAWAMAGAPPASLPCCSLI SDCCASNQSDSVGVGPSEPGVGYSLVVR RFLSRSEKRNIRVGVTFRSRCV/LSPLS LTRKGNCLTPCASQVRQCLALLRLAHGA
7007	20908	A	7065	392	183	GGLKP/IPGNPGNSLFSQKKKQPGAGG SPRGSPPPGGLGGGIFFGPKGLGSINPN FGPAPPFGGQKKKSLF
7008	20909	A	7066	538	248	FFLKQSCSVAQAGVHWGYLSSLQTLHPR F\KFSCHSLSSWDYRCAPPRLAN\FVL LAEMGFHFFHIAQAGLEPTSNDLPTSA SQNAGITGVSHHT
7009	20910	A	7067	2	127	VTGQAVVHACSPGTLGARAG/WIVWAQQ FRTSLGIMVRPCLYL
7010	20911	A	7068	379	217	KKMFCKNE/SFTIFPRLVLNSWAQTILP PWPPKVLGLQVQTTVPGSYSPLSLYKE
7011	20912	A	7069	386	176	KRDVKDKLKKMWCIHIMYYLAIKKET LPFATWVNLQ\TFILSEISQEQDKYHMI SLICGIKMLIYRIE
7012	20913	A	7070	30	408	NSELGSGVGPTPEPGTGGNLLVCWLLR LWEKCSVWAGVSRFFQ/CTDYDGFPPWG KGNPPTPCASQVRRHPALLRRTLHGLHP CASHEKNQVQLEMOKSSVFCIDLTGSC RVELFPFGHLGSKNP
7013	20914	A	7071	310	414	HVPWRSFAPAHCNLGSLOPPPPGFKRFS CLSLPSSWDYRCPPRLAN\FCSGSLQS WLTATSASWVQAILLSQPPR
7014	20915	A	7072	353	243	IFIFCRV/RGLTILSRLVWNFWDQVILL PEPKVLGLQV
7015	20916	A	7073	1	276	ELWDFKEFNITLYLSKERKEVCERGR RDNRKLTLEDIMAKNFSNWKIINPQIQE AQQTPN\QETGRKLALRHITIKLLKTND KKKILKAV
7016	20917	A	7074	362	133	GGGGGGGRYSPQKKGTLPLTPPSNWGPK GAPPFRGNFFFFFFFFS\RDGCLAMLRL VLDSWAQVMLLPQPLKVLKL
7017	20918	A	7075	3	177	KWSPHSLPNN\WLYRHMPPCPANVEFF CSLAVLPRMVSNSWPGAILSPWPTRMLG LQT

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7018	20919	A	7076	1	169	PQLPSSRNRYRHVPFCWANFCIFS/RRRCFTMLARLFLNSWPQVTRPHWPPKVLGLQA
7019	20920	A	7077	402	231	PSCLSLRSSWDYRCMPPHLTNYYYYYYYYFVEMGSHSVTRPQDILPPWP\PKVLGLQV
7020	20921	A	7078	422	316	FCRDK/SLPMLPKLILNSWVQTTHLPQPKVLGLQA
7021	20922	A	7079	58	293	DPICTKSKKLKKTQ\TDKEDITTKKAKKAKSKIKIEEDGEEGKVVVVEEVSVKKKDKKKKPWLGMAHTCNENTLGG
7022	20923	A	7080	363	123	GVFFRDHARAFSLHTGCAVHISRCF/HVLTHFKEFLPHWFLTIIHTHTHTHTHTHTPSFPELGKAVPMHRIVIVPTNYQH
7023	20924	A	7081	3	181	YFLL\FFWDRVLPCHPGWSKGWSQTGGLGQSAHLSLPKHWVCRREPPHPALFLLEKNTIS
7024	20925	A	7082	453	142	FFXXFFXXXXXFFFFFFFFFPFFFFFFF FFFLKNSFFYFFLFFFFYPFLPLPLFFF FPPNFFFFFFLFS*NNFFFFFFPPLFFP FFFLPFFFFFFFPPFFP8F
7025	20926	A	7083	268	92	KNNLPSSWG\YKCSPPHKGNRFFFYIKDGGGLIMLLRLISNSWAQVILLSWPSKVLERQA
7026	20927	A	7084	413	0	SCSVAQDGVQWDDLGSLLQLLPKNKPPFCLSSTPAA\FPSDWDYR
7027	20928	A	7085	400	125	KTRSFVSVRGGVQL/CI/GSLKPRTEGVKSSSPSASPVRNTGMCPPPPQIFFFLVETGSHYAAQASLKQSSCLGFLILFLSQPLGEKEGPTICT
7028	20929	A	7086	377	38	NPGGPFYFWGPKKKIKPFPFPGVKLVSKRAPPFFF/CFFETGSPFVAQTSLELLDSHNPPTSASQSAGITDMSHARPMSICMIQLWKS YHRFHFISQGSRDCSSSRRET
7029	20930	A	7087	1	151	SFCRD/KRLIMLPRLVLNSQAQVMLLPQPPKVLSSHHTWPIIKFSFMHFNLF
7030	20931	A	7088	405	111	PRLVLN\SELRRSAHLSLPKCWDYGPFP PCPAQMHVLKSGTAAHKVHDFLASWSHL PTHSPFPVLCSTQISVAFPIQNLRAQQRSGQRHFGKQCQSIH
7031	20932	A	7089	1	309	KQINKSSLRISGKPPNCEVLHLGKSVN KSLLPEPHKLASDP/HLCDFLESS\EQVK SVKELNCHV\TSLYTLGALES DMAEYF\N KTYTLGPGMLAHAYNSSILGG
7032	20933	A	7090	414	240	FSLF/CKNLKGLTMLPKLVSNFWPQAILLPQPPKVLGL
7033	20934	A	7091	460	328	RHPPPYLGK/FFCRDR/SLTMLPRLVSN SWPQVILSPWPPKVLVL
7034	20935	A	7092	388	199	KQFSCSLSPSRWDY/SALPPRAHFCIF NRDGFSPYWSGWSLGLPKCSDYRRRIFL RAKAHVRE
7035	20936	A	7093	18	271	MHSFATYLLVNLHLLVLCRLCPLSMYSG EKSYILLTKRPMWLF/SSGFPFNSWSPSS ITLRIFLTCLTLKLSCCSCCCCCYCCCC C
7036	20937	A	7094	415	291	GDLGSPQAPPPG\SRHSPASASRIDGTT GARHIMNFKNLAIK

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7037	20938	A	7095	21	428	DKGLTVTQARVQW/HDPSSRQPPSPGLK RFFRLSLPSNWDHRCAPPRVANYFFFYR WGSYHVAQAGLELLASNTPTSASHSAG ITALFLRDTLVRFMGSFCFPQSGAAF TAQIPQRGRTEELFIFLFLNDYLF
7038	20939	A	7096	320	134	LPL\PKTTFYLFNLRDRVLLCCPGWSR\ ILSSKQSTLLGLPKCWDHRHEPPQOAVD HTLDFS
7039	20940	A	7097	402	221	DYRHVPPFPANF/LVEMGFVHVSQAGLE LLGSSDPNTSQSAGITETSHQAQAYTF IFIY
7040	20941	A	7098	427	259	PPPRFKRFSGLSLRRWDYRPPPCPGN FFFFF\CIFVQMGFHLVGQAKMLKLHD
7041	20942	A	7099	422	275	VQWYNLDSLQPASSGFKRFSHLRLSTW DYRH\PRPANFCIFSNTKDTFI
7042	20943	A	7100	3	404	HASGATWRNPVSTRVWHIPIVPATQEG EMGGSLEPRK/LKAAVSHCTPVWVT
7043	20944	A	7101	539	336	FETESRSFTEAGVQWRDGLSLQPPPGF KR/DSPALASRVTTGTTGAHHAGLIFVF LVRAGVSPHWPGWS
7044	20945	A	7102	408	287	WLILFFIFCRD/RGLTMLPTLVNSWAQ AILLPQPPKVLGL
7045	20946	A	7103	1074	705	SFLRWSFTLVAQAGVRWRGLGSLQPLP WFKQFSCSLLSWD\YGRPPRLANYF F\VILVETGFHRYWPRMVSNSQPQ/CDL PAVGRPNASAGI\TGVSHCAWPKMFLNNC TCTHSPYLQGVISLG
7046	20947	A	7104	227	55	FSQHKINIQFYISLSPHTITMSFPLCRD /RGLAMLHRL/VLNSWPHVILPWPPKV LRL
7047	20948	A	7105	479	314	PRLLIFFFFIERGL/LCSPGWSQTFGLQ ESSCFGLPKSWGPRKEPQPCALKLTLQ
7048	20949	A	7106	37	143	NSFF/CKRRGLTMLSRVSNWPKVILT PQPPKLEL
7049	20950	A	7107	441	106	GAPSPASLPPCSLISDCCASNQDSVGV GPSEPGVGYSLVRRFLSRSEKRNIRVG VTRFSRCV/LSPLSLTRKNSLTPCASQ VRQCLALLRLAHGAHTHPAPTVMHSLV R
7050	20951	A	7108	413	207	CCIQAGPAFFGGPPPPRWGCGVPPPGY /MPSPPVFRVGLLVFRGPPPNWFLPMGL QPDGPGLDPKKFAK
7051	20952	A	7109	92	409	PHLPDGAAGQRCPPPGRGCCVRAGPQL PPGRGGWPGGLPPPSRTGWLPGGGAP HFSDGAVARQRVSSLLRRGGRAETLLTS QTGSRPGRGTPHISDDGRFGRD
7052	20953	A	7110	408	13	PPWGPFGGPPPEAGSNPPGPPWGTPLS PKKPKNYSQGGGFLNPPPPG/SGPGI PFSPEGKGS LNPGGQKKGIGAPSPPPG PKKPPSQKKKKGKEKVKIGESSQI LLFKVSKILSVNLFHLSSLI
7053	20954	A	7111	290	175	LKKNCR/DRSHTMLPRLVLNSWPQTILP SQPKVLGLQI
7054	20955	A	7112	1136	552	ILFKEMGCEAGQRCSPVITITLGRPRR ADHLRCGVDRDQPGTTLKPRLYSNTKIS WAWWRVPA\IPA\IRRPEATRTFNPRR WRLFLNLRSHPLHSHPGRQSKIPIKKER KKGQDRKGKGCQNWGQKQRRKEGKKE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						MGMGRIGGKKNKKEGRKERKEGRKEGNKW VWAE LGAFPEQGGKGLRRGPFSEEAVGVSP L
7055	20956	A	7113	570	199	LCLLKQAWLMAGAPPPASLPCCGLISDC CASNQDQSVGVGPSEPGVYSLVVRRL SRSDKRNIRVGVTFRSVCV/LSPLSLTR KENSILTPCASQVRQCLALLRLVHGAHT WPAPT VWHS LMR
7056	20957	A	7114	466	284	RTRGIGWTANRRMKATQPGLTFFHLIHK QEGGNVGSQKGQRD\VTNSAPHWRLHDQ TANCL
7057	20958	A	7115	474	224	DSNFEKSSTLGKMLSNSIKCYREIFCER KSQMQQTSM\FKKL PQSPQPSAITTL ISQLPPTSRQNP PPAK\RLQLAEGSDGC
7058	20959	A	7116	377	111	FXKNFXSFLFFSLTRKNWVAHITFFF FFFLPTPPFFYFIPLLIFCFFFLFYIF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFL
7059	20960	A	7117	417	148	VPPCLANF\NFFVETGSPYVAQAGLELL GSSHPPTLASQSSQITRVSHCSLLYFLM HSNTSISFFSFWALVSFLEMPSSCQDGI TVLAR
7060	20961	A	7118	2	196	RVPPPCPA\NFVFFVQTAFCHVAQAGPK LLASNPPASASQSARIAVLSCYCLPSL RLRSHLDFF
7061	20962	A	7119	2	417	EAGGSLEPRNRLHCA/LVAPMNSRCIP AWAT
7062	20963	A	7120	801	450	GPKFLGPPGVRRIN/RRPGGGGLPRVYK NNYPEDRPVLPAPFFSGGGR/GPGPHDK HPLPRKKQKNSPGRGGEPFFPPPGFPP GGERKNPLTPQRKRVHWGGLAPFPFPPS LSAKEPLF
7063	20964	A	7121	3	199	DANGFALVVQAGVQCCDLSSLOQSP/RL ANFVFLAETGFLHVGQAGLKLITSGNLP ALTSQRLRLQ
7064	20965	A	7122	407	164	NVAGLTGAYLDSFFGRDRV/LTMLRLV LNSWAQAILPPWPKVMGLQACTIEVSS LVAQIASKRLSGVQESDEAAWIRDC
7065	20966	A	7123	33	192	RWDFTMLPRLVLGSKRSAHLGLPKCWDY KHBP/PCCPGWSWAQRDLPTLASQSAGI TSMHLHQAIPKFLFQFIRFSILVF
7066	20967	A	7124	3	399	SIPVDWPSRAPTPRGRESAAHQGN/YPV GQRN/RMAGLSRPSFCWREVSFSR/SHS C/ICWVQLGKSAVL PQSRGPGAHEGSR RRGGSSPPCPPLQTQLVFSPQELSMSAP IHRLSVTLQGDICISTGGAPFRCLA
7067	20968	A	7125	1901	1574	FFEMESCSVAQAGVQWHDGSLQPLPPG FKQFSCLSLPSSWDYRHLPPHRANFFV LVETGLHHVGQ\SGLELLTLGD/LLPAS ASQSAGITGVSHHAWAKNPCFLTSTDT
7068	20969	A	7126	408	234	LPSSWDYRSPPPQANFYIFSRD/MGFTM LARLLTSSDPPALASQSARIAGVSHHAQ PVYF
7069	20970	A	7127	88	277	KLSTEYKKQRPEDSFFFL/VEIGFRYV AQAGLELLSSDPPTLASQSAGITGVSH HIQPFKK
7070	20971	A	7128	3	140	QRWCVPATRKAEAGESLETSSRLQGA MITP\CSPA WATEQDLAS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
7071	20972	A	7129	1	212	PLLFSVSPILLSVSPPLLPFP/EPAASPP PSTHSLPSVQSESIGQFLHPPDPPLA FPAPLKHQDLHISHL
7072	20973	A	7130	361	3	RNNISQDIIVIGNDSSNRSGSKLKIFW KGFTILHAIKDFCDS/WEEVKISRLPGV WKKLIPITLMDDF/EGFKTSVEEVADMV ETETELERLELVKPEYGTGLQSRDKT LTDEKLLIMD
7073	20974	A	7131	421	201	NFCILVD/TGFHHVGVQSLELLTPSNPP ASASQSSGITGLSDHSQKSELVLSFNF FALFHILLCVMLAIDRND
7074	20975	A	7132	221	529	LIKFTIHSFYFIYLFIFPSGDGCFALSP RLESSGVISAHCNIRLPGSSDSPDSASS VAGII/CMRHHTQLILY/CLVET/EFHH VGQGGVDLLTSGDPPASASQSV
7075	20976	A	7133	1	227	KGIHFSSANDVKKKTVLTWLNQDPQLF RDGLDGWYHRLQKCL\ELDEVYVEK
7076	20977	A	7134	1242	300	DFVLPDGRVIP\KGIVCLINIIIG\THYN PN\LWPTPLEVYDPPFRNP\ENIKERSP LAFIPFSAGPRNCIGQAFAMAEMKVLA LTLHFRILPTHTEPRRKPELILRAEGG LWLRVEPLAGTSRGNPRASSRPSLSDPW VLRRLPPPIFLFLLLLTPLLFVSMAR EPPSLRVEAPGPPEMRTPPAIEATPKG TLQPAQRRLRFLSGCVPILHGVAGHRYG KDKMGIHQHPDGTVLKQLQPPRGPREL EFYNMYYAADCTDGVLLRLQYLPKYG IWPPPAAPNDLYLKLENVTHKFNKPCIM DVKIGQKKL
7077	20978	A	7135	1	259	GTSCILASMLTRHRLRFSP/CLFETFC SVAQSGVQWYDHSSLPQPPGLKLFSPV NFPSSWDYRHMPPCLASASILKLEFTID LGFYS
7078	20979	A	7136	1132	900	CSGVISAHCKPRLPGSRHSPASASRVAG TTGTRHARLNFCIFFLVEMGFHRVSQD GLHLL/NLVVCPPRPPKVLELHA
7079	20980	A	7137	1	501	FFLRWSLTVTRLECSDVISAHCNHLPG SSDSPASAFREAGT/GHDAQLIFVFLV ETG/FHHVVKDGVDDLTS
7080	20981	A	7138	2	229	WHSGLLWSQPPL\YLSLSSWDYSHVS PCPAGLCFLVETGSPYVAQAGLSLRGS ASQSTGIIGMSQPAGFWKQL
7081	20982	A	7139	255	58	IFGKGFPFPFCQNGQFGVPPPPRAFFFF FF/CPAKYYTMLPRLVVSNSWAQAIHPP WPLKVLGLQA
7082	20983	A	7140	422	274	TMLPRLVSN\GLKQSSRLSLPKWWDYR YKPPCLVYTFPINRPEVPKE
7083	20984	A	7141	417	60	VWRPLEELETLPDPAIPLLGILHKEH KLLYHKDTC\WNQPKWPSMVDWIKEMWY INTMEYYTAIKKINAIFRDPLTSPWDPF SWRKFCPLLEIWPASYFLPGINTRSLDE PLHIKGER
7084	20985	A	7142	391	70	SPPPHPPRKGDYRGGPP/RPGKKREIFF FFFFLVDTFCHVAQAGLKLLASN/LP TSASQSAGITSVRHYIQPTLLKIIPQFL DILLFLKIFHSFLKSFNGLGSFY
7085	20986	A	7143	405	304	FCRDR/SLLMLPRLDLNSWAQGIILPWP PKVLGL

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7086	20987	A	7144	3	159	HASEKIWMYTMHYA\SQKKNKIMSFV ATWMRLVNLKSLMKNECMSVNGR
7087	20988	A	7145	343	115	CEFYFLSCIYVFIYFCR/DKGLSLLLRH VSNWPQVILLPWPPKVS HQAPEFYFR NKQTKIDLSFEETAADLAYYS
7088	20989	A	7146	453	119	RCWKGCGLWISLRTT/WREWLQVPPFWK TVWRCLRLKVEPPYPATPLPGIHLKK TKAVAQRDMCTPLFIVAFQHLLKRLFF SRCVFLAPLLKIA
7089	20990	A	7147	3	105	TIEWGEVIS/SSYSSTMANNEGLFSLVA RKL SRPL
7090	20991	A	7148	295	23	FANIFSHSAETLQTRREWGPIFNIL/EK NFQPRISHPAKLSFISEGEIKSFPDKQM LRNFITTRPALQEFLLKKEFMSFPGTWMK LETIIIS
7091	20992	A	7149	1	161	RTRGFFYLDGVRSLAMLP/RLVLNSWPQ AILLPWLPKVLGSOTLAMVAAYTVFV
7092	20993	A	7150	1	219	DYRCTPPHPAHF/SIFIFCRQR/SLTMF LSLVNLSWTQAILLPWPKLLGLQACTA MPIPGVELLWVSGCFVKES
7093	20994	A	7151	177	34	ELVSFLSFLSLSFPPSFLPSFLPFLSF LPSPNPSF\LPSPFLPSFL
7094	20995	A	7152	398	40	MNDVLLFHPGWNVAQSWFTGASN\FG LKQSSHLSSLCSWNYRHTPOCPASLLAY VCMYVCMYVCMYVCRD/RGLTMLPWLVS NSRPQAILPPQPSKIMGPLLGAHAHAYN TSPKGSQRR
7095	20996	A	7153	418	179	RNSCTQMRNEALPNSGYFPKLYYYDF/ CQRQDLAILPRLVYNSWQAAILLPWPPK VLGLQHEPPCLAVIQFLKGNLKIV
7096	20997	A	7154	767	537	QALLCLPGWS\AVAQSWLTAASNSDDPP ACLPSSWDYRHVPPRQAEWSFRVSVSSP VKRDPGSPWRRMRPCSE
7097	20998	A	7155	421	301	HAQLFFCRHW/SFTMLPWLVSNSWAQAI LLPWPPKVLGLQV
7098	20999	A	7156	410	269	AGGPQTGSFFFF/CYERGVSLPRLVSD TWSHVILQPHPKVLGLQA
7099	21000	A	7157	3	237	MQIKA/TMLYHFTPTNMTVLGFKNSRG WQARGEIGTLVHCWGCIMMQLWETVW HFLKRLNLKGVVHACSPNYSGG
7100	21001	A	7158	435	211	LFLVEMG\FAVLASLVLTLE\PRDSPTS ASQARMGTGMSHHTQPLFLFVSKFHIA KKLSLIWQNLRRAGICRLS
7101	21002	A	7159	3	220	SSASQSGGITGVSHHARPSERQ/SCSV AQAVVQWCNYSSLITPTPLKRSRLSL LSSWDY\GALPHPSVAS
7102	21003	A	7160	1	172	FRKVLGRGTSGNLCTQVRVEFMDTSRS IMRNVK\SPVREGDVLTLLELELETLLR R
7103	21004	A	7161	1	180	DAAPVLKATARPTRPDRWK/IDIDSLDI HGETPSLQKNTNFRANWCIPVVPATRE ADMF
7104	21005	A	7162	3	108	KKKKTGRFKLV\MQYNRRFVNVPTEGK KKGNANS
7105	21006	A	7163	409	110	GQHGLTQSLPLSAPPRAVPRWAPRPD/ SGLSLSPLLPTAFATTGASSANRFVSG PRDGNFLNIPQSQSWFL
7106	21007	A	7164	35	371	YFHLSLLKFLFLASMMVFLTVVVRLLK

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						LLFFFLGETEPAFVAQPGR\QGPNLGSL RPHFPSVKHFPGLTPPRAGTSGLDPPSP AIFGFFKKKRGSPCGPGRWTGPRGGP P
7107	21008	A	7165	3	382	YTGPAAWMSMLVVLAEEAEVGSLEPRS SKLQ\QPPLRHCTPAWAT
7108	21009	A	7166	1	305	TAVTVDPYHSVYIEVNARPGACMNGGGL LNGEQNSLKRKQLVQTLNKRHGEELAMV DSLTLGPKLEEA/ASPPAFARVRLRARQ ACRRKGSRLCWEHLVSKV
7109	21010	A	7167	383	55	RDLMSVMRMSMLAIALCPTALMGFMNSI FYGRVVAKLPPFPLSYIQGLSHRNMMD DTTDCSFIPLYICTMSIR\QNIQKIVG LAPSRATKQAGGFLGPPPPCGKFS
7110	21011	A	7168	465	166	SPQGAQIKGVGFQKLRPWGP\PGFPRGK PFFWFKKLPPQGGGPLCSRFSGGLSQK N\SGPWGEIFPWGQNGPPSPPGKETF FSKKKKKKKAVDYLNS
7111	21012	A	7169	2	323	IQGFKTLSEEVSADEVEIVRELGLQAE EDVTLLHFNSTACCRIEHERKRQMQ QTSLVSHF\RKLLQSPQSSAIATINQSQ PSTLRQDMPATRLHLTGGLDNE
7112	21013	A	7170	3	509	FGTIPVLCADLNSLPDSGVVEYLSTGG VETNHKDFKELRYNESLTFNSCHGKNGT TNGRITHGFKLQSAYESGLMPYNTYTFD FKGIIDYIFYSKPQLNTLGILGPLDHHW LVENNISGCPHPLIPSDHFSLFAQLEL/ YTAFPPAPSRHPPSWQEVVKHLQRTALI HL
7113	21014	A	7171	1121	320	SSCFQTSSHACFVTEFVPGDPMQIHE DVFFEPQARFYVACVVLGLQFLHEKKII YRDLKLDNLLDAQGGLKIADFGLCKEG IGFGDRTSTFCGTPEFLAPEVLTQRAYT RAVDWWGLGVLLYEMLVGECPPGDTTE EVFDCIRLHGRPPTAPFLSVQG\VKFIQ KLLQKCEKPLGAGDQNAEEIKVQPPFR PTNWQALLARTIQPPFVPTLCGPADLRY FEGEFHRAA\PALTPAPHSLLTARQQA AFRDFFDVSERFLEP
7114	21015	A	7172	355	3	GPLLMLGMNIFLTLPLLLPLSMLEGG VCGNF/ITNCCLEIDDNRKVIDITAKI QKLAHVVPQIWKWSPDTLFGWFFSLG RFKTLVGIVLVILGVCLTLPCLLPLLVK NIQSANV
7115	21016	A	7173	184	2	EKKVEDDDDDDFEMESRSVIPAGVQWR NL\LHPLPSGFKPPSCLSLPRSWEHCA PLHQCI
7116	21017	A	7174	1190	407	SLKRRFSARGSRFMSMYETGSGQKPYLP MGEASRPESRMRLQPPAHIGRSALVT SSSSLPSFPSTLSWSRDESARRASRLK QNSTPESDYDNTPNDEPDGMGSSSRKGR QRMVWPVGDGLVPTAEAPHVAPSPTLPS TEDVIRKTEQITKNIQELLRAAQENKHD SYIPCSEIRIHVAVTEMAALFPKPKSDM VRTSLRLLTSSAYRLQSECKKTLPGDPL SPTDVQLVTQQ\VIPVCVRPFAKAKQL VTITTKENNN
7117	21018	A	7175	3	136	AIHLASLKVFYRYRVLSL/LKRLVNSW

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						PQVILLPWPPKVLGLQV
7118	21019	A	7176	3	316	GIVKFFFFFFLTKRRTVTQAGVEWCSLG SLQLPPPRFKQFTCLSPVSWDYRHLPI CLANFCIF\ VETGFHHVGMGLRLTSG YPPTSAPPDAEITGVIHRTQP
7119	21020	A	7177	529	217	LLPRLEYSGMVIAHCGLLQLGSSQAILG ACYCAW\HNFKAFFVETKSHYVTQAGLK LLASSNPALASQSVGITGVSHCAQATL PFKTVDKGPSFNLSFTPLL
7120	21021	A	7178	3	150	YTLCKSKKDIKSIYHIMT/HLKTHHTH THHTHTHKPSTTFSTYTFIM
7121	21022	A	7179	540	69	ACRGAVHVGQDGSALTYVEDGTACGPTM LSLDHLCLPALAFNFSTCTDSGERRCS HHGVTAWSLGWREKLTRGDRPLLTSPGP ALPIC\CSNEGKCIQPDWTGKDCSIHN PLPTSPPTGETERYKGPSGTNIIIDSLA GAVLVAIVLDETGWGYK
7122	21023	A	7180	452	279	CIDSIYQEIYHLSISILSVYLSIYRSY LSIYLPWF\SLYLGPRFLRTRDQLLS LT
7123	21024	A	7181	501	183	HVRCIAFICALIGFPGSYFSIMPVVT/V DLVGIEHLNAYGIIICVNGISALLGPP FAGWIYDITQKYDFSFYICGLLYMIGIL FLLIQPCIRIEQSRKYMGAHV
7124	21025	A	7182	446	245	LRVRSALNQVSSASRYWDTGVATKLAT F/SLFWKDRNLDILPSMVFNWQVIFP SWPPKVLGLQM
7125	21026	A	7183	420	73	DSSDDSGQSKLP/FWKGFITLDAIKNI CDSLEDFKISLTGAWNLIPLMDDYEG FKTRVEEVTADVVEIARELEVEHGLG AVAHAYNPNTLRRLSLKPRSLRPGQHSK TSL
7126	21027	A	7184	567	174	FFLRDRVPSLTQAGVQWQDHSLSQPRPP RLKQSSH\PALLSSWD\YRHRPLCLAKF LIFLQRRGLAI/FARGVVSNSWSQ/CNL PASVSPSAGITGBSHYSQFLLSDSQTK VYKTHRSTISSTITEMGCERKD
7127	21028	A	7185	345	59	RNGSSCLWQVIQSLTLLPRLECSGVTTA QCSLGLVGSSNPPTSASC\VESHCFAQD GLELMGSSNPPTLAGITGMSHCAQPLYD LFLYEYGLSVHY
7128	21029	A	7186	1	209	LSVVLEIGSHSVTQAGVQWVHSSSLQP* MLGLKPSSRFSPLPKCNDYRHEPWCLPGL LRLKFDPSVGGVA
7129	21030	A	7187	3	225	EKTPVSDRGAKGCTESLVNRRPCFSALE VDETYVP*EFNAETFTFHADICTLSDKV RHFLLKPIALVILNHHIF
7130	21031	A	7188	1	377	ES*RNHNGDEDDSHVRAQACIEAKHDK YMA DMDELFSQADDNRKRDIPDYLRGK ISFELMRQPCITPSGITYDRKDI EEHLH RVGHFDPVTRSPLTHEQLIPNLAMKEVI DAFISENGCVEDY
7131	21032	A	7189	1	359	SRATDHVQRQGHG*GIHNSDWENTDWF RETKNQSVPLSCCIETVSNNGSLAHFY DLYABGCEALVGKLLFMMHVIWAEIA FAAIQLLSMLSACIVMCRKSTDPAYELL ITVGTYA
7132	21033	A	7190	496	118	QNQKFPFEPGTS*LGLYPKKYKLYHKD

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						PKTCMFTAALLTIEKFWNHHKHLMSADW IKKVWYGTGVGHACNQSTFLFWFFEMES HAVAQGGVQWLNLCSIQAPAWATERDSS QKRPKIDPHKYIVN
7133	21034	A	7192	1337	342	ISEATRTFRESIWQFQSSPREDDRNRL SASGSRQSHPGPRSTPGPGQGHRSRSHQ CAPVSSAARPGGPSFRLSEGALSRSQFS VLVYIP*VAAGQFVKACLGASSPPSRL* GGLGTGHRTPGKEARSWPETSAPPAPHL LRSCLPSRGEKLAQARSQKHLGWKWL KLCPTKYKSWSGPDDSPSVLRDPEAGTT RWAPSGNPEBEVVLQKAKYLQNTISEVL SVLHLLHIKALQLHSTNPFVFNARHLLV GQISSALTNNLSQILFLLLRFPFLSQV ERHSPLOKTGTTETNLVLFQDTPVPMNFP SSILLPSKYSCLPDLKASHFYQ
7134	21035	A	7193	469	130	SASWDYRRPPRPSPNPLY**RRGFTILA RMVSVS*PRDPPASASQSGACAYSIIYLO ERFARLHPACLAPRYMASDPLSSLHHSV PPGLHLEHEHWHCLLPQQICRPGKLW Y
7135	21036	A	7194	430	149	TVWQFLKQLNIELSCDPVILLGICPRE LKTYVHTKTRT*AFIVALCTIVPKQKQL KYPVSDEWVIKMWYVHTMDYFSVIKKNK LAKHRGSHL
7136	21037	A	7195	257	412	TATSNKEPLKKVRCLIWRRKDCWARGFT ACNPSTLGC*GRWIMRSRDRDHPG
7137	21038	A	7196	1	124	PLISGVVHPCNPSTLGGRGWRIA*VQEF ETSLGELAEPCLY
7138	21039	A	7197	2	120	YGIILFITSEVVFVAGFF*AFYHSSLGK KISKKESVIIY
7139	21040	A	7198	234	416	GVHAEVLISPGQDRRLRALVVIPIIFGI LFAILLVLFVFKKVAKKPTNKVGHP*EP GTEF
7140	21041	A	7199	372	3	VHYVPVQTGSPCCVPHPRGLSTIHPLH SRYTGLGMVAHACNCSTLGGQSGKIA*A LEMEISLGNMVRPCLYERTNKQSKPRHM GITTFGLTFSLTLDKYSLIISGFYLPQV LISLHPLGPY
7141	21042	A	7200	396	21	GLKESHKCCAIACQLQORDPLVRVLGKAG F*RKSLSISTELQSLFDSPDFSKITGKP IKLTQVEHRAGFEWNEGAGTTSPGLQ PAHLTFPLDYHLNQPFIFVLRDSDTGAL LFIGKILDPRGP
7142	21043	A	7201	2	148	REPPHSLANF*KFPVDKGFLLPRLVS SSWPQVLPPLPPRELGLQA
7143	21044	A	7202	1	291	AEGFRMHALVSQAACGTSGYKLSVGVMV QGPLTHMLGLLISLIFLSRGSGRTWAF SHS*YKTSDDLPCRNRREVIEFLHYRNL HSHICLSVTKTFL
7144	21045	A	7203	262	406	ILARMTSVVNSIKHLILFLK*SSHLSTP SSWNYRCVLPHQANFLFL*R*SFTLM PRLVETVLLIQNSPTKIDSSPDDPSGKF YQTLNIVFENIRRGNTSNLLHKNSRILI PNLTKTLHD
7145	21046	A	7204	2	247	DTVLERSGQGTAAALPRSTSLDRDWAITF EQILASLLTEPALVKYFDKPECMMARIT SAKNIRMMGKPLT*ASDYEISAMTG

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7146	21047	A	7205	2	168	FFFLVETGFTVLARMVSVS*PRGLPASA SQSAGIAGVSHRAQPALRFILLENRMC
7147	21048	A	7206	1	237	GKCAHTHTHTHTRDTHRHAHAHTHACTH THTYVQGCSSLQWSQDCVRMWACHIFGV PRE*ASRYTSSLVYKPGCTGVCG
7148	21049	A	7207	2	239	KVDSEHKLERSSGGVLGRFKGKSGGLN LGNFFASRKGYSTRGFDRLNTEGSDQDK EDDGSESE*EYS*PMPALEPCSS
7149	21050	A	7208	1	405	GSRDNMNVILICFPNAPKVSASVKNDA QLDKYLECTAQEII*NHWEDVPDLFHV RTLPSDNMPSLPPGGELASMRVTIEAVY YRLNFIYINDDTDSTDDMWFNCSSSHG VYLDLHRRVQVNFDETFSMHPPL
7150	21051	A	7209	2	761	QDFGTRFATVLLFVGYFKCTRTLKGTCL YNAILYKVCSPRNDQPDVCYNPSFLLP IKTGELLGLFLVYASREKRSIAIGD*KDD KWPPERIIQYYPAT*AQDSSWGYRIPI YMLN*IIRLQAVLEIITNKTGRALTVLA LQEIQMRNAIYKSLALDYLLAEGGIC GKFNMNTNCLHIDDQGGQIVEDIKITKL AHVPMQIPDIVWKNIVKIPVLFCSVLIT GTCSPPQSGTPCWLRSRSPSHVDFPRVVS P
7151	21052	A	7210	147	390	KTGLSDQMPRAIQLSYSYLSPLLY**SY KKKKKKKKKKKKKKKKNPFKGPKN*SF WGGEKKSGPGAGLKNPGGGKNTFY
7152	21053	A	7211	433	214	WGRGNALTIHPPWVPFQSETPPSPL*G ITLLDNPPSPPIPKQPPPH*SIIVPYLL SSPQPGFPHPFQADGLA
7153	21054	A	7212	532	253	KVINVFHKAAIMSDFSRDRSHSTLKAS E*GFTMIDAINKICDL*KEAKISILGTI *KKSIPITLMDDF*GFKTPML*VTANVGF QRFSSKKFYW
7154	21055	A	7213	456	24	DAQAFSWYSQGYFNSSQGSISLPGDTS PVKIKRMGGPLFFS*LLKSTCWACSKTS RVPKGLVKTGLPRPR*FVYKDLGGFY RF
7155	21056	A	7214	2	445	ILRDLQVRVPTWSGFPSWAMELLVEKAI SSASSPQSPGDALRTVFECISSGIIKLG SPGLLDPCCKDPFDTLATMTDQHREDIT SSAQFALRLLAFRQIHKVLGMDPLPQMI QRSNIHNNRKRDRSDGVDGFEAEGK*D *KDYDTF
7156	21057	A	7215	203	3	VRPGVVAHACNPSTLGG*GGRIA*SQEF ETNLGNTVRPCRNSEVLNRKTVSIRRA LRVFSPLHTA
7157	21058	A	7216	1	285	GKCAHTHTHTHTHTHTHMTHTHTHART HTHMCRAV*VRGARTVCTCGSAPFLES PGKEPKDITLRPLFVSQAARAFIGEKAFC SVYRQREPPPI
7158	21059	A	7217	1	386	GDSNCEWSVLYVIAITPGIGVALGILSW TVICMLKQNGKPKMKSKYKNLDATDQ SL*LKPASRAGIKQKGLLLSSSLMHSES KLSDDAIFTWPDREKGLLHGQNGSVL NGQTPLKATSPREIL
7159	21060	A	7218	70	379	NILYFNIFFFFK*FLKFLWVFFVFF* VFFFNFFVFFVFFLNVFFVFFVFFVFF WGPFFLFRFFFCGLGFFGTQSWRWF

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						LFPWGLMFLFPLLFLLVFF*LVFF
7160	21061	A	7219	1	208	PRLAASVSPGDMGLGMQVLGLTASACN CSTLGGRGMGIT*G*EFETSLVKKARTC FYKRLKRQKSANL
7161	21062	A	7220	455	96	HYLYGSQGLSRFYFVTQGRVQWHDHGS LQPPTPGVKQSSSLSPKCWDYKCEPPCL ARPCPPFFFL*TSSTDVGLLLNQQPIL* IMTFPPYLLRKSLSFHQIYEPTICS HLLSFCYT
7162	21063	A	7221	201	319	IYELWPGPVAHACNFSILGG*GEQIAQV QEFKTSLGHLG
7163	21064	A	7222	307	3	NRRQAGPFFAKLGRPSPKGGFPNFFKLF FFKSSF*KNPKGQGWGFPLIPGFQGPQ VGGSLGAPGLKPPWGTQNPFSKKKKK RSNCTDTGTTIAHRRQM
7164	21065	A	7223	331	141	SETITANVSPNL*DANDVPIQCEISPLI SYAGEGLERYVADKEFHAPVIDENG VH EVVKNGI
7165	21066	A	7224	157	314	WLPGRDGGEDGVCHVAQAGPKLRT*GD PSIKASQRAGITGLTHRTGPK*KF
7166	21067	A	7225	2	392	RDVRSLOPLPPSLK*FSCLSLSSWDYR CAPPTT*LIFILLVEMGFHHIGQAGLEL LTSGDPPASASQAGVTGVSHRTPPSF VLVNPPIPLLPPVSPDGPNISSSTTSW RGYPEVLRWGLCSFWGCG
7167	21068	A	7226	84	204	FIFFFFKR*SLTMLPRLVSNWARVALP PQRPKVLGLHV
7168	21069	A	7227	3	307	DRAAPRGAGRAGAVGPHRTGDWGLAGTP AGRGHARHIGRGPKQGRAAGRGHLHPG GLLGRGGNSEP*RKQRTPGSMRRAAPLL STGQVWEGPASVGDRVP
7169	21070	A	7228	52	1176	GSQQPLLHISEAQGDTLIKAPAEAAWP PLIAFSSGGRLPCSHES*SAAGYKRLDD TAAGGPPSPGGSPRSPATAPGLHPVWGG QLRPRGGRGLPATGSGEAFQALTQLSRG RACTGPPAPGSEDAAPSGCSAARWSP*M AGSSSCAIPDSAASCIPOGPEWRW*SR APARNRCSASSGRSRC*QLRRRYIPGL LHPVLHEALPDSWCETQLGPPLASEAA PPRSRRREEG*RGSGRC**KPSLPRWS LCRNQAEAGFVSILVWLSGLAGAPSRPA AAAPQIAPNQHRSPPPRLAPVFAASGSP WPWERDLGVLETINVGNFQDENPSACS GPQSTPDITYYPVQKPKTGLRLHFHSRPN TIVKSVGNMCL
7170	21071	A	7229	3	112	ASNLSRGCSEPRPCHCTPAWV*E*DSI SKTNKQKN
7171	21072	A	7230	103	299	AMSQIRNAIPFTIAT*RL*YLEIQLTKE AKDIYNENYKILPKIARDVTNWKNI PC S*IGAQLCK
7172	21073	A	7231	2	137	SLTSLSLICFCL*RWGLSVLPRLISNSW PQAIFFPPWPKVLELQV
7173	21074	A	7232	3	273	LTHIVDGNFLTMYQCLMCVC*QELGY QPVTTERCHNVNDCLQRSFKAQVFSCH ACRHDLGQNYIMIPNEIMQTLDDLAFPG YSLGR
7174	21075	A	7233	338	136	RPRWEDCLSPGVQNVCGHSESFPLOEI *KISQTIWCKPVVPSYQEVGELLEIRG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						STCFGLPKCWD
7175	21076	A	7234	437	261	HLGFPECWDYRHEPQHPT*FLEHFM*RR GLTTFPRLVWNSWEPQAIFFRWSPKVLEL QT
7176	21077	A	7235	41	264	VTVMEIKGKINLVLDIIKDIIYVEGFSTY YF*RGGLTMLPRLLDLSWAQAILPPQPP E*MGLQECNHHAQLSRYF
7177	21078	A	7236	1	154	GTRDFSVKTL*ARREWHDIPTGMKEKNF YPKKVYALKIPFKNEABTKKVEV
7178	21079	A	7237	1	179	SCLSLSSS*DCR*PPPCPANFVKSFFRN GVLTMPLRLVSNFLPQANLLAQPLSGFI ILL
7179	21080	A	7238	340	140	KINWVWVPVPVIVPTPEA*AQKLP*PGK LKFPILT*IPPLPSRLGHQSQTSPPKKKK KFYILSSDSV
7180	21081	A	7239	2	175	QFESKPSPAWATEQDPVSKKKKKKKKK KKKKKKKNSSKFKMIPFTKRQY*EGNWK N
7181	21082	A	7240	336	192	QSETPSQSNQKFIF*GGIALLPRLVLN SWAQAILPPWPPKMLGLQA
7182	21083	A	7241	1	186	DRPGQHGEMLSLTFCFFCRDGGTLMLP RLVLKS*AQVILPSRPPKALGLQDTVHC SKFDAV
7183	21084	A	7242	2	111	VKTLNKLGDGTWLRITRAIF*KPIANI ILNMCSFL
7184	21085	A	7243	360	217	LPSRGDYKRKPPCLVNIFYL*R*GLTLL PRLISNFWAQMILLPQSPKC
7185	21086	A	7244	35	276	VQQRVKQGRKYYSIVLKNKKLKNYL VGE*MG*RNIGWVQ*VAHTCNSTLGR GGRII*PWEFETSLCNIG*TCISG
7186	21087	A	7245	1	356	IQHTFSLTIFGIKYSYVVLKIVSWLAAV AHACNLSTLGGRGWIT*GHELETNLF AVKPWVYDKNSFPPTLNLRFKSGHLWE PRGKNHGGPPETPPLSRVSPQRFPPGGT RPLKKE
7187	21088	A	7246	3	293	CKCGKAFHNFYSFQNHESHTGEMLYDI RNVGK*SIFF*HHCQHKTHRAEKLCEC KICREAFSHFGNLKVHEAGRSGSRL*SQ HLGWANCLTSGI
7188	21089	A	7247	6	387	ASIPCLTYPSEWFL*FI*QAGHFSFSK KLFI CAFFSNRDEVSLMLPRLGLNSWAQ VLLPWPPKVLGLQVRATTPAKLGIFWG FMSVSLGGVCLCRSLCPLPLPGQVH SGCSQS FVEKMNEL
7189	21090	A	7248	373	146	HLGKKVLI FW PQYLALNPPNGGVSRY PRCRPLMVFFFFF*GRGLAMLTRLV SNSWSQVIFQLQLPKVLGL
7190	21091	A	7249	2	184	AILRGI*KKFISTLMDDFEGIKTSLEBV TADVVEIAREVELEVEVPKDVTELLQS HDTT
7191	21092	A	7250	795	544	EMKSCSCCPGWQWRDLGSLQPPPPRFK RSPASASLVAGITAAACHHARLIFVFLID TGFHYVG*AGLKTPEA*ATAPGPIFLYF
7192	21093	A	7251	34	242	KNTSLKKKFFWCQKLRLNVLVEEFAFWP GAVAHACNPSTLGDGRGVA*GQEFQTS LSNIGRPRLYRKI
7193	21094	A	7252	216	57	NIQVLKYVLTSTYLKKKKCAFLGPVAHT CNPGLGAQGRRIIS*AQEFETSLIS

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7194	21095	A	7253	126	366	INLTECCQQLDKAIFFFFLKKGLFAP*A EWQGGSFASLQPKPRLKKSSHLTLLST WDYGGALPCRFNGIFFFWKGG
7195	21096	A	7254	2	213	RPTWATQNPASTKKKKNSFFFEFEFRT VAQAEVQGGNLG*LQSLPPGLKRFSCLK MPEAPKQSCSLIG
7196	21097	A	7255	150	263	EGVSLPRLACNGAILAHCNRLRLETSSD LCAFS*TTTRYKYSGYCFSHPNMLIC SRFTLLSSSSSLGHLTLFLLIVCFEKES HSCPGWRAMVLSWLTATFASRRQATFAP SLELSR
7197	21098	A	7256	386	93	PPGGLPPQSIPSPRAQLKPKSPRGKKRG GPKPGGSQPGFWGFFFGPGPPFKRGGGL NWLGAKN*KGVKKNQKKKGKMPQETK RGNRSIDMKFEGGS
7198	21099	A	7257	153	369	KENSRLQGYGPLFSHS*FTNSCPGQVQW LTPVILALWEAEVGGSKDQPGQHGKTPR LLKIQKFARCGGGRL
7199	21100	A	7258	180	3	CSTLI*IRKVWLGAHAHNPNTLRGRG GRIA*GQVFKTSLGNNVKTCLFLPSPHN QQ
7200	21101	A	7259	22	265	QLRAIPDLKLDPLMEGKEILSRTLGGSG TVAPICDPSTLRGQGGWIA*VQEFKTSI GNMAKPHLYRKKLLGQVTKLEYKW
7201	21102	A	7260	326	2	KSAMQICIVDPLNAFCLEICCHANLHCR PSNAFCFLKVDNVRFAVSPSIPQVSLIL KNFSWPGVVAHTCNSNTVRGQGERIA*A QEFETILGNTGRPCLYFLKNNRKS
7202	21103	A	7261	1	68	VNLCFILWLGPVVAHACNPST*GGRGG RIA*P*ELETCLSNTA*PGVVAHACNPS T
7203	21104	A	7262	282	176	GLKKTFFFLVRERVLLCPGWSAVV*SQ LTAN*TPGLKLFSLCLSPCSWNHRHVAL HVAENIC*CHMPVVPATWEAEAGEQLEP RSSVCSEL
7204	21105	A	7263	588	351	NNTVCLLESISSVNLCLPHLQHSVPKLE IFLFFSSDNFPPSTHHITVRPLSPS*AI IFPVCTYTSRWPEATKDPQKK
7205	21106	A	7264	327	2	KIKERINNFICRDRVSICCPGWNAV VLNSWAQAIRFCLSLMSS*NYRCAPTHQ QVTTIFFCRDQIEIHMVPKYHLGNTLNY FFVLFCFVFLRHPFSAHRNFRLP
7206	21107	A	7265	121	270	AQEAGFELLTSGDLPTSASQSABITGMS HRAIPSCY*FYVTLHGLTVACA
7207	21108	A	7266	3	227	SSQVSLPNNWDYRREPPCLRFVFLFFVE TRSCYVASLELLGSGDPTVLAS*SARVI DMGHCDWPNLSEILLHVR
7208	21109	A	7267	300	1	KMLLNTIMCNREILCKRKSPRVQQTSTFV SYFKKLPPQPPQSAATTTLSQPPSTSKQ DPPAAK*L*FAEGRLLAFFSNVLYQLR YIMCFLPHTGIVHLVN
7209	21110	A	7268	29	344	ASLLALKKKSGLGAVAHNAHNASTSGGRG GRIT*AQEFATSLGNMARTCLYKKKKKK KKKGKNTGVTGGPQRGAPIFGPWGGGKS PAPGKPGGPNPFPKGAPTLF
7210	21111	A	7269	3	209	LHPLSPGPPAPVAAGIPGPOASR*GPCR PDPSPDASVDASLPGPALSLWSWGSNR GEYGTTPASQIH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7211	21112	A	7270	86	206	CQPGVVAHAYNPSTWGGRRGQIT*GQBF ETSLGNTARPPL
7212	21113	A	7271	45	274	GLGTVAQACDNPSTLGG*GGWIA*GQBF KTINNDKSNKQWYLAIIEQINNRMCLICK NKKELTDICNNTDEFQKHRE
7213	21114	A	7272	1	122	VLVETGYLRVGOAGLKLITPGDPPALAS QSAGITGISHRA*SYMHF*LVETGYLRV GOAGLKLITPGDPPALASQSAGITGISH RA
7214	21115	A	7273	3	242	LLKQLDYRPPHPAKFFFFLEFLVKKGPH LVVKGGFKTQTSGLLPG*ASKVGIGIPGV SHCPGLIGVFNLTLLKVAVSLMDL
7215	21116	A	7274	2	169	LALVAQAGGQWHDLSLQPLSPSPFPQFF YLSLPSS*DYRHEPPHSAWFSFFSNYR
7216	21117	A	7275	353	76	FAHLGLPQCWDYRREPLCAT*KLFLLK GK *PSKQVIFSSLGTGHFSNACFSCVMWT IVLLIINFVWTGIDGRTSGSSSVKCGNH SIYPMVLL
7217	21118	A	7276	6	87	RRGLTLLPRIGSNSWPQAILLPWPPKVL KL*AQTPGLRQSSCLGLPKC
7218	21119	A	7277	1	203	FQVKMLCSGMMWLTVPVIALGAVAHTGN PSTVGGRGQII*S*FYTSLDSGNPPA SASQSAGITLA
7219	21120	A	7278	272	51	IFFPVN*CGGHDVQHFNPS*NNLSSWS SWFMPIILPLWEA*AGK*LEPRSLRPAW ATKLDNSKKKIIIEIHA
7220	21121	A	7279	1	131	SRDYRHGPHLPTDFVFFVEMRFHHVAQA GLKLLGLSDLPALTS*SRDYRHGPHLPT DFVFFVEMRFHHVAQAAGLKLGLSDLPA LTS
7221	21122	A	7280	411	36	FLECVPNFFPPKKKFFPKNTGQVFFPV TFL*KGPALFFFIFFYCKKFFFLSSAK DFPDRVFF*KGPLFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFCKHFIYKKVHF *SSVHFQPIIFF
7222	21123	A	7282	395	181	RKHESIHDSDVISVTFNMSLRLEFFFI FILSL*LRFIFFFSFFLVFFFCFF FFFFFFFFFFFFFFFF
7223	21124	A	7283	392	2	IKFFGVNV*FNYILKNGLF*QLLI*LIN LFILRQGLIFVQVCNVLVFFFIFF FFLFFFFFFFFFLLFFFIFFFIFFFIFF FFFFFFFFFFFFFFFFFLLTQNMFLIVN FCKDTFKQONIHLRTRGR
7224	21125	A	7284	113	291	YVCVCVCVCVCVCVMEY*SAIKRDKIVA FTVTWMELETIILSEVSQEWETTHMLS LIN
7225	21126	A	7285	327	44	LIKVSENFSPPKKVLPPKPPCTIFPPS PF*KTPPEPIFIKPPHKKKNFNSPPQK *GPPQGFKSPPEFFFFFFFFFFFFFFF LGFSSKLLIR
7226	21127	A	7286	3	215	VILIIEMI*EAFAWKRVLIVEBPSINL E*LYDGGYYDGLVLTSGLGPY
7227	21128	A	7287	367	119	LKAPAPPFLNPPFWGKNFILSPPERMG PPRGFFKRGPPFFFFFFFFFFFFFFFFLG FFFFFFFFFLLQYNNMYFH*ILLINQ
7228	21129	A	7288	73	259	INKYLQN*KKKKKKKKKKKKKKGGP FKTTPRGAQISPGVKKNFPPKGGFKK QAPGPF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
7229	21130	A	7289	337	53	LRSFAPFHLPIINNLLTDIHMVPLPPSS LCSHYLFNEVTVTLFKITTHLQLGTMA HTCNPNTLGG*GGRSA*AQESETSPGNM AKPRLYLNNF
7230	21131	A	7290	1	96	KHHFGFEAAA*YWHFVDVV*LFLYVSIY **GS
7231	21132	A	7291	288	2	SRVEFKGPFMAHCSVTIPGSSYVFTSAS *VAGPHGARHHAC*FLP*FLV*MLLEM SRHVQAGL*RVSSDPPARACQSGGIP GVKPHAQSVSV
7232	21133	A	7292	121	233	YFPKKKKKKKKKKKKKKKKKKKKKK* KGGGRSRKSYLG
7233	21134	A	7293	3	346	NPLNPLVNLTVSEPKRNSSLDTRKKPCRE RHREKETLRKKRNQHTEARGRQRENHPE TE*ETGQRDRDKQTKQKQDIDIQAYTYT DREKRDKKRHRQIR*AEAERIRDTERQR DI
7234	21135	A	7294	46	346	ETGLKKWGDLSNGTVRAVLNLAQADFV SIPSYHIKHGNTKNNCGEGKKKILVVT AKKSEPGVVTHACNPNTLGG*GGRVT*G QWFKTGLGNIVRPCST
7235	21136	A	7295	254	12	RKDAENNGSRAR*IKRVKDLVQSKLKPF QELEKEGILPNPFYEASITLIPKPKDT SKEDYRPISLMNIIDAKILNKILAN
7236	21137	A	7296	258	1	CIGQCVLVAVGRELLCVSRSCGLLHVD EVGGEALGRLLVVPWTQRFSESFGDLS TRDAVMGNPKVKAHGK*VLGAFSDGLAL LD
7237	21138	A	7297	191	263	VCSKCEPFIYIMDYAAIKRKNKIMSFA RWVQLEVVSSELTQEQTENNMF*VVFG FLLLC
7238	21139	A	7298	2	164	SRVAGITGAHHHAQLIFVFLVETGFHHV GQAAFKLLTSNHHARPQ*LHFFYFFK
7239	21140	A	7299	307	8	VMIITFWLPHLSGYIEKSTPYECGFDPI SADRVPFSIKFPLVAITFLCDLEKALL LPLP*ALQTFNLPLIVMSSLLIIILAL SMAYE*LLKGLDCSE
7240	21141	A	7300	205	317	KSSPACTPSTLGG*GGWFA*VQEFETSL DNMVKPOLY
7241	21142	A	7301	140	22	FNFLFLYP*NYFFFFFFFPPPPPPFL PPFAMNINVY
7242	21143	A	7302	382	151	SIHRSEFRPRRSHSVSRPESRGITLVYC SLYFLGSGDSAPVVS*VAGITGVCPWAS LIFGFFFFFFNRDGVLLSCPG
7243	21144	A	7303	318	17	LVPTKRQVENYYPVHTYIWIYCTKGKRR WAGIGGSCLSQHFGRPWQDPLSLGV* DQPGQHRETPSLQK*KNWWQBPVPAIQ EAEAGEWCEPGRQSLQ
7244	21145	A	7304	310	132	QWCDLGATTPANCFIFVRNGVSPCWG WS*PPDLKLSARLHFQSVFFNPISIGL FFL
7245	21146	A	7305	338	168	REPPLPAANFVFFVEMRSHHVROAGPEP PSSDLPASASQAGITGVHCHAWP**T YK
7246	21147	A	7306	276	161	IINAAIKKNEFMSFAGTWMKLEAITLSK LTQELKVK*KLKFNNTDTILLLLIFKI F
7247	21148	A	7307	310	61	ITLVYCNFFYFINFNFLKLFDSFVILS

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3						LKQIYSCTAIVYILIL*APVQPKFLCFY FLYFKNIFYKNIIFYKIKYV*NMXYFYF
7248	21149	A	7308	257	1	CGRVDLH*AVFFFFKRWSLTVLPSLDLD SWAQVILLP*PPE*LGQQSCTTTPSSLS TFLYAFLHIPVNKMSCFVGKDRGMFFSY H
7249	21150	A	7309	2	181	RDGFCHTGTGL*LLTSGDPPASASQSA GITGVSHHARPCLSLTAFFKNMVMWPG QQE
7250	21151	A	7310	25	340	FCVENTMDVKNI*IFLIFVPDVHLG*QK NLLLDTI*KKKSIRIQE**QYKSISKRN YNTVSDKSWLGTVAHACNPSTLGQGGGR TA*TQEFQTSLDNTPVRPCVY
7251	21152	A	7311	2	193	FVDFSMHILDMLSLYLSIVICYITLFLS IIDNIYVNGPHKIIPIFYCIKIFYIY IWFCEWFFETVLLCCFSVFTFNDYCSYL HYFLLLGVEGLFHFH*FLYLYMVLFLVF
7252	21153	A	7312	1	245	RTEGLKQSSHSFSLSSWDYRHVPLHPAN AFFFFKGP*SEPLTLASSLHWYFPGGHF LQGPAKIDDFNSPILGKLKKKSPF
7253	21154	A	7313	167	2	GKPCLLVVMCRDSQKCGEKGTLKREAL RMGK*GOARWLTVPVIALWELEAGGSP
7254	21155	A	7314	334	152	CHVAQAGVQWYNHSSLQP*PPGLR*FSH LSLPSGWNHSWTPHPANFFIMGSCHLP LINK
7255	21156	A	7315	2	164	PHVQDGLLELLTSGDPPASAFQSAEITG VSHHARPTFYLS*QVGLTVTSFRNPQ
7256	21157	A	7316	155	9	QRIKH*FHWLGAVILTCNPSTLGQGGW ITGGQKFETSLAYMATPRLY
7257	21158	A	7317	1	293	GIPSTWDYWCTSPQPHF*FFFFFF**KR DLAMLPGGVNLSWIPAILQPKGPKVLGL QAWTILYKGYGKEMWHKEICKGTHDVL SKLLTTKRFRLL
7258	21159	A	7318	262	73	SNSLVYLKPDVYIFLLFVETVSSHVA QVGLBLVASSSTPI*ASQSVEITGVSHH ARPKVT
7259	21160	A	7319	169	265	GGRMALSPGRGGCSEP*GCHCTPAWETE QNPA
7260	21161	A	7320	169	260	KPQKIPVACDQQFTDKRNC SHGDYECNM VDDFFFFFRERVSLCHPGWSAVV*SGDH TTALQPG
7261	21162	A	7321	580	400	FFFFERESRSVARQPGVQWRDLSSLKSP PPGFKRFPCLSLPSSWDYRRAQPCPANV FEFW*RWGFTTLARIVLLS*PCDPPTSA SQSAGITGVSHCAQP*FFFFERESRSVA RQPGVQWRDLSSLKSPPGFKRFPCLSL PSSWDYRRAQPCPANVFEFW
7262	21163	A	7322	130	26	SPGFLFGLIEPLPSRFKGFVNLNLP*TW EYRLALTAPIKFKFLIKTGPPH*GIKL RG
7263	21164	A	7323	17	303	KSSGTIKGRAQSPFLQLVAIEQCQDCPH FRSQF*YLKKQLQPGMMHAYNPSYSG *SRRIT*AQEFKRLGNITKLCKLKINN SLIFKITEIE
7264	21165	A	7324	194	8	DWVEVLKKSTYRPDTVAHACNPSTLGG* GGSIT*GQKFEIRLGNVVGPCCLKNLTN QLGVGG
7265	21166	A	7325	413	72	GVPIFLKTLTGKTISSERESKVPLEKCK

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						ANFRDKRGIPPHKRVIPAEKKL*KGRS PFDDGFQKKLTQPRVSAFKGHPPLQPLY AFIKSFREGTHHQDCPFWHLTLLSARRQ Q
7266	21167	A	7326	394	177	NVNHHTHTHTHTHTHTHTHCWCKSDTGYS SDS*CITPRCIHDPTWPSSSQTVNLAMG LTLAKEVLNMTQTEV
7267	21168	A	7327	232	22	SRPSGSKKGAPALQQSSCLSPFLSSWDYR HKPPYLTNFCIFL*SQSPMLPRLLSNS QPHSNLPKVVLEQV
7268	21169	A	7328	232	3	YHRSSGSLISLIQIRLSKI*APSIPIY KEWLSSVAHVYNPTLGGQGGRLT*GQE FETSLGNIARPCLENCLKN
7269	21170	A	7329	364	3	PKARRATVRRTRVSKAPSNRQCLGVNTH VLGHRPVPKGNKTRWSASEQAHTCNI TTLGGQGGIT*DFEFESSLATMQNFVS VSGWLQKMFQKLYSKPPFNVAKAPR IWLICARA
7270	21171	A	7330	177	2	DPHLHKKFKARCGGMTL*SQLLRRLR*K DQLSLGVGGCFELLWCYCTPANVTERDP SC
7271	21172	A	7331	413	40	RHMYLMFYTYIYVLDIYTYTVFFMYTYI P*CVCKYISCLHIMYRFISMPCVYVYV CMCVCNVIHVIVENAGSCLALSALIEME GMARDSKMTFTNPDEKMRSLYKKQLEKL NFMILCPTWKEF
7272	21173	A	7332	147	49	KNYIYFCRRGLPMLPRLGLNSRAQEILL PQPPM*LGLNSRAQEILLPQPPM
7273	21174	A	7333	148	361	SWLGTVAHAYNPSTLGGGRGRQIT*VQEF ETSQSNRIARPLLVSVALAYVQPLPMVA MRKLWLIPTSRITAL
7274	21175	A	7334	305	2	CPGGFVTRVHR*YVRLSQPDRLRVFTSGA MPASAAQSAGITGMSHRARPVCSIIIFL NIFKVTICIFVELTIPNQKQNTFLSSTV ASCRILASRPTPIVVVL
7275	21176	A	7335	1415	1164	FFLRQSLLYCPGWSVVAQSOLIASSTIQ A*AILPPCSWDYSSQHTWLKFFFC*DGF SMLPRLVSGSWAQMVLLPQLPKAQAKL
7276	21177	A	7336	1	206	GTRADHLMMSGFDQDPGGHTETLSLLKIQ RSQAWWHVPVMLPTR*IDARESLERLMT IALLKVRNRYIF
7277	21178	A	7337	65	302	KSSLFYFLKIETGFHYVAQTGL*LLSSD DPPASVPQSAGITSMSSHQPKELLKST RNTLEEPNREWAKAREWAHRRNT
7278	21179	A	7338	208	38	NPVSAKNEEYPRGTFDLGTQAEVQWHDL GSLQPTPPGLK*FS*LSPRV
7279	21180	A	7339	2	198	ARADHPRSGVRNHPGQHGETPVSTKNTK N*AWWRVPLVPECWDYILFYMFNCDN KLPKWLTL
7280	21181	A	7340	2	227	ARGEIMSFATWQLEANILSKLTQE*K AKYCMFSLLSGAKHWLNMNIKVGTDTR DYLGCSTQAVLKNLGRAE
7281	21182	A	7341	3	300	HEGRNYTLTGRDSCTLAASABKACGACP LWKGCDAAESSKVCREASDCREEGISIC VDVNCKEQTMPEC*AVL*CTVHLIYVT INNALCLPQLTLFL
7282	21183	A	7342	210	351	RGLGTVAHACNLNTFGG*GRWII*AHF ETSLRNITKPSLRENPDML

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7283	21184	A	7343	306	164	IYMLYFIYITLIYIHTHTHTHLYLDKYI YL*CVHCFL**AYMICHQR
7284	21185	A	7344	442	8	SQMSKLKTWFRVAHAHWNFSTLGGQGR IT*VREFETSLGNTARPNLYWN
7285	21186	A	7345	3	248	HELSSLSSLPFFPKNEKGR*VAHAGL KLTSSDPPT*ASQSARITGISHCARPL LSHFLAYLALPCHQNRLCTGHLPT
7286	21187	A	7346	2	246	HELYQSILSPLFPKNDIGSR*IAHAGL QLLT*SDPPT*ASQSARITGISHCARPL LSHCLAYLALTCHQNRLCTGHLPT
7287	21188	A	7347	1	130	GTRLLKRLTQETRLNPGGRGCREPSLHY CTPTWARQSQTVAHN*KRLTQETRLNPG GRGCREPSLHYCTPTWARQSQTVAHN
7288	21189	A	7348	516	288	FFETESRFTQTGVQWCDLGPLQPLPPG FKGFSCLSLSS*DYRCLEPPHPANFCIF SRDGVSPC*LGWSQTPDLK
7289	21190	A	7349	417	148	STSVVQAGVQWHDHGLLPGPPRLK*S SHLSLPHG*DYRHILSCLANF*NIFVEA GFRHTAGLEPLGSSDLPASASQSAGIT GMSHLA
7290	21191	A	7350	143	2	TQKFKTSLSSWDYRRVSAHVANFCIFSK DRVSPY*PGWSRTPDARA
7291	21192	A	7351	189	37	EATAVRRII*NLFFFFFF*RWGLTVLPK LVNSWAQAILSPQPSKVLRLQA
7292	21193	A	7352	131	2	KSLRGTVAHACNPSTLGGRHGWIT*SRE FKTSRANMVKPRPRA
7293	21194	A	7353	1	106	GTRGQCLTMLPRLVLNYWAQMLPPWPP *VLGLQV
7294	21195	A	7354	939	653	KGNFIFLRQSFTLVAQAGVQWRDLGSPQ PPPPGSK*FSCLSLRSSWDYRHGPPHPA NFAFLVEMGFLHVGOAGLELPT*GDPT SASQSAGITGR
7295	21196	A	7355	270	26	EARFLGLLRDIAQLCYPGWSAAV*S*LT AASTSWAQVKASTHLSLPNN*D*ARATM PG*LKKYVFF*RQGLAILPRLRLVF
7296	21197	A	7356	329	206	HHLANF*TFCDRGLTMLARLNSWPOAI LLPQPPKVLGLQM
7297	21198	A	7357	128	253	MRPDTVAHTCNPSTLGGQGRIT*THEF ETSLGDMMKPYLYK
7298	21199	A	7358	2	108	AREGSGGQGCSEP*WRHCTAAWVTEQDP VSKTIKK
7299	21200	A	7359	1	340	GTRERNWHLA*ALHTHTHTHTHRHTHTH THFSFPANS*RTDFVIF*QSLLEIMTS FSPSLGLKCSFSQPSGLLSSIAGERDS RIHGENTVSMCLHNRLKAE LRSDVISLR V
7300	21201	A	7360	385	1	SVGSPKPCAGYNLLVCHLLRPLEKRSIR VGVT*FSRCHLSPLSLTRKANSITPCTS WMRRCLILLRLTLGVPHMSTHCTPLP SEMNLGPQLEMOKSPIFCVAHAGSPRLE LFLPHGLGSTPNLPSC
7301	21202	A	7361	234	29	LSTEPKGSKALKFNVTLLNLNIAF*CNNG CNSNL*S*QY*RVIQSHHLSQTLWLTP VIPALWBAEAGG
7302	21203	A	7362	68	339	DRDIANKPAWQLCQSRILYLAQLQFIDQ GELLPDFRIHYKVI*TCATW*RRNRLI DQWNRADIPDLNCPQANRLTEVILVLWE ADVGGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7303	21204	A	7363	168	2	CFYSTHAHIFKELRQRPQAVAHAYNLST LGGRRGRLT*GQKFETSLANMVKPHSC
7304	21205	A	7364	399	62	QPGQYQKHPVLIKNSKIKPFWGDPFVVP NAREG*A*KMVEPGKVRVQSAQIKALEF NLGPKKKVPFKKKNPWLAQGGGLRPEIP AFGKASKGGSPPSRILRPPGFLPYPAHF
7305	21206	A	7365	289	76	VCDVLRRESRAQLSRKCSGII*AHCNVS IAGSSNCHASALRVPGSTGVWVESERGD VDRFEAYGSRGYVCA
7306	21207	A	7366	364	182	QWHDHCNFKLLGSSNPPTLAP*VAGTAG TCHCAWLI*FLTWKIGFKTSLRIIVLLG YFWF
7307	21208	A	7367	155	2	ELGTRKREGWEKSATVAHACNPSSLGGRG RWIT*GPEFFPTSMANMMKAHPRA
7308	21209	A	7368	342	184	LSLPSNDRRYTPPRLANFFKFFKR*S LIMLRLRYRPFYITTHQTLNSAMTF
7309	21210	A	7369	2	211	AREPKCL*TDWINKMQYIDAVEYHLAI KLNEILTHATTWNLENMLIGRS*TKRA TCCVIPFMDSIYV
7310	21211	A	7370	190	344	YKNVTVKRILTWFTVAHACNPSTLGGQ GGRFG*GQEFETSLGKIARPCLY
7311	21212	A	7371	24	254	KPGGIGAHASSQHYGRPRREDHLSLGV* DQPGQHGEPISLQKKKKKGLPGRGGVCL KPWFLKILGEKNVWVLTPKG
7312	21213	A	7372	43	358	DSNLNYSLFFHGEADLGTQVLTHPSTT AMYFVHYCOSP*ILYGTINT*PPVVHKN PIHIKTPSPCLOASTAINQLSHINCNS KATPHPLGYQQTYPPLTVHST
7313	21214	A	7373	2	288	IHIILAFSTSLGILVYRSHLIASLLCL HGIILSLTIIAPLIPLNTHSLAPIGPI AILVIAA*QAAVGLALLVSISTTYGLNY VHNLALLQCCN
7314	21215	A	7374	335	1	VQWDFGSLQNPFGVSPFFWLSLPPNNL GFKGPPPRPGPFLKF*KPGFSALTRMV SLSRPRDSAPLAPPKAGVSRNLNPRARAP FFFFFVFCFHFFLLSGEKKSLAHKGGI
7315	21216	A	7375	399	91	RIFFFPPSLKAPPHRQKPTPFPPTKKPL VFSIPPIFPFKFLKKNPFSPWEVFLFLS FFQKDAFFGPOV*KGNFFFKGPPPLTQ NSPQGVPPKKKKKKKKKN
7316	21217	A	7376	377	131	YLYIKFYNFIIIFYIFIFNIF*FNMIF NLLFYIFYILINFNILILIINFFFYPI LLIILNIIILILYIIYYPIIKNIKT
7317	21218	A	7377	2	156	FHHVV*AGLELLGSSNPPTWAFQSAETT GVSHHAQLPHFILRKQELLSLGL
7318	21219	A	7378	319	59	DTKMNSQDILYSIQSNRT*W*LIKRQ*T KQKSAPRNGNEVP*THQSTATTLSISQ PSTSKQDPPAAK*L*FAEGRLLAPPSNN VF
7319	21220	A	7379	308	12	FSPTISNFNYKSNPSPLIYLFQ*PITQL IPTNISTNTPLNL*FYRLIYSTSISLL PISNNVKIK*QFHTKPTPFLPTLIALT TLLLPISPPILIL
7320	21221	A	7380	11	169	RRDLAMVRLFFSSSPGLK*SLHLGFPEH WDYSHEPPSWLLFFFLITEGYFF
7321	21222	A	7381	300	2	KFFPPPGFFFGFFSPL*SHQKKTQIFF GEEFFWGFKKFFLFFFPGGFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FF*INSLFIQNSFLT
7322	21223	A	7382	163	160	PGTSNDEIQRRNSRNRISPIAER*GLSL LPRLWWMGSNEAHSNLELQSSNPASAS SKSTMITGVSHCA*PRLEWWMGSNEAHSN LELQSSNPASASKSTMITGVSHCA
7323	21224	A	7383	1	183	VVCVCVCVCVCVKWDSYSAIKNELVA FVVTWKRLLETIIILSEVSQ*NTIYHMSS LICGS
7324	21225	A	7384	2	196	KIQMWPGVVAHACYPNTLGGQDGRTA*G QEFQTSLSGNIARPCLYQQQQQQQPRCS LTYDGDKS
7325	21226	A	7385	3	192	RNLSSLQPPPPGLK*WSCLSLPSSWDYR RPPPCPANCFMLCEFFRTNGVFPSPGV YFPRN
7326	21227	A	7386	266	198	TMLSGFLRSAGLTMTIS*PHDPPASASQS AGITGVSHRARPLVLFRLDSLYSGTQAG VPWRDLSSLQSRLEQMRFCFP
7327	21228	A	7387	164	311	SKQQKGLSGVAHPNCPNSILGGRGRWIN* GQRFETSMASNVKPCLSLLKL
7328	21229	A	7388	3	218	EIMSFATWMOLEANILSTLSHE*IAKY CMLSLLSGAKHWLMNIEVGTGDRDYL GCTYPSSSTEQLGYYS
7329	21230	A	7389	521	58	SDCGLTPIAQTGVHWHHLSSLQ*LPWL G*FSLHSLPSSWDYKYVPPCPASFLYYF LVETGFCHVAQDGLLELDSNPPSSASQ SAGITGMSGCAGLRRF*KLRSWRYLVLL AMQVNEQGTSGAGEAVSEADAGQGCCCG LCLHRILSQYALF
7330	21231	A	7390	169	322	APGNFKTN*RXNGFWAGNTLGVSUKNMK NGAWAWLTSVIPALWEABAGGSP
7331	21232	A	7391	1	353	GTSFHYGSFHHQKDVTKGQSRPRER VLGSHARKNSLPVHEVKAYLL*KYLSIL RATHILISPDGCWVPFIFIAQSYIFLSSC GFFLLFFLLLLTSLFCSWHLLIISFLALF VIRLY
7332	21233	A	7392	372	3	IQAGACCAECIPSKGIRWNPISIVEGLHS DMSWSLCLFLSGAISVLCNFRLSGSSDS PMSA*QAARTAVIRHHTRLIFCIFSRRR ETGFHEVGQENLMLLLQLFSLGFSIS ATLLTLMLLV
7333	21234	A	7393	362	176	ARMECSGAI*AGLRGSSDSLASAS*EAG YTGKCGHAQ*TFVFLVEVRFHHVQNAI NIRTSI
7334	21235	A	7394	2	304	ARADCCARNE*GSVGMGSPBPGVGYNLL VFRFLRPLEKHSIRVGETRFRCSCLSQL CLARTGNSLTPCTSWVRQCLALLRLMLG ALHPLSCTQRPTSHSE
7335	21236	A	7395	256	3	MYAARYWNKAKITTESLRHWAGHGGSH PYNPSTLGG*GGQIS*AHKPETSLGNMV KPHLSKNKQTNKQTNKQTNISWSWCTCL
7336	21237	A	7396	346	2	RDHFYRESHSLITYICLENVKSNLKCGE GPLNFTFHLQRKNCNLGHTRSPPGVYHV GRTEATGPIKRRNGLGAVAHTSNPSNL GGQGGWIT*GQEFKTSLSLPRWLTPVIP LV
7337	21238	A	7397	2	242	RRYSDYPDAYTT*NILSSVGSFISLTAV ILIIIMI*EA*KKKKKKKKKKKKGGPF KKTLLGGPKFNRRMEGKNFSLKGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Methiod	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7338	21239	A	7398	1	289	TKLLGLYYTLLQASNDKSPFSIFDGIY GSTFFVTTGFGHGLHVIIGSTILTI*FIR QLIFHTSKHFGLEADA*YWLADARR HSESIHQCCSL
7339	21240	A	7399	346	40	IIIFTNKIYIKINKRLKLFIIKILDLYI I*IFFFRK*FTFKQ*KP*IININKIYYN NIK*IIFYLFFFFFFFPLFFFPF FFFFFFFPLKK
7340	21241	A	7400	1	334	NSCRRQRLLDLLLPITL*LPQLIGYIE KSTRYECGFHPISPARVPSIKFPLVAI TFLLFDLQIALLLPLP*ALQTNLPLIV MSSLLIIILALNLAYE*LPGGLD*AE
7341	21242	A	7401	2	302	HTINLLGERYVLATTY*STMTLLLTGL TVLHTGLYSVYLMTTTQWG*LTPHIINM KP*PTR*DTLVFIHLSPILLSLNPDII TGVVLVLLSYELYLLT
7342	21243	A	7402	57	338	TTINVIIGYIEASTAYESGCDPISPARVP FSIKFFLVAITFLLFDLBIALLPLP*A LQTNLPLIGMSSLLIIILALSLAYE* LQKGLD*AE
7343	21244	A	7403	407	68	QEELVDPLTTVREQCEQLENCVKAR*RL *LCDERVSSRSHSEEDCEDLFDLHAR DHCVFLLIYLINLYMCELT
7344	21245	A	7404	494	154	SLFIFYLYLIPLP*FFHYFFYPILLSI FSFKLFFFLHFFHMFPLFFSPNK IPFPKIPRFFLPPLF*KFFFLPFPF LSPLGFFF*SPFFFPFFFPFFFPF F
7345	21246	A	7405	1	400	NPGRFLSTSNSSLYERTREIRPTSQSAF PRK*YHLKKKKKKKKKKKKKKKKKK KGGGPLKKPRGGQK*TGGEKKKFPFPR GKKKPPGKF*KKTFFWGGKMGKTPQK KINPLGKKIKFGKRGKTPPL
7346	21247	A	7406	2	257	RASLCHPGWSAVV*SWLIAALTSWLKQF SHLSLKCWDYRHEPPHLA*LRFEHRHS GSSICTLNR*ILLSFPILSIRYKNGLIL Y
7347	21248	A	7407	259	47	YVFFFLFLFFIRLQSVSPFFFPFF FFFFFFFFFVVK*SPIEMFSFV LYLLRQVSISIAITLFG
7348	21249	A	7408	3	248	VTFL*CDVEIAVLIPLP*ALPTNLALI DMSSLLIIILALRLAYE*LRGGLD*AE EHQATHSAYERAPPL
7349	21250	A	7409	2	350	RSGMPRRYSYDYPDAYTT*NILGSGVAFI CLTAGILIIIFI*EAFASKRVLIVEQP SINLE*LYGCPPPYHTPEEPVYIKSRHI RKESNPPKLVSQPHGLHDFPKKGLGTI TEKN
7350	21251	A	7410	2	232	LDQTYAKIHFTIVFIGVDLTLPLQHFGL LSGMPRRYSYDYPDAYTT*NILSSVGSFI ALTAAILIIFI*EAFAKKF
7351	21252	A	7411	2	321	TSLAVLLIIMTL*LPQLNRYIEKSTPY ECGFDPICPGRVFPFSIKFFLVAITLLF DLETALLPLP*SLQTNLPLIAMSSLL LIILDLNLAYE*LQKGLD*AE
7352	21253	A	7412	2	194	SIECFVLPITLLCDLEIALLLPLP*AL QTSNPLPLVMSSLLIIILALNLAYE*L QKGLD*AD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine; W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
7353	21254	A	7413	1	197	LYTTYFVTKLLLTSLFL*GRTAYPRLR YDQLIHLL*KNFLPLTLALLI*HVSIP I TISSIPPQT
7354	21255	A	7414	1	185	STPLP*ALQTTNPLIVMSSLLLIITLA LSLAYE*LQKGLD*AEKKKGA AVLKDP SGGPS
7355	21256	A	7415	347	228	LE*LYGCPPPYHTFEPPVYIKSRLLKRKE SNPPKLVSSOPHGLHDFFKHIKNYRKNK RKEGLASVKENDRGP
7356	21257	A	7416	1	296	HAYDHASQALNGYIEQSTPYECGFDPI RARVPFCIKVFLVAITFLLFDLEIALLL PLP*ALQTANPLIGMSSLLLIILALS LAYE*LHKGLD*AE
7357	21258	A	7417	3	202	TCST*HVLVRMT*LIYDLEIALL*PVP* ALQSTNPLISMSTSLLLIILALSMAYE *LQTGLD*AE
7358	21259	A	7418	1	321	SNLLALVLITITS*LPQLSGCVGECTP YECGICRILNARALCCMQIFLKAITFLL FDLEIALLLPLP*ALQTTNPLIDMSSL LLIILALS LAYE*LQKGLD*AE
7359	21260	A	7419	1	212	RTRGIIFRPLSQSLY*LLAANLVILT*I GGQPVSYPTIIGQVAVLYFTTILILI PTICLIENKILKWA
7360	21261	A	7420	2	257	GRVGRGVGYSTAFPLQAITVLVDLESA LLLALP*SLQTTNLSLIVMSSLLLIIL ALSLAYE*LPLGLD*AEYWGEMMTTLD A
7361	21262	A	7421	367	269	HCDLKLGGSSDPPASAS*VAWITGTCHH TKLS
7362	21263	A	7422	2	116	ALQTTNPLIVMSSLLLIITLALRLAYE *LQKGLD*AE
7363	21264	A	7423	2	336	KPECGREGILPCCSSSAWPEGSFRPPQM NLGSFLSFFFLFFFFFEKGLFLCPPV*S PYGKSNLLEPSASRFKQFFCLGPLNNWD YRLFPPFPNGFVFKNRVFPFWPSLV
7364	21265	A	7424	3	154	LFL*IRTAYPRFRYDQLIHLL*ENFLPL TVALLI*HVSIPITISSIPPQT
7365	21266	A	7425	3	154	LFL*IRTAYPRFRYDQLIHLL*ENFLPL TLALLI*HVSIPITISSIPPQT
7366	21267	A	7426	1	314	INTLLTLLLIITL*LPQLNGYIN*STP YECGFDPIPARVPSIKFFLIAITFLL FDLEIALLLPLP*ALQATNPLIDMPSL LLIILALS LAYE*LHQGLY
7367	21268	A	7427	1	331	ILIINTLLALLLIITP*LPQLNGYIEK STPYECGFDPIPARVPSIKFFLVAIT FLLFDLEIALLLPLP*ALQTTNPLIVM TSLLLIILALRLDYE*LQPGLD*AD
7368	21269	A	7428	2	373	SDRNHIIHALVITILLGLYFTLLQASEY FESAFTISDGIYGSTFFVATGFHGLHV IGSTFLTICFIRQLIFHTSKHHFGFEA AA*YWHIVDVAGLFLHVSIIYRGGSYNHQ IIPSVAQESTPA
7369	21270	A	7429	378	63	PSFFPPFP*NFFPPRPLFSPPGFPFPF FPPPKGPPPKIPPGFFSPFPWEKFPF PPPLILPPRFFFNPPPPFFFPFFFPF FFFPFFFPFFFPFFFPFFFPF
7370	21271	A	7430	1	109	QTTNPLIVMSSLLLIILALS LAYE*L QKGLD*AE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7371	21272	A	7431	358	290	FLLVIPNLFHFLIYIIISIVPNVSFFH IIYILSIFFPFIIFILLSSFNILFFF FITSFPFFYFFFFFFFFFFFF FFFSFFFFF*FFFTN
7372	21273	A	7432	1	95	PTRPTRPHNSLQL*TPGLKQSYRLPS SWD*RHMPSPHPANFRKF*RWHLCPGW S*TPGLKQSYRLPSSWD
7373	21274	A	7433	1202	870	HNIFKIRPHCRLTHRGKPFYWGLLVTPV FSPSLRPSFLPSFLPSFLPS*LPFLPS FLFLSYSPCLPLFLCLRCIPSAFFWG NPRQVQENCIVITTYRILSFTALHQL
7374	21275	A	7434	163	1	SVVVKRIGLGRVAYTCNPSTVGQDG*Y T*GQEFETILAKRREPLFLACFLFI
7375	21276	A	7435	148	362	NDDNSVEFGIRLHKGLGTVARTYKPSL GGQGGHIA*AQEFMTSLGHMT*SSLYHK LTEYGWRDTASLLMC
7376	21277	A	7436	61	233	GGDLRHWPSSDSFFLSLFFF*NKNGGG LALLPRLDLNSWSQAILPLKPPNALGLQ A
7377	21278	A	7437	44	242	FVCLFLFFFEKESTFQHDLSLQPPFLP RFKRFSCSLSPSTWDYRLAPQCLANF*I F**KSGFTFG
7378	21279	A	7438	119	300	YCVSLLIFFIFIIYIFILLIFKFLFITL NYISFLFFYF*H*FYF*KNFIFVFPFGY FPRP
7379	21280	A	7439	1	221	LKLQHDPTTISLVITRNWKQKCPNVQ QIVH*SAIKRNELLIHAKTWMNLRGIML SEICQPQKILYLEIPFI
7380	21281	A	7440	35	345	FSFCCVCVCVCSLPHKHAIEMLNQTTP YVPKGVAYLPEREPFIVPMDDELTA*YE DYRTHESAQEPSEPHQLSRRSLPH*PGH ATRDHSPPTDSWGRRTSH
7381	21282	A	7441	3	384	VIHL*AGAVTIGSRKSTNALAHFLRQG TPTPVILVLGIIETMNLIIQPVALAERL TDNITAGHLLMHLIVSATLAILTINLTS TLIMFTVLILLTILQIAVALMHAYVPAL LVCLYLHDDAYDHGG
7382	21283	A	7442	15	277	GLAILPRLVPNSWPKVILQVWPPKMLG* QA
7383	21284	A	7443	21	694	NGGLNAHLASASEFDHSGVQLIEREEI CIFYEKINIQEKMKLNGEIEIHLLEKI QFLKMKIAEKQRQICVTQKLLPAKRSID ADLAVLQIQFSQCTDRIKDLKQFVKPD GENRARFLPGKDLTEKEMIQKLDKLELQ LAKKEELLEKDFIYEQVSRLTDRLCSK TSGCKQDTLLFTKRMNGYSRRIKNATEK MMALCA*LSMKQAPTIELQKEVQGERP
7384	21285	A	7444	141	428	DRSLLEAGDGRIAGDFFFF*TGTFNFAQ AKVQWGIHSSLHP*PPGLKQSSYLNILG SYHHWLRPHALFFFLKNGSLFCPGWFG TGERGTTFWGAK
7385	21286	A	7445	35	343	GYSIIGCPKFLDEKIFDSGHEKERKINS LLE*KKKKKKKKKKKKKKRGGLLK TSGGPKIKRGGIKNFIKGGVKKTSGE FFGKKPFFGGEKFWELP
7386	21287	A	7446	403	193	EYIKQGAENNQPKLHAHRKRLTWKETP RCIHEGIAPAIMNSDCLVFDTSIAQLFA ENGNLGINVTISMC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7387	21288	A	7447	411	110	LTDSLINIVYR*KMSYIS*NSA*VYLY IFCIYIYIYIYIYRIYSIYRC*YIYVG PAHIVLVYSSSYILVYYESHKYGYIMGL NILSYIFTYSYFSACS
7388	21289	A	7448	1	380	PTRPQKLKKNCGVSNGLCFFGGGQFL IWGFFFFFCILIEGGLNSKNYELKSLIK TYGAKKAEIHTEN*KNRETLLEAAQL AIKVTNPAMLRTEVHDYAMYMHNPWLN KLNNCHKVAISCKQ
7389	21290	A	7449	200	437	VQSNNKNFKRRRL*PGVVAHTCNPSTL GGQARRIS*AQELETGLNLMRCPNYNK FINVLDDVHGVTSPPVSQYKKVC
7390	21291	A	7450	405	3	PPRFPGFFFPYPLKFFFPKGFNFPGG FFPIFFPPKKKFFPKNSPGGFFLPPLG KIFFFLPPFKFGPPRGFF*RAPLEFFFF FFFFFFFFFFFPPFFFLQRIINF ARPGTFLSRAVPLRGALPPSA
7391	21292	A	7451	2	348	PRVRPRVRYKLQTKRCDLTPS*GHSV SLRNTTFDALKS*DTDSLSPKLECHGV NTPNCNLRPLSLSDYPASLSREAWIAT RLRAWEIFVFLAQMRODYCMNPGGGCN ELK
7392	21293	A	7452	1	168	LVHDGHAGLKLTSGRDPA*AYQSAGYT GVRPLGPPTYYYFRTASMTFICEFATV
7393	21294	A	7453	184	260	SSRGGLASRSSR*STLLGLPKCWDYRC MPPSLANFFFFNF*I*NFCFW*RRSLGM LPRLVVNS*MQAILPLRIRLQIHFAQT QTFFSL
7394	21295	A	7454	405	64	FFFFFNFF*KKKI*DVFAKIFFKIFFFF SGLKIFWGGGFQNAAPPQKQFFF*KIKSF FFLNFF*KNIFFFVAGVFFLLNFFFR GAPLEFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFF
7395	21296	A	7455	368	2	SQSFGPRWRNRLGPEQHIKISRYRPAQ VHACHPSTLGGGRGWIT*GQEPKGSTHL GLPKYWDYMEPLLVLVYICFHFRTFCN KAAIHCFKPEQLLYNKTSYFKESYKVKA ALVACKPTRP
7396	21297	A	7456	2	183	TERDSVSKNKYIYIHTHTHTYICVHG VIYVI*SLLLIYNIAYILYHVFIYLL IFKA
7397	21298	A	7457	281	127	YNFCIFM*RCGFNNVGQSLKVLRLGYS PASASQIAGITGVSQCAQPVAYS
7398	21299	A	7458	2	194	TSVRKYF*VFPTITDRIYGSTWVATGL HGLHVIIGSTFLTICLIRQLIFHTSYH HFGSEAAG*YWHFVEPARLFLVVCY** GSTWVATGLHGLHVIIGSTFLTICLIR QLIFHTSYHHFSEAAG
7399	21300	A	7459	22	319	GGSVTGAYHRILDHNRNQIFLA*GGSVT GAYHRILDHNRNQIFLALLISMLGLYF TLLQASKYFECPTICDGIYGSTFFVAT GFHGLHVIIGSTFLTICWIRQLIHFTS RHHFGLEAAA*YWHFVDVV*LFYVSIY **GSVTGAYHRILDHNRNQIFLALLISM LLGLYFTLLQASKYFECPTICDGIYGS TFFVATGFHGLHVIIGSTFLTICWIRQL ILHFTSRHHFGLEAAA
7400	21301	A	7460	1	222	TILGLYVTLQA*EYKATFTYDGIY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						GSTFFAATGFHGLHDIIGSAFLTICFIR QLIFHFTSEHHFGFEAAA*YWHFVDAT* LCMYVSIY**GSTFFAATGFHGLHDIIG SAFLTICFIRQLIFHFTSEHHFGFEAAA
7401	21302	A	7461	3	246	LNYSLFFHGEANLGTQVLTHPSTTAMY FVHYCQPP*ILYGTINT*PPVVHKNPIK KKKKKKKKKKKKKKKKKKRGGGF
7402	21303	A	7462	2	155	SRSRAALLLELP*ALQTTNLPLIVMSSL LLIIILALSLEYE*LQKGLD*AE
7403	21304	A	7463	1	136	PTRPAPSHLLYCKNIKKLFPSGTANEAL IADI FLRCKKKKFKVK**VLKASBB*N GCKHLHGMH*NSAVCTVPWLKQIMNSD* **KVNTQ*KKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKGGENN*KNIKKLF PSGTANEALIADI FLRCKKKKFKVK
7404	21305	A	7464	166	192	NIN*MWYMHTEVCYSDFKRKEILIHATT WMNLEDIMVSEISQSQDKYCMILHIEY KLYIHM
7405	21306	A	7465	416	55	LFFLRLGYFFLPNIRVFFPLSTLFFFFF VWGGFFFGRRFFPPPPQEVCFFFIF*G IFFFFLFLK*KNMFFFFFLWGPFPFFFF SGAPLFFFFFFFFFFFFFFFFFFFFFLR KANTKKMF
7406	21307	A	7466	295	84	IWGNVTLQLVSCFLCFLPLH*GFFCCC CCLFLFLFVCLFVCFNLNPKSIKCLLP FSLSLGCAEIPSSF
7407	21308	A	7467	142	258	PGTVAHTCNPSTAGGQGRIP*GHEFKT NLANMVKLHLY
7408	21309	A	7468	3	192	PSEYFESPTISDGIYGSTFFVATGFHG LHVIIGSTFLTICFIRQLIFHFTSKHHF GFEEAAA*YWHFVDVV*LFLYVSIY**GS TFFVATGFHGLHVIIGSTFLTICFIRQL IFHFTSKHHFGFEAAA
7409	21310	A	7469	2	110	GRVGKHHFGFEAAA*YWHFVDVV*LFLY VSIY**GS
7410	21311	A	7470	380	8	TPQKRKKLKKAGEGVFPKKKTPPPPP PIFIYFIFFFFFIYFFFFFPQYMSF FYSHIMIQRHFLNF*ESFYSCISILQ*L FKFFSFLGGLIKL
7411	21312	A	7471	1	107	PTRPHHFGFEAAA*YWHFVDVV*LFLYV SIY**GS
7412	21313	A	7472	2	360	VNTLLALLLIMITF*LPQLNGYIEKSTP YECGLDPISPARVPFSIKLFLVAITFL LDLEIALLLPLP*ALQTTNLPLRAMSSL LVVILALGLAYE*LQKGLD*AEWLHSL TQPTNNN
7413	21314	A	7473	423	167	VKVHKCFLPGVAPHAFNPSTLGGRGRI A*AQEFKTSLGNIVRPPSDTCNPVLGL QA
7414	21315	A	7474	1	73	IKPE*YFLFAYTILRSVPNKLGGV
7415	21316	A	7475	131	3	ISWVGAEWLTRVIPAL*EASGVSRGQE IETILANTVKPDAW
7416	21317	A	7476	2	103	PRVRSTGFSSIAHITRDVNYG*IIRYLH ANGAK
7417	21318	A	7477	2	325	NTLLALLLIITF*LPQLIGYIEKSTPY ECGFDPISPARVPFSIKFLVAITFLLE DLEIALLLPLP*ALQTTNLPLIVMSSL LIIILALSLEYE*LQKGLTERDT

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7418	21319	A	7478	423	170	FFSFFFFFFFFFFFFEIDKNVYLIM*C TNPQEKRNLLFCFLVMSPVCITPHTYI CVCVCVIYYIIYIIYIIYIYPPIFSCCD
7419	21320	A	7479	433	50	RVFVVFFFTPEKKTFFFOEIYLFSSFPF L*NFFFSPPKLFFLLGGFAPNFPPPKKV FLKFPPGFFFFSPPFKKKFFFFFFPRFFFA PPRFFF*GPSSFFFFFFFFFFFFFFFFFL TVKPTRGRFGCGQI
7420	21321	A	7480	401	337	FFFFFGKFFFPQEFTVFPPPFKIFFF SLRLFLFWGGGAQFFPPQK*VFFSKFPR WFFPPPLFRKKFFFFFFPG*FLAPQGFFL KGPPPPPPPPPPPPPPPPPPPPPI*VGGR VGNPNPNPTNVLPN
7421	21322	A	7481	1	84	KNFLPLTLALLI*HVSIPITISSIPPQT
7422	21323	A	7482	562	412	LFSFHVSGTMAHTCNPSTLTG*GRIT*G LEFKTSLGNTVRSHRYRKKIA
7423	21324	A	7483	12	233	DIFHFTSKHYFGFEAAA*YWFVDVVR FLYASII*GSLL
7424	21325	A	7484	385	56	GNEFTPCKFNFPYFVLISIFFFPKCLK FF*BIFIIPPPKFLFLPPNFPVLFFF FLFWBFFFSFLWFFFPFFFFFFF FFFFFFFF*KTEFFVNSNFQHTK
7425	21326	A	7485	424	6	FFFFFSGGSLIREDPAGALYDYGR* LVVVVTG*TLFGVGVIVIEIARGNRLCD
7426	21327	A	7486	16	129	FXXRXKLIXKEPSINLE*LYGCPPPYH TFEEPVIKS
7427	21328	A	7487	183	387	IASGLDIFLLLLETGSHSVTOAGVQWH NHDSLQPLRTGLK*SSRRSPRGSDYRV LLCHPGWSAEA
7428	21329	A	7488	351	169	EKKIFFFSPRGYGPPPPFFLKAPPHIFF FFFFFFFFFFFFFRGGGDHKNNFFFF WGFLKNPPLFPFPPRV*I*IFFFFFFFF FFFFFFFFFLGGGGGTIKIFFFFGGF
7429	21330	A	7489	47	212	THASALFL*IRTAYPRFRYDQLIHLL*K NFLPLTLALLI*HVSIPITISSIPPQT
7430	21331	A	7490	98	273	TSGSCCSAHILAFKP*AGMATFITKSL* *CHTHTHTHTHTHTHTMYIYTHMHTY IF
7431	21332	A	7491	70	405	LYGCPPPYHTFEPPVYI*EAFASKRKVL IVEEPSINLE*LYGCPPPYHTFEPPVYI KSRQRKESNPPKLVSQQPHGLHDFKK KKKKKKKKKKGGGPLKKPRGGPNLTGG GKKNFFFFRGGEKKPPGGFWKKTFLGG GKLGTPPPRRF
7432	21333	A	7492	22	208	RSSLPARPTRAVALIIFMI*EAFASKRL VLIVEEPSINLE*LYGCPPPYHTFEPPV YIKSYV
7433	21334	A	7493	2	204	KLPETVKKKKKKKFYSFRSIVMLLLYLF S*SLSFDLLYSLLFFLFLSFYIYSFLC FPLCKTATTEH
7434	21335	A	7494	2	104	TTLLLSRT*NKLT*LTPLIPSTLLSLGG LPPLTG
7435	21336	A	7495	291	160	PRHF*IFVEMGSHYVAQAGLKLVAASN LAWASQSAGVTGVSHGSLITSL
7436	21337	A	7496	422	180	LGAPQGVF*KGPPFPSSSSSSYSSSSSS PS*QNIFNKIFLFCVPVLETESVTQGV QWRDLGSLQLPPGPKRFFTITTH
7437	21338	A	7497	244	296	FFFFFFFFFFFFFFFFFFFFFFFFFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFFFFFFFFFFFFFFFFFFFFFFFG GNF*FYK*LLGNRDGVCLPSSYL
7438	21339	A	7498	1	410	PTRPDQLIHL*KNFLPLTLALLI*HVS IPITISSIPPYT
7439	21340	A	7499	51	478	PQKYTLIMKICIIIPGKGFPRVEMLAGG NENTRCLIEERSYKYHYSLIKLGLOQQC IFSSLLYKYNMIYCLMLCYIIGYIFIFY DMYYRQSVLYYKLYNYVMLI*YIILYL FMCI*KYIYFIFM*YKIFIYLYLY*YK YIFYIYLCVYKNIYTLNINIYLYTY IYININII
7440	21341	A	7500	3	110	FTSKHHFGFEAAA*YWHFVDEV*LFLYV SIY*GS
7441	21342	A	7501	168	327	APCYKATVIKTI*Y*YKHRYTEQWSRTK NPDINPYICGQMIIFLQKSLHKI
7442	21343	A	7502	400	159	NNFSPLRNLQGGFFGLKFFPMGFQAGPPG *GFSFFLRNFFLDVFRGKY*TFGF*DF FYCPSNEVLGEPPLMGGNKPGFP
7443	21344	A	7503	401	257	TSQKKKKKKKTPKKKKKNREKPPKKKR GTRGEPFKTGGGKEKKKPKKKKKKGK PP*PQLVKRGGREKKKNLWKKKGAF*K KKKKKKKNPKKKKKKPGKTPKKKKGDPG GTF
7444	21345	A	7504	44	344	LLASLANLALPPTINLLGELSVLVTTF *SNITLLLTGLNLTALYSLYIFTTTQ WGSILTHINNIPKSF TRENTLMFIHLS PILLLSLNPDITIGFSS
7445	21346	A	7505	286	252	I*FAPHVHGAGLEFLTSDLPASASQSA RITSVSQHAMPVHNIFYSLL
7446	21347	A	7506	3	213	RELPGKRFLLSLSSWD*WRMPSHPA TFCIFCRDEVLPCCPAGLLILVWNLKN CCCYHHHRYYYCY
7447	21348	A	7507	400	20	SLPQKKVSLKLSAVQLVMF*DRFSLC HPGWRA*GQSGVTTASSLRAR*SSCLTW EYRPSPLADFLFW*RRGLPI*PRVVS NS*GOVGLLHQPSKMLKFSSSLPCARPL FFFFNRSTNLRVQS
7448	21349	A	7508	349	227	SDFLTSANPPASAKSFGITGVSHHTRP *PRFLKVNLIYSEMEVYN*ASFRHVD*G GLELLTL*FTHLGLPKLWDYRREPPHPA LTKIFKGKPYIQ
7449	21350	A	7509	371	21	FLVETGFHHVG*AGLEPLASSNLPASAS QTAGITGMSHCAQPNPGSLLNKTMLAVA TEQWGYMWPSVFGHITARPEGKRLSDC LHSDTNVCVVCVCSGLIFVCFETGCRFA LQPG
7450	21351	A	7510	330	14	DKVCSVTQARVQWHDHGSLLFLSSGLRQ SSHLSLLSSWDHRHMPGPMANFFFY**R LRSHYVAQAGLKLASSNPPTLTCQSAG ITGVSHNTWPKALPSVTDLKH
7451	21352	A	7511	417	33	APPCCGGPPKRIFGFSRKRKGPPPPKR FF*KNKPPKGGGKSPPPPKNFPPKKKN LGPKKKSGFWGRFAPPRAPGGVFNFP FKAGGEKFFSRGEINPPRGAGKKKGFFL GKKNTKKKTTPKKKDL
7452	21353	A	7512	81	296	CLREGASHSAAQAGLHWHDHSSSLHP*NP GLRGSSRLNLLSIWYRCVPPSLANFES CLLKILGSPFPKNL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7453	21354	A	7513	412	279	KKYTQGLGVVAHAYNPSTLGSQGRRI* AQFETSLGNTGRPCLH
7454	21355	A	7514	74	126	KI*DWVPKGAPLQGPVF*NSTFRPRVRN RGPPWPRPGPTVWKG*NKKN*PAPRGSN PFFFFPGNPGPFKLKGWPGSS*GSFQNC KKAQAG*APT*KPGPPPPQNKV
7455	21356	A	7515	332	20	GERQVGSYFFMNTERLEFGMTKKF*KWIV SMVAQHSSSISGVVWVRGQELAFPLSPD WQVDYESYTWKLDPGSEETQTLVREYF SWEGAFQHVKGAFNQKIFK
7456	21357	A	7516	1	167	RTRGQRFVTLARIVLIS*HCDLPASASQ SAGITGVSHCTRPGLSFLYTPAKHST
7457	21358	A	7517	2	223	GRMEEMGSHYVA*AGLEFLGASDLPA*A PQRAKILLLLGGHKPGLTILPRLSSNSW PHVKWPRWFLKALGLRG
7458	21359	A	7518	151	476	SLGKFVAFSFSFLK*RRALAVLPRLCS NSWP*AVLLPWLPVRVGIAGMSYHTQPDY HFQARAVAEIILGLVSTQHSSVTGLPVEN SFRAGHGGPRLQSQHFGRLRWADC
7459	21360	A	7519	3	134	CSFRLGAVAHICNVITLGGRGGRIA*AQ EFETCLDNIARPCLY
7460	21361	A	7520	14	219	APSIHGFGFLYTYIHTHTHTHYMYI*V YIHTHIESIKQPLTQLQSNKKANRIVF RTQFMLTCYFMR
7461	21362	A	7521	134	334	RKHSC*IFFNFCFYLSELETRSHYVASTG LDLLASSNPPALASQRARITGMSHHAPP VLTRFKKSLF
7462	21363	A	7522	406	145	FLKTGFSPFGPFVF*TPPPGFPFPPPPP IFGVPGGGPFAPPLFFFPQTKHFPFPL NPPSPPPQGRGFFRGFFLPPPAFFLKTTP FFF
7463	21364	A	7523	3	382	HPQEGGRLTSLE*NTSLRLKKKKKKKK KRGGPFKKNPWGAQI*PGKKKNFLKR GAKKNHLGNFGKKPYFWGGKLAKEPKK N*TFKGGKKFLRGKGKKTTPKWLLKIF FSGFYLLKKIFPPGP
7464	21365	A	7524	319	106	GTRSCSVT*AGVQWHDHSSLQP*TPWLK RSSWLRNRWDYKHEPPCLNNFFFCRDG GLLCHPGWSQSPELK
7465	21366	A	7525	433	228	MQPYNWEVNSSSQLSSARQVTHVLT GNFFIK*ERWDLPLVLPRLVSKSWPQVIF PPWPSKVLKLQV
7466	21367	A	7526	26	351	CRSLVFSLPKPLRFVSILHIQVFSHPD FFFLTGNQTK*RK*TPFIFPA*LFKTPA PKPGMVAHTCSPSYSGGLDGRIA*AQBF RTSLGNKTNFSLGGGRKKKPPSGS
7467	21368	A	7527	438	62	QLSKIHRPPAGGRFFKSGGGFKPFCFVG LPPFGKKANQTPKNPPKKQKPSGGGLS PMGKPP*FPCSMPSDSPGSVSFSRGGVA PAPKDYCPIV*AALIPSKKKKSKPG*V KKGKPNLYSIYNK
7468	21369	A	7528	3	132	FYYL*RRGFVPLPRLVLNSWLQVILLPW PPKVLN*AAHHPHG
7469	21370	A	7529	2	628	FFFLPGVVNRVLLMGRGLGEANSREGRG PSQPRGMHGQLEVRGGRSQDGDWHGTL PPWGRIRYRGAPPTFAAPQAPKPFRLLP M*LPGRPSSCLLPETPALSPLPSAEWGG FKLLTGTSETPGPSGSPSVGSANAQAAG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ATTIVARGHTPCTRGPLDTHASSLRWHAHTRPPRPLAHEGHTHAHPHTPGAWVGEFPFGWGRA
7470	21371	A	7530	63	205	GRPTRPRTRGVKIL*QFHTKPTPGLPTLIALTLLLPISPFILIL
7471	21372	A	7531	390	56	KTFFFNLIATFEAKSVLLFLLFFETGSRSSAQPGVQWHHQSLLQPPL*LKSSCLSLLSN*DYRCAPPCQ*SPCLSLKWCVDYKREPPHPAKESHMQOSYLIYBLYIA
7472	21373	A	7532	543	335	LAAYGGTCLQS*LFSRLRWEDHLSPGVQGCNELQLQHCS PANATE*DPVFKGEKKE RVLVKVFS
7473	21374	A	7533	3	145	WCDHGSLEPRSPGLKQSSCLSLPSNWDH SSEPLHTTSMWNF*IFKFLNLK
7474	21375	A	7534	386	106	SWVTDEITMEI*ECVLNDNSDTPYQNLWDTEKVVLRAKFTALNACMKKSERAIQIRH TCVHTHTHTHTHTHTGSKCLLRKYLIT IQQNIRIN
7475	21376	A	7535	398	2	SLQPLPRVKCFSSPSPPRRWDYRGAPP RGGKFFFFGKKFPPVQGQGF*FLPPGV LAPPPQKGRISGSGSPRPPFFFFFKIR ISYPILAKQLKLCFLKKKKSIQAIKLY HHQKNPITKSSVFVESQRA
7476	21377	A	7536	2	344	HSKCVPAEVTMAYYIRYLSISLLHIL ENIVHFFFFHLY*GPNLFFFYFAGTRL IQRSWK*PMII**VHVQIKREGQIFNK* IFCMIGRG*ITCGQEFETSLVNMVKPC LY
7477	21378	A	7537	116	224	LHTHTHTHTHTHTHTHTQFNKLP*LFIP CGHIPRRY
7478	21379	A	7538	1	383	WHERTHSRITILFQGLTLLPLIAF**L LASLANLVLPPTINLLGELFVLVTFS* SNITLLLTGLNLTALYSLYIPTTQ* GSLTHHINNIPKPLFTRENTLMFIHLSP ILLSLNPDIITGFSS
7479	21380	A	7539	31	332	DNYLSSYSSSGSWRELILASQIRWEP IVDRTPSHRTHHTHTHTHTHTHTV LFRIGPWTHAREPRGHICGN*IRNQSP* KNPRTRGKNLRTPHGW
7480	21381	A	7540	199	15	NNVQIK*QFHTKPTPPLPTLIALTLL LPISPFILIL
7481	21382	A	7541	337	157	AEIVPLNSSLGNRVRHL*MESYSVAQAG VQWHDLGSVQPLPPGFKRFSCLSSW DSRLYFRCHD
7482	21383	A	7542	28	313	RARIGSDQCLSAGTQVVENKSIQSGDFM WNDFRS*SVTRVGVRWRNHGSL*PWIPG LR*SSGFLPNCWDYDRNEVWGGKKEV TCPTVNLOKSQ
7483	21384	A	7543	493	180	GGFRGSWLVRDGGQGVGFCSLPPPPSR VKQFFCLRFPRRWGREGSPRPSYFFFP *EKPRFFFLGRVVLNFLGQGVGPPWPSQ RVGFPLTPGPRASFFFNLI
7484	21385	A	7544	403	426	FF*KFFITFHTLEFFFFFFFFFFF FFFFFFFFLAPPPGGFFFSFYQKIFL KFPQPEKFALPFGGGFF*GKFPQFFF CFLVFFFFFFFLFLENGVSLYCPGRSRTP GLKLSSRLASLRAGITGVSH
7485	21386	A	7545	3	335	RHSDYDPGYST*NILSSEDSLISLTAA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LLMVEMI*EAFAYRRTGLIA*EPSMNLE *LYGCPPPYHTFEEBPGYIKSRLKRKRSN PPKLVSQPHGLHDFKKKKNRGGPF
7486	21387	A	7546	424	140	RRVKFVGGGAPQGPPEKRGVLPKIPREK VFPPPPG*NGPPGPAFKTPPKKKNISS PPPGNWAPPGLLKGPPIFFFFFFFFFFF FFFFFLNPLK
7487	21388	A	7547	2	348	FCHVAQSGGLKLASSDPPTLASQSARIT GMSHHGGLK*GEFLGPSSNKGALLLWRA TWLQSFMKASLFLVKPRPTFVYVFAFV GYRDIYFTASSLIKVIQEGLYTKMKCAP LTL
7488	21389	A	7548	2	90	RKQAYTHNTHTHTHTHT*KKGTGIAH KHTHTHTHTHTLKAQKQIBGGK
7489	21390	A	7549	256	405	CELYSGKEMELVFGLFIFTGVTRLETFF KKECSSFFHSQSRGHLQPSILNEWHI RNPLGLTHFLLL*KTGVABYKNSLNVVH HPFLLSYAVSFLLQGWSFAMLSKLSNS *VQARCLPQSPKVLGLKESPOERTVNVS SIRGKKNSWYLDYLFSQLQGLKLFIRK SVHSSIPRAEGINCNHQY
7490	21391	A	7550	2	362	ILIMNTLLALLLIITTF*LPQLNGYVBK STPVECGFDPISPARVPLCIKFFLAAT FLLYELEIALLLPL*ALQTTNPLIGM SSLLLIIILALSLAYE*LQKGLD*AELK EEQKTLOC
7491	21392	A	7551	1	317	TTFDNSALLFFWDGGEIEFHVSQAGVQ WHNLCSL*POPPGFKQKLILPQIVKENV SKISSQLLFSRVNINISPSQCITPPSL QLARIGIFYAAKIHLTKGLRG
7492	21393	A	7552	479	183	YLFHVHTTASHNSGACTGPTVGDIIVSS TL*SMTEQVTMPASAVSDGTVPVSVRTA SRGSEQAAESMVSEHIEILEHAGELVI ASPEGQLEVQTVIV
7493	21394	A	7553	454	105	KPPWGNKIRPPLFPGRKVPPPRF*NPVR GSPPKK*FVPVGRVLGTGVTPLSPFLK TTPLLLDWPPLSQPPGGVKPENSLYPGK KRFR*PKFPPCPPAWGTRKKPPLQKKKK QVVL
7494	21395	A	7554	439	1	LLKRCVRKDSPPPPQNKIFFFILKKFVFF FAPY*VRKFYFLTAHFGKRPPQIYIFGP PPVFLIFCFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFNKQVFI ERLLCARHCFRPPPEEKTKNKIEAANPN SEGEER
7495	21396	A	7555	323	82	FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFR*AYL VRSPLLFI FVSFY*LI*HVYHRYSVYI ELDVLLTGSKIILI
7496	21397	A	7556	194	412	KMVRTSLGHLVEAKKKKKKKKKKKKKK KKKKKKKKKKKKKDSRGVV*KKFGGG HNRGVKIIFFSLGG
7497	21398	A	7557	414	219	KGFKKLFPFVPF*FFLCPPPIFLKGF* GRKPPPKNPQGGPPFFFEQTTPPLFFF FFFFFFFF
7498	21399	A	7558	377	25	THVGGVFWGKFFFSRRVFFFFHYLIQIL SPPPKRPPPKGTPEG*IFPLFKEINFF FF*DFFFAPPPFFFFFFFFFFFFFFFFF

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
						PPPGYFVLVNGVFFVPGPPGFELPSPS *VAPPASQKGGVSGVSPCRVWVPFFKK KKKLRGVEQRCTMHLVYSKNVPVKPQK KSSIGSL
7514	21415	A	7574	2	383	PRVRSTAFSSIAHITRDVNYG*IIRYLH ANGAKKKKKKKKKKKKKRGALKKKPG GGQKGGGGEKKNFFFKGGEKKKPGGIFE KKTFFGGGEGAHPQKKKTPGGKKKIL RGKGGKKPLYPWGEK
7515	21416	A	7575	402	69	KIFFKNSPLWKISHPPTYRGFFPPFP* NFFFLPGPYFFLGGCSHLGPPPKGFFQ KIPPLGLFLSPFFKKIYLFPPRIFLAPP GVFLKAPPPPPPPPPPPPPPPPPPP
7516	21417	A	7576	1	119	LIHFHTSKHFGFEAAA*VWHFVN*V*L FLYVSIY**GS
7517	21418	A	7577	219	69	NDISANTAIKKFWLKPCKPTTEGWLNT* LYIHLVEYYATLKVCGLDYVR
7518	21419	A	7578	3	287	HASAQNLNGYIEKSTPYERGDPISPARV PFFIKFLLVATIFLLLELEIALLLPLP* ALQTTNLPPLVMPSSLLSIILALRLAYE *LQKGLE*AE
7519	21420	A	7579	10	125	ALQTTNLPPLVVMSSLLLIIL*ALQTT NLPLVVMSSLLLIILTLILAYEGLQKG LN*AE
7520	21421	A	7580	3	299	DAWVRLDFFD*VELPTEARIRIITSQ DVLHS*ADPTLGLKTDAPGRNLQTTFT ATRPVYVYGCSEICGANHSFMPIALBL VPLKI FEIGPVFTL
7521	21422	A	7581	3	116	AFASKRTGLGVEEPSLTLE*LGGGPPP* HTLEBPVNI
7522	21423	A	7582	398	2	RVFPAPKNSLQIFPPLFFFWGSPWKFFF TPFFHFVFWGNFKFNPPFAFLRLPFP GEKIPLVFFFFFTD*NFVENFFFLSLL FFPGFFFFFNM*S*LF*SPANFNV*VTH LFIFMVFFHDFWFSFGPILW
7523	21424	A	7583	288	9	RGSKNLEKNSFPYKVNNGNGSPLEPHL FFSPRGVGPFFFFFEFTRSRSVIQAGVQW HDLSSPPGLK*SSHLISIQSSWDY*RAPP HPANFVYF
7524	21425	A	7584	1	124	RDGGFTMLPRPILLTGLKQSSCISLPK* WDYRCEPLHLASC
7525	21426	A	7585	339	76	THPGHNGISVSPKKKIPRGGGPPLFP PLPRVGGGDSL*PRKGGFN*TKPAPFPS SWGKKKELPFSKKKKKKRKKGSISTPF SRIB
7526	21427	A	7586	205	87	SISLSLSLSHTHTHTHTHTLHSPRCV PQIGLPIISKWAKVELIT*R
7527	21428	A	7587	353	256	PHPSVTTLVTSQQYQDPPPAKRL*LAEG SDDC
7528	21429	A	7588	159	195	QICRHRVHINFLMSGSIMITPPSFLF LNFL*SYVAQAGLKHLSQSDPPASASQS AEIRGMSHNAWPHF*YFVELVHFYINK FVGIELFILTS
7529	21430	A	7589	76	205	RKKPEPEKTCFDNITGNTYPCLSYEH SD*YVNR*LCAR
7530	21431	A	7590	218	20	LSLYLASHLWLKPPHLEWAPSKSSLRL GTVASPCNPSTLGGRGGW*GQESETS LANMAKPCFY

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7531	21432	A	7591	142	12	QIDYYLYLFI*RKGLTLMRLVSNWLH IILLPWPPKVLGLQM
7532	21433	A	7592	2	224	QIIEALLITILLGHYFTLLQA*EYKAP FTISDGIYGSTFFVTGFGHLHGIIGST FLTICYNPQLIFHTSEHKFGLQAAP*Y WLFVDVARLFVPASII**GSLFYPTSL RVLQGSLLHHFRDLRLNIFCNHRLPRT RHYWLVNPHYLLQPTNISLYLRT
7533	21434	A	7593	1	323	HAYGNTLVA*LVVTMTF*LPLVDGYIKK FTPYEGGFEPKSAARVLFSIKVLVAIT FLLSDLQSALLPLP*AVQTTNPLIVM AALLDDIILALSLEYA*LLKGLE
7534	21435	A	7594	1	104	RACVCVCGVCVCLCLLMCVCCVVCV CVFCAC*KMCVCVCCVVCVFCAC
7535	21436	A	7595	383	43	VFISETLCEHVAWSQTTIESLGLGTVAH TLNASTLRG*GRMIA*GO*SKTRGNMD SISSHSQTTIAQSPHLLGRHQPKWCMCVQ AAEAVLKGQVETDASFQIQKIPINSLIN L
7536	21437	A	7596	2	331	WPPTGITPLNPLEGPLLNTGGLLA*GVS MT*AHSLSGENNRNQVIALVITILLGL YFTLLRASEYFESPTISDGVDRSTFFV TTGFGHLHVIIGSTLLSIWFIQILCNF TSKHFGFKAVA*YWLNFYKLVHPPTN M
7537	21438	A	7597	384	23	LFKTKQYRFLPPFPPLKIFFFPLKA*IF LGGFSSHYPFPPKGFPPKSPWF*IPPP YRKKHFCSHTPKNLAPRWF*KRPPHF IFFF**RWGLAMLPRLFNS*QAVALLL QSPEVLGL
7538	21439	A	7598	401	189	RVLPFCFAGNS*TPGLKCTCLGL*KCWD YRRBPCLIRFYLFYFLRQGLAMLP VLNSWP*VTLLP*SP
7539	21440	A	7599	81	368	KCVIYFPLSITLGAKYDFFFFLEKELA FFPQGMQGGNLG*LKPPPLR*RDFFSCL ALPRGGNGRGAPPSPTNFGFLGNGVYP SGPGGFETPDLK
7540	21441	A	7600	264	25	AVEHFQRLFCSHY*NNIVEERLGLVAR TCNCPLEDKAAWIT*RHEFETSLANMV IFCLDIGSKSFLSMRFSRCLLWKL
7541	21442	A	7601	1	196	WEPSLVGETNVNSFNQKYNWPGAVAHT YNAGTLGGQGGWIT*GQLEITLSKKVK PSTYFTNTR
7542	21443	A	7602	315	82	TCTQVFIALFITAKKFKLICPLTDNWIS RVWYVHTMKHISAIKRKAVIHATMWVKL ENIILSEIKOSQKATGCMISFI
7543	21444	A	7603	334	118	PKIKTEGGPPPKNAGGMYK*KKFIILVL AAPHPFPFVFSVFSFYFWFFRFFFFF FFFFFFFFFFFFFLR
7544	21445	A	7604	3	288	DAYTT*NILSSVGSFISLTAVILIIFMI *EASSSSSSPPGGLRPRAFPVRPPGAGL VF*VSVPPDLPCQSLAGLQVLRFMELAR LAPHIRWIIQ
7545	21446	A	7605	354	33	EGRARYTRVPQRFPHLLGIFAPQLGK KKKFSFSKKKKKNQNLGAVSHANNLS TKGG*GRGSRFT*A*EFRTSQKLGTKGN MVKPISTNTFKNERGGAELSOL
7546	21447	A	7606	401	161	YLVSHLLQITLPPALFVVIFFF*DRVLL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CGPGWSAVVWSYCSLCLLGSNSSPCQSL PSSWDYRHLRLWRFLMPRGILCVYV
7547	21448	A	7607	354	50	SGAQDPAGQHGTTPFSQKVPKKVYPAWW CMVVPATQEA*LKKSLEPWRRLRLREA FFVYLGWVLSNGEPPPLGGGGSVFLEAL EKSVGFSSSLGFGWVFFF
7548	21449	A	7608	370	115	TIKNICNSWEVKIPRFTGVWKKLIPATL MDDLEGFKTLVEEPTEDVV*ITGELEVE PENVIEFLQSHDQTSSTDEGLLLMDEQRR W
7549	21450	A	7609	120	358	TTAVYLGHYCQSP*ILNGTVNT*PPVVH KDPILFLTPFCFHASSAMNQLSHISC NSKATPHPLGYQQTYPTPLTVHMT
7550	21451	A	7610	3	164	HE*ASIP*NTHTHTHTHTHTHTHTHFYK EENLSHLWNISCIPLGAHKGGKKMN
7551	21452	A	7611	85	324	FRFFAFFFF*KKISFCPOAGGQGGILPS LDPPFPGLKKFSGLTTPRSWN*GPCPPP GLIGVFLKKRGFPPLVGREPNLWT
7552	21453	A	7612	268	317	FLNCFNPGGGGCSQPKLGPCPPAWGAK *ASLSKKKKKNKN*LSYKAPSYGYKKG
7553	21454	A	7613	101	339	AVPLTMVKIHALWKRVRFRHNSKL*LP CDPAISLVSMYPKEMKSVCLKDVCSPRL ITGELTIAGMWNPNRSMDSYG
7554	21455	A	7614	366	208	LELLTSGDLPASASQSAGITGISHRARP GTLFF*AVNGGGNQVFLFLRLVNLGL
7555	21456	A	7615	30	328	NYCLDPHGETELGTHFLTHPSTRAMVF EPYCOAL*IL*GVINT*PTVLHRNRSHI KAACLCLQARTVVNLQISHINWKY*TTT HPL*YQOTYPALEYI
7556	21457	A	7616	39	159	TPGLKQFFHLGLPRCWDYRHEPPRCPN MYLI*ISF*CV
7557	21458	A	7617	290	91	KMSFLIFFRDMASLCCPGWT*TPGLKQS SCFHLPRSWDHRCTSLHLAVKTFLYYFL KMFYYQNVWH
7558	21459	A	7618	37	246	TQQELVYIYRIDTHTHTHTHTHTHS HTHYWIYTWKHTLKGPKLF*EKTMGST PIISWKERLSLYRS
7559	21460	A	7619	23	190	IPPQFCPFLLSLFT*IDMSCNMCAVC VCVCVYVCVICDMVLLPFCCKLECSK
7560	21461	A	7620	367	2	FFSPKALIFLGGGGPIFPFPKKSFFSKI PPGFFPPLPGFLKPPPPPLF*NPPLKKK NFFFPFPPENWAPPRVFFKGPFPFFFPF FFFFFWSRFLIFPQFFFLNNKIGKK KIFRHLGAG
7561	21462	A	7621	6	25	SVILQSIIFFIATTNLLGLLPHSLTPTT QLSINLAMAIP*AGAEIIGFRSKIKNA LAHFLPQGTPTPLIPILVIETISLLIQ PIALAERLTANITAGHLLMHLIGSTTLA ISTI*LLYNP
7562	21463	A	7622	383	67	AFLNPGKKFPFPGFKRFFCPPPPKKGK NRGPPPRGKIFFFVFVKTFVVGPGG F*ILTSGDPPGQQGGLGGFFFFQIGGT GDLNLSHKSMPPTINTHNG
7563	21464	A	7623	372	35	TGGFWGVFFFFFKQGFPPKSTGGNLGP KNPCPKGPRVSPPPPP*NRGPGGPPPP PGKKFPFFFFFIETGFPHVALAGLEL PGSGNLPTSVSQSAGIPGISTWPNGVFQ
7564	21465	A	7624	287	6	LSGVEWVDHMINICLFFKKLPCCV*KWL

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						YQPVAVAHACNPSTLGGRDRWIPGGQEF KTTCLSLPKRWHRREPLYLAFCPPYNG IGCLLIIGF
7565	21466	A	7625	271	277	NRGKGKTGSLGILEKNPFFGGGPFWANP PP*GLKFWGGVGPKRPPPKRVFFQNSQ GTSFPLPPVLKSGPGLVLKKAPQKEKNI TFQPPGKFGPPRGSLSKRAPPFFFFFFFS LRKSSVIEK
7566	21467	A	7626	2	269	LLGELSVLVC*FPPKHTTFLLTGLSILF TGLYSLYILTQTQWGLSTHHIINLKPLF TPKNTLMFIHLYPILLLSLNPDIKKKK KGGAF
7567	21468	A	7627	397	164	FPPPKKVFQKNPKKKFSPPRVF*TPPP PPFFLPPPKKKKFFFSPPP*IWPPPGIF *KPPPLFFFFFFFFFFFFFK
7568	21469	A	7628	3	324	DGMNVSTLYGATGSGHLDIMGSALLTI WYIRQLLHFTSKHHFGFEAAA*YWHFV DVD*LFLLCGSIY**GSPGGPKFSRGGK IAPVHWGDD
7569	21470	A	7629	2	246	SGLGTTLS*KNISVLLTGLKILVTGLYS VYIFTATQWGLSTHHINKIKP*LTRENT LMFIHLCPILLLSLNPDISYPGFTS
7570	21471	A	7630	112	290	LISGKGQWTQMRPLVLTFTDSFSK*K NPSTLGEQCGRIT*QOELETSLGNIVRP HLY
7571	21472	A	7631	248	2	KVPASGKRPEPHWYPYHAVPGCGRIPAT AIWTQXWYQGFPPALSPRLCSGAISAH CYFGFPGPSDSPASPS*LAGTTGTRP
7572	21473	A	7632	383	106	GWGQCCKPAIPALERPNPQECFRPGVLN QP*PQNKSPFFFFFFKKKKYIYICMVV HAYNPSYSGG*GGRIT*AQKPKTSLNNT VRPHLYKK
7573	21474	A	7633	435	133	YACLGLPKCWDNRHEPPGLANFCIFSKN RGFPISDRVINSWVRVFG*PKPPKMG FQTLVQASLGFLIFLKTGFPFSSQHE EQGWDTSFQHRFFRGK
7574	21475	A	7634	1	209	NAYRIVILCQKLFPLLSGKMNFKTRCW LGMVAHACSPSTLGG*GGRIA*AQEFGT SLGSILRPCHCKK
7575	21476	A	7635	117	495	STSFIDKVLRRHSFLFFSLFFETKCSL TQTGVQWHDGSL*PPPPRFK*FSLG LSSWDYRHAPRPASFFVFLVEMRFHHV GQAGLELLTSGDPPASASQSAGITGMSH HALAHLFYSSGKS
7576	21477	A	7636	1	241	LPGSSDSPTSASQVAGITGMCHHAQLFF FLAF*LIFFNF*FFFGNSFFVFPAGGHW GIGG*LNPPPPGLKRFSCLTLWGG
7577	21478	A	7637	3	93	EAEAGESLEPGDRGCSKLRSCHTTPAWQ QSVTLVSKKETKNTKTSEVPFGVLNLLY KVSINILIFKBIFYQAPLILV*DNPDS TLSSALQPGQSKTVSNKTKQKTVS*PG NRV
7578	21479	A	7638	46	228	GIPHIQPSKSVFNNVHGPGTVAHTRNPN TLEY*GGGIT*GHEFETSLGNIVRLPPP SLQSI
7579	21480	A	7639	1212	1023	KNHSNEWIKKM*YICTMEY*AIRRNEIM AFAAT*MKLETIILSEVTQEWKTKYCMF SLVSGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
7580	21481	A	7640	479	318	AEFLNLGDDGCSEPR*HHCTPAWATRAK FHLKRKKK
7581	21482	A	7641	470	172	RNIRPRENQYPVFMVAFPLIAKNW*QPK CPSSEAMNKLRCIHTTAVLHSSEEQP TDTHNSDLRSIAPSWRSQTRAAHRMI PWHSGKGKTPSTENA
7582	21483	A	7642	2	201	AGAPPPAWLPFCRLISDC*ASNQRDSVG VGPSEPYATVRKYLELLLCQMHHDMCTY RFSIRIVLNL
7583	21484	A	7643	521	385	GGSPLETH*YTSQGGGIPYTDLTGHHP QGRIQEAPKLTHL
7584	21485	A	7644	331	3	DLVPKKGKGGKKTTPRIKKFPPKGEDFF FFTPHYFVVVFWGGAFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFT*DYIIS F*EERFNKFYRCQSTLVQIGHTSNL
7585	21486	A	7645	88	367	HCSFLLGKKKKKKKKKKKKKKKKKK KKKTKKNEYKNLLGGAPP*KPPSGALY KYRRENFIPIFSFERVSKYPPRDLCCKNL FWGGLNIPS
7586	21487	A	7646	378	37	FFFPXFFFFFSPPPXFFFLXFFXPPF XXSFFSLPPLPLXXPPPPPLFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFNI*TI VL
7587	21488	A	7647	34	293	TGIPGVISAIFMI*EAFVSKRKVLIGKK PSINLE*LYGCPPPYHTFEPPVIKSTQ KRKESNPPKLGSSQPHGLHDFKEKKKI IK
7588	21489	A	7648	22	106	KNFLPLTLTL*KNFLPLTLTLI*YGS IPITISSIPPOT
7589	21490	A	7649	1	231	FDRITISKDISK*MVLVSKKKKKKKKK KKKKKKKKKKKKGGGPFKTPGGAPKNP GEEKIIFFFLGGGKNTWGF
7590	21491	A	7650	79	286	VVSRCLVSLRNPCIKTCS*AKKKKKKK KKKKKKKKKKKGGAFLKIPWGGPIFP GGKPPFFFGGGY
7591	21492	A	7651	57	375	SGKSEFHRVPQWPGTGADACNPSTLGGR GRWIT*QGEFETSPQGDPISTKKKKKKR GALLKDSLGGPNLPGFGLKVFSFRGGI LKPTWEFWEGTFILGGEKIGPN
7592	21493	A	7652	3	357	LAFLALSKIHTASIPVSSPSKSPRS KGTKKKKKKKKKKKRGGLKKTLLGGPK INGGKKKKIIFPKGGEKTPGGILEKKL FLGGKMGPNPPKKIKPLGEKKNF*GEK GEKKP
7593	21494	A	7653	113	378	MGAFLNLPFLMGGGNPSGPNGHVWLG GSYLGPGKTPPKKSQKGGPPDL*GRGG QCSPGTKPGGGGKTLGAPPFTKSLPLG LQKK
7594	21495	A	7654	341	147	NFFPSLKPFIFFGGFCPIFPKPKSFFS KIPVVFSSPPF*EKIFFPPPLNFAPP RVFFKGP
7595	21496	A	7655	395	3	FFFFFFFFFFFFRKGSE*FVLFVSPAP SLRG
7596	21497	A	7656	2	162	ESKGYTHTHTHTHIYTHIYTHYTPREH *PKKADVAMLILNKLFPKPRCVALL
7597	21498	A	7657	333	28	LEFFFNFFSYFLFFS*RVWGPERRPPP LKKAV*KFLFLDIFLFFFFFIPLGFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFLEHIRLLMFVTFSSHR
7598	21499	A	7658	1	137	HSSLGDRVRPCLKKKKKKKKKKKKKKKK KKKKKKKKKKKKGGGLF*EKKKKKKKKK KKKKKKKKKKGGGLF
7599	21500	A	7659	236	32	IIFLIKFLVF*FIFI*F*FILTFFYPKR LKILEFFFFFFFFFFFFFFFF*KNFIK NIIYFFIFVLFYLYLKFFIYIKTFLFLKI
7600	21501	A	7660	301	65	KAPPKIFWFFFFVFFVVSFYIFFFFF FLFFFFFFFFFFFFFFFFFFFFWKS LAAT*FLRGFETP*LAYILKTT
7601	21502	A	7661	70	273	KHSPPHKPAD*NTLTKKKKKKKKKKK KKKKKKKKKKKKKKGGGALIKNPWG GPIHRGGEKFFFSFLRRD
7602	21503	A	7662	1	353	ILIINTLLALLIIITFGLPQLSGCLQK STPYEGGSDPISPARGRFSLKGPLQAMT FLL*ELEIAL*PLP*ALQTTNLPLIDM GCLLNIIILCLSLAYE*LP*GLDCSRYP SQRIQ
7603	21504	A	7663	1	131	FIRQLIFHFTSKHHFGPEAAA*YWHFVD VA*LFYVSIY**GS
7604	21505	A	7664	2	192	PLSQSLY*LLAADLILT*IGGQPVSYF FTIIGQVASVLYFTTILILIPTISLIEN KILKWAY
7605	21506	A	7665	356	2	TFFFLSSPGSGSGSPTPARPKKNPPPWG GGLPLFSRRGALFPKNFPWGGYPFFFLF *KKPFFPPPGPQSPVTSFKDVVPPLRM PPPRPHVRPLGLPKKSFSRPRWEKQVKK TKKRAA
7606	21507	A	7666	312	2	GFFFFFFFFFFFFL*DRVLLLLPRLECNG VISAH
7607	21508	A	7667	1	233	FWLSSNAEFDSANSCECLEVQRMIDQD SFPTYHYFDMYVCIV**RSLAVSPGLV SNSWFQAILQPQPQSLGLQE
7608	21509	A	7668	174	295	IFFLEFCGEHSLAVLPRVLNSWTOAIL PPLPP*ILGLQA
7609	21510	A	7669	183	330	NKFKLYWSPVAMAHACNPRTHRGWIT* CEZFETTLANMVNMVKPCLY
7610	21511	A	7670	3	319	TSNTLLALLIIITTF*LPQLNGYIEKST PYESGFDPISPARVPFYIKFFLVAITFL LFDLEIALLLPLP*AVQTTNLPLIVMSS LLIIILPLALAYE*LQGLD
7611	21512	A	7671	1	313	ARGERERERERERERERERESGGGGP TQTDCKGGRNT*RGREIYRESB*DDRPP FLPTYRVNLQRPVGLRLKAGDKTFCL ILTLARDYVWPDYRMKRAHDM
7612	21513	A	7672	3	91	TRRERERDR*REREREREREIFREKNSQ S
7613	21514	A	7673	1	115	DELANLFII*KAGFPVLRLVLNSWLQV ILLPWPPLN
7614	21515	A	7674	3	232	TRRERERERERERERERERERERE RYRE*DRERERERERDCVWGGVISLSR AVALSGAPAVGRQTRERISR
7615	21516	A	7675	1	234	ARGERERERERERERERERERERE REIERERERLTQRERERERGRGVWHAFL AIERG*KPQGGFWWKEERVKKBPGLKLL
7616	21517	A	7676	1	262	ARGERERERERERERERERERERE RERERERERERERERARAPQNL*ERWAH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1. 26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TPPAPGVSLSWREHTRGGPPWKGKREGGW GRLGHPPPSILRAKGG
7617	21518	A	7677	214	2	QQASVAQAGVKWFDLCSLQSMPPRFK*F SCLSLSSWDYGPFPCCAGLHIWRRNVT LALQGLPTTSLALV
7618	21519	A	7678	3	341	HERHELEELIKTLFFFFFRKKNHLCKP GGKKRGPIWFLKKFFSPPQKKPPPPPPF LREIGAMAPQPGGGLLI*NKTPFRPRGQ GGPKPPTPGKPNPPPPPKGNFPL*GPNP QPPGSPTPPPPQKVIFFFEHQA
7619	21520	A	7679	1	357	GTRINTLLALLLIITTF*LPOLTGYIKK STPYECGFDPISPARVPSIKFFLVAIT FLLDLEIALLLPL*ALQTTNPLIDM SSLLLIIITLSLAYE*LQKGLD*TDFY SVGGEAN
7620	21521	A	7680	365	1	PDAQ*HCTNGQSNRLINLLIKALLTTA KIWIQPKCPVDARIKKMQ*IPRMEHPS AIKKEILPSVATWMSLEDIVPSRISQAQ KDKYHTVSCMWNLRMLNAEPEGRFVVR GVQGWGAARA
7621	21522	A	7681	387	3	FFFKKEFCPRKKAKK*NWGPGNLGPRG* KNFPPPPQKRGKKGGPPQGGIILGFL* KKGFPFMGRGSKLWPLGFSPLNPPKRG GKKGEPPPPQKPGGPPPKGLFFFFF FFLRQSLTSPRLLV
7622	21523	A	7682	107	290	ELNKRWGLGAVAHACNPST*ELNKRWG LGAVAHACNPSTLGG*GRWIT*ALEFKI NLDNKARSHLKIKKHQQQKNSGLDA
7623	21524	A	7683	1	348	GTRERKPTWLWYHRERGMERDCSCVPGS SGISESRVWVQVGMVYPALIIYLCLEPK YLVISEFSAPFRIWFLGLSVVAHTCNPS NLGGQGGRI*SQEFKTNLANIVRPHLF FFLF
7624	21525	A	7684	364	77	GGPSIFPRLALLGGGGPGGPPLPGRNFS FFNFVKKGVFFPPGVFPPLPPGVLPFP PPFWAPG*PRPPNFFLGAPGFFPFFFLG GGFFPVAPGGV
7625	21526	A	7685	3	24	HEETIIQVKREPVE*KKIFANPTFNKGL TSEIYKKQLNRKKPNPI*KQSSK
7626	21527	A	7686	1	125	GTRPGMPGTYSNPDTYTA*KIISIGS FISKTAQPGPWE
7627	21528	A	7687	459	298	LSLPSSWNHMCALPHPASFFL*ROGLAL LPRLVSKSWAQVMLLPWPSKVLGLQV
7628	21529	A	7688	374	248	FPHHNVEHIVRPLSPRYPIISHVTCTY RSRWP*ASEGSQKK
7629	21530	A	7689	284	163	GTVAHTCNLSTLRGRGGWIT*GQEDTS PAWPKVLGLQA
7630	21531	A	7690	83	255	KVDYVSIKSEFF*DRVSLYHPS*GTVAR S*LTTTPNPGIKQSTCPTVPSSWDYRHV LPLPTRTIFSVPTQSLATILI*ITLNL INLGIHFL
7631	21532	A	7691	3	193	HERLDPADFSFNFFSVDVGLAMFPRLVL NS*HQVILLWPLTVLDYRHELLRPWAG FYLNFT
7632	21533	A	7692	1	364	NFKSFFP*LFYLYHLLFFGFGFLFFFLI KLGSFLFINFSKKSVL*FTNWIYFSVLY FTDFCFIFIISFFGFSLIYFIIAVFPLK FIGFILSFI*ITVFYQQAQWLTPVIPIL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Methiod	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WVAEVRGSL
7633	21534	A	7693	370	151	GKKYSVASPGKLNPPQGFCKTAPPPFF FFLK*RCGFTMLPRLVLNPPQGILPPQ PPKVLGLQVLRHHIWL
7634	21535	A	7694	3	373	WPGYTLNQAYAKIHFTIIFIGANLTFPP QHFLGLSGMPRRYSDYPDAYTT*NISS AGSFISITAVILIIFMI*EAFASKRKVL IVEEPSQSAGITGVSHCARAEYLFIDRR DGLSLCWPGWT
7635	21536	A	7695	406	394	KFF*KKFLFPPTPTFLLEACLFLLPPI KGFLFKYIAPGIKTPPPKKEKFFSSLKV LFSPPYFFFI PPPPI FFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFF ECWRL*W*FYFFFKESPHCIP
7636	21537	A	7696	2	334	ILINNTFLALLLLITFWVPQLAGYIKK STPYECGFDPISPARVPSIKFFLAIT FLLFDLEIALLLPLP*ALQTTNPLIVM ASLLLIILALSLAYE*LQGLD*AE
7637	21538	A	7697	2	95	LNLTIYIILTTTAFLLNLNSSTTTLL SRT*NKLT*LTIIYIILTTTAFLLNLNS STTTLLSRT
7638	21539	A	7698	423	326	RQCLTMLPRLVSNS*SQVILLPWPLKVL GSQA
7639	21540	A	7699	400	32	FHKEYESYFFSPNQPFPPFFPHR*NFY VGVLKKQPPKKKFFLLPTPERFFPFL *KKNIFFFP*YFFPLVIFFL*PPPLFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFSSNSFFPY
7640	21541	A	7700	125	407	FINFSSTFVVRPTTCNMQKHTPIARTKD LCITIFFFLEKNFLFVPQVGGQGGILG *LKILLRG*KQFSCFTLEGRWTNGGIPP PPKNFLKKFF
7641	21542	A	7701	50	225	PWNMVKMSCWLGVAVHCNPSTLGGRGR RIA*AQEFETS*VTQ*DPVSVIKRRKN FK
7642	21543	A	7702	2	146	EIALLLPLP*ALQTTNPLIVMSSLLLI IILALSLAYE*LQGLD*AE
7643	21544	A	7703	1	93	ILIINTLLALLLLIMTMGLPQPKGYIKK STP*ECGFDPISPARVPSIKIFLIAIT FLLFDLEIALLLPLP*ALQTTNPLIVM ASLLLIILSLSLAYE*LQGLD*ALLL LIMTMGLPQPKGYIKKSTP
7644	21545	A	7704	2	112	GRVGKHHFGFEAAA*YWHFVDVG*LFLY VSIY**GS
7645	21546	A	7705	1	325	TAGQFLPKLSILLSYNPAITFLGIYPKI LKTIVYMKCTCTWPIAALFIVQTWKQQ SKLWYIQTIKYYSVLK*NELSSYENTSK KLRCILLRERSQYKKPPYFLIPTM
7646	21547	A	7706	2	169	SRSRAGTLAI*TNLPCTLMITILIVL TILEIAGALIQAYVFTLVVSLYLDST
7647	21548	A	7707	263	346	MLINVPLGLLFVGVILSKESPSVDQGGV QWINLFSMQPPPTGFK*FSCLEA*ASDN LSPHEQYRLALSFLKLT
7648	21549	A	7708	343	163	PKEF**RQGFHVQAGFKLLRSGNPPP SASQNGKITGVNPLAWQTNNISPPMAP
7649	21550	A	7709	459	144	FWPGASSHAFDPTTLGGRGGRIA*AEHF KTLGNIVRPPSDTCNPKVLGLLA
7650	21551	A	7710	2	83	NFLELTALLI*YVSTPITISSIPPQT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M ethi od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=-possible nucleotide deletion, \=possible nucleotide insertion)
7651	21552	A	7711	19	181	KYVHTKACT*MFISSLFIITKNWKQPIF SSIGE*VNKT*YIHTMEYLLFRNKRK
7652	21553	A	7712	392	49	SDIFNSDIFSHY*CSVF*SYLAYNRYLS FL*LFLEFIYSYP*IDHAFHCPLHPVSS FWLDFFLFIFSFFLFSYFYSFYF*FYF *FIFNFIFNLFFILFYF*FSFFSKCLKF PC
7653	21554	A	7713	334	208	FFF*EWVLTTLPRVLNPOAPAILLPWP PKVLGFTGVSHIKI
7654	21555	A	7714	2	408	WNGMEWNGLKWNRLERYGMQWNGLEWNR TE*TRMVWNAMEWTRIELNGLEWNGMEC NGMHLNGLEWNGMERNGTDPWNGTDP WNGTDPWNGTEWNGMEWNEVDSNGMEW NGIDSNEMGWTRMEWNGMESTRV
7655	21556	A	7715	362	223	VWVFMPIIPTLWEAEVGG*LEPRSSKPA WATWQDAIPKKKFKHQHP
7656	21557	A	7716	2	335	LIVIINTLLALLLIITF*LPQLNGYIE KSTPYECGFDPISPARVPSIKIFLVAI TFLLFDLEIALLLPL*ALQTTNLPLIA MSSLLLIILALSAYE*LQKGLD*AE
7657	21558	A	7717	2	142	SITL*LPQLNGYIEKTPPYECGFEPICP ARVPLSIKFFLEAITFLLFDLEIALLLP LP*ALQTDLDPLIVMTSLLLIITLTL AYE*LQKGS*AYMPRPFPVHKILLRS YLLLI
7658	21559	A	7718	6	92	FFFAAA*YWHFVNVV*LPLYVSIY*GS
7659	21560	A	7719	417	164	PLEPLISGRGLPQIAPPPKGSPPKSPR WFFFFPP*KKKNYPPPPKILPPPGFF* NPPPPPPPPPPPPPIFFYFFKTALPL
7660	21561	A	7720	25	401	TENS*DPNWD*IPHYA*P*TSTVKKKK KKKKKKKKKKKKGGGLIKKFRGGPKY TGGGKIIFFFFMGGKKKPLGDFLKNFF LGGGNLGKHPKKLSLQKKKNFKGRGG KKTPLCRRGKKFS
7661	21562	A	7721	388	2	APPPFFYFFFIFFFYFLGVGFSFK*N SKVFWISNFKKILRVFICSLEKGINPF LEKCFYMFFFVAFIIRLNFSLOAKFFL LNFALLPFPEIFFFPFFFPQIEDFW HPYIEQVYQLSLFSL
7662	21563	A	7722	389	71	FFLPHQKQVFPFPFKIFFFSSRVFFF WGWQAQKPPPKKFFFLKTPPGFPLPPP *KKKFFFSRPFPLPPPGFFFKPPPNF FFFFFFFFFFFFFFFFFLN
7663	21564	A	7723	77	220	TPRRGWAYWLPAYPAILEA*AGGLLEP KSLRSTWPTWRNSISPKRK
7664	21565	A	7724	16	258	ISSFVKRRSFAMFRLVLSNWPVLP PRPPE*LGLQACTTFSNFFDGIPLRP LKEDVTARDQREILYVFALFYGGGA
7665	21566	A	7725	353	111	IFGAGPRFVFKAGGQGANRSLSLKFFPG NKWSFFPSKKEWGRG*PPRPFFFFFF FFIREGVSLCCQGSQIPGLKQSS
7666	21567	A	7726	2	185	MSMGHTRLSSAWTGKPPLSVEDDFEKLI WEISGGKLEAEIDLDPGKDEDDLLELS *MIDT
7667	21568	A	7727	346	143	SOAFLYLESFLLLLLY*FLFFEMESH VTQDRVQWRHLSSLQPLPPRFQPSRLT LPSSWEAEVGG
7668	21569	A	7728	411	221	NLRPPGSSYSPASAS*LAGIPGARHHTQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LIFAFLEILKLNLAFLYLIPKPNITYYL PNCYINI
7669	21570	A	7729	2	303	AAASTNMLLFGLGRHLVVEWLGHMVGLI FTFKLPLNQAGRRGSHL*FQHFGQRWE DHLRSRVQDHPQHSKTPSSLOKNKMSI ESNLLNIHKLFFSTGRM
7670	21571	A	7730	67	65	SICEYCFVSSVFLKRLFSVMQAFSLEG CVSCQS*AFLQHYLFKKLYFLY*WGLTM LSRLVLNTWQVIHLPPWPKVLGL*APC GNEA
7671	21572	A	7731	354	238	QSILDDVAMVLD*QAEVFIVKMWRLLIY VHEAKKIGLVK
7672	21573	A	7732	33	186	RGALAVLSRLILTPGLKESSCLDLPKGW DYRWEPPRPGCF*LMVLVLSF
7673	21574	A	7733	1	181	VNAGADCSSIGGVPLQHKKCHGKDYEP RGITTLERSYVBETTEHLVSKSK*PLRA QINL
7674	21575	A	7734	336	80	HKLKEPPGVFPVFPFKNLEFGPGPPKPF FKKAFSPILSFFFGKIFKIPFRGENFA P*NFGKNS*KPRFSPPPKKKGPPFFFF F
7675	21576	A	7735	2	163	TPVSTGTPVPTLT*VPSPIIFPVSEKWA GCLHLCNFTCTELRLTSLLTIRS
7676	21577	A	7736	87	258	KAPSVCLFSALLMLLRMSARTSVCTVRP LSPS*AVISPVTCYTTSRWPEATEDSQK
7677	21578	A	7737	1	103	LDKGIYMTLQPSKLEPKLEANVEIREH MLENSSRP*RDLYDSAAFARTKARSKC RDKRAHVGEFF
7678	21579	A	7738	193	300	GGLPPPPPPFFFLKKRGFPWVTRGGPN PPPLEMGGPTPPKGWNYGGPPP*FHPF GGVGPPISKGGGLGPPRVTTQKKPLFFKK KKKKNNGGGKPPYPSPFLGGVKQKGVNP KGGGSKPKFPPPPPPGGKKKKPFLKKK KKKK
7679	21580	A	7739	150	17	GRVAQVWMLMHAIPAL*KAEAGRSLEPR SWTPDWGTWHLPISTK
7680	21581	A	7740	1	358	SPPRPPPPPPPPPKKFKKLENPPPPPK NPQKQNPPTKTKKSPTTTPKKKPKIGT PPQTPKKINCS*KKQNNPENKKGLNYP NKPNNHPAPPKEPKQREKPLVPTKKKKG PSPKKKK
7681	21582	A	7741	235	147	F*FFLGDEISLCCPGWSLTPGLEQASCP GLPRRWNYRCEPPHSVKTI
7682	21583	A	7742	131	12	AASTYGO*FKICGAILRLMPIVIEFIPL KILQIGPVFTL
7683	21584	A	7743	1	184	NQYPWCFCNHSMSGESKTLNRSGMVAH TCNPSTLGGQGGRIIT*A*GSKSSLGDKV RPHLY
7684	21585	A	7744	347	202	SLFVETGYHYVD*AYLELLASGSPASA SQSFGISSVSLCTQPMFQFE
7685	21586	A	7745	138	263	KKRKTYIHTKTCM*MFIAALFIRVRKWK QSKCHSADEWINKF*YIKICLSIHQLND IWIATF
7686	21587	A	7746	358	169	AAAVAERTONTTEKTEDLVGLWIKKVTY WPGVVAHVCNPITLGGRGWIT*GQEIE TSLPTRR
7687	21588	A	7747	78	346	AIQMLRNQVKIKLPKSPVEIIPFKIVPQ FQVQKIKSQNNFLLLFQESQIFATSTG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SVRPLSPS*AIISPVTCTYTSRWPEVTEKSQKK
7688	21589	A	7748	222	98	KKKARHGLGAVAHACNPSTLGGQGORIT*VQEANIVRTCLY
7689	21590	A	7749	314	52	LNNVDLQFFLGPRKKRNLDSSLFVSAEEVRLMYCFNKLAILHYF*FSNKFIVFV*KFGHLLDENMGSKFDNIGMNAMANKDNASK
7690	21591	A	7750	371	216	YHTHTHTHTHTHTQIPSLPLNLEGPVGYLLSCGSLHLKNLW*KCMRKERKK
7691	21592	A	7751	3	238	FLIQTFGHHVSQAGWELLR*GNLPALAFQSAGITGMSYLCVAESLYLLPPLKILCSSLLTSLSPYDTWKVALLCSYTV
7692	21593	A	7752	2	247	NSDIFDIYIIQYIFLIYLIYIIQYIYLI*VFLIIFPKFTLK*EFIFISLSISFRLAFIVYRDVILLFLFFFS*NFVGDSIS
7693	21594	A	7753	359	2	TLKIRPLLYLPLFFPPPP*KKKIFFPPPGGGKGV*SGFYLMGRGTSLFFKRFFLYPPKEGGLRGSPPPPSFFFFFKRGFPFLARGV*KKGPQGTPLPWLPKSLGLRG
7694	21595	A	7754	3	174	CSVIQAGGQWCGHSSLP*IPGINQSSYLSFPSSWDYRHATMPS*FLFFIEIKMLQ
7695	21596	A	7755	292	219	IWPLSHVHNSPLTHSPSQVDQGLFTLLPCLSGMYVQFPLAEMPFISSLLLENACLSLCEGSEAQKPLLWEGLSYLPPLNQLPLCL*LCVCISGGVCRCILMCILGVCVCMHVCVSVCPCTHTLAQETKGC
7696	21597	A	7756	2	195	VALMADGAIDTESNDYGAFMPLGIERGLDRIWEMPELWLRPNFEFCMTD*PCIQHAPSVSCGLA
7697	21598	A	7757	4	280	DHIVDMITPSFTRRTIAVF*DLNLYIVI RGHITSILKPNKNLKLWYIYTYEYSSAL KQNEILIHATIWINLENMQDEINQTKD IYCTISLI
7698	21599	A	7758	352	107	FLTRASRGHNGETIVTSWPGAVAHVCNPSSLGRRRWIT*GQEFKTSLANMVITTFISKNSNRFLSQFPISLRPTHYKVL
7699	21600	A	7759	92	4	RPSRRRGWTA*GQEFKTS LGNMVKPCLY
7700	21601	A	7760	92	4	RPRRRRGWTA*GQEFKTS LGNMVKPCLY
7701	21602	A	7761	328	124	PLFSFLFFPPPPPPPPPPRRRDGVLPCCPGWS*TPGLKLSSSLCLPKCWNYKHEPLHTAHNF
7702	21603	A	7762	1	167	VDSTDKRPGAVAHNYPSTVSGQGQIT*GKFNPSLANTVKLFKKKKRKRGLF
7703	21604	A	7763	309	226	RPRRRLTSLPRL*CSGAISAHCKLRLEPG
7704	21605	A	7764	349	7	QVFCFLFFVCFSSIFMTFNE*QGLKVTSGISSNVY*FLLIWILGKITQDIGRCFSEYGSPEQHNGLIVRNASSRLGVVAHTCN PITLGG*GGWIT*GEGFETSLANMGKPLLY
7705	21606	A	7765	43	339	FFFFLFFFFFIIFLLSFFF*DHFFVSLFISNFVFLFPFIIFTVFOAHLFICLLFFPICMFLNLFPNPNFYFYPPLFFYL LFFFFG*FFNHLFYL
7706	21607	A	7766	352	102	HTSCLIIKSSLSKMNISCVSSSISFFF*FILIEIGSR*VVQAGLQLLGSTDP PASA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SQSARITGLSHHAQLSSTSLVVENVW
7707	21608	A	7767	346	90	TPPSSFFSFPPFFSFIPFRFFFSNR DRVLVCYLGS*TPELK*SSQFGLPKCW DFRCGPPCLTSTAFYISITVNFSPNCY S
7708	21609	A	7768	278	87	AASTGVGPSEPSAGYYLLVCRLLRSLEK CSIRVGVT*FSRCHLSPLSLTRKNSLT PCASRV
7709	21610	A	7769	5	272	AVVHPINESCVLNIGKDSCLLY*LFEKK KKKKKKKKKKKKKKKKKKHXYE*FNTFP G VARKINLFLCTIQVDAGGTLWGGGPPI FFFFL
7710	21611	A	7770	198	33	QRQSRQCRAWLGMVAHAYNPGLTGG*D RRTT*GQEFKTSLGNIVRPYLYEKM
7711	21612	A	7771	97	410	A*WLMPIVPIIWEVKVVRLLPEGLRPS WATWRKP
7712	21613	A	7772	5	415	ILCVYLHFGVTHPVL*YMHFLPLTLA LLI*YVSIPITISSIPPYT
7713	21614	A	7773	1	342	VVRVTSCHSG*AAAYAT*YILSAEGSFF PLTEELLI*FMKREAPT*KR*VLIHHP SINLD*LYGCPTPYHTFPDPVYLSKRR RRDSHPKLASRLPHVLHDFKKKKGG RF
7714	21615	A	7774	398	122	SPPPPFPSSPSFFLPPSSSFFLFFLFF FFFFFFFFFFFCD*VSLC CPA*SQTPGLK*YSYHGLEKFWNYWHRP PCLAYFL
7715	21616	A	7775	1	336	FNFLIIIIEMESRSVSAHCKLSLPGSS NSSASASRVAGSRGAHHHTWLFFFFFF F*KKKGAPPGGGGFLTLKKKNPPPRAP QGGINGGTTPRPNQGGKFFPWGKKKF
7716	21617	A	7776	1456	1232	FAIESHCVTQAGVQWNCNLASLQSPTEF K*FSCGLPSSWDYRCVPHANFYIFS RDRVSPCWPGWSKTPDLK
7717	21618	A	7777	400	2	NTEFPYGPPIISLGM*P*EMETIYIPRK P CTQMFLEVLFTIAKK*KKPKRS*LING* ILVPLMEYYSATKRPDMHTKNVDI GNIILSERRQM*KTHIVYSIHRASCTAE VRIKVSYKRAATWIKSILIA
7718	21619	A	7778	360	218	PYLANF*NLL*RWHLNMLPRPDSNSWPQ VILSLWPPRVLG*QRGGRVEQRGARGNW MSKCEGGDCLCWAGA
7719	21620	A	7779	1	372	FEVRSCSAHAGVQWHDHGFELGSSD DPSVSASCISRTGASHCTQG*L*LLTK VL*VSACLSVNTLRLTSLKSDTFLGS RSKLSLGSLSQTYISPSRHFQLLCFR SLFPRFLVKHKK
7720	21621	A	7780	372	219	ATSLLSYFKLPQPPQSSATTTIISQ*S STSRQDLPAKRLELTEGSDDP
7721	21622	A	7781	358	145	IKNIHDSWEDVKISTLTRV*KELIPVLT DNSEGLKTSM*EVTAEVVEIARELELEV EPKDVLVQFHDITNR
7722	21623	A	7782	317	146	GRVDCCKPFYRFQMLLVRLGMVAHVCNP STLGGRGWIP*QGEFKASVSRMPRPHL Y
7723	21624	A	7783	13	186	DRVSITQTSWAHPPTSAS*VAWTTGMHH HTWLNPFVVFVEMGFHHVGVQVIRLPLLS WK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7724	21625	A	7784	339	221	KWDLAMLARLVSNWLGSSSYLSL*NCW DYGSEPLCPAL
7725	21626	A	7785	355	3	FGNSGRVDLFFFFFFFLDRVSLCCPGCSA VTNLEVHHLSALQPQTGPKPSSHLSLS SWDYRRVPPHPS*GLF**GK*YSITQLR FLNLHLESGLRSLPKPVASTVRIRTQS GLGLX
7726	21627	A	7786	1	201	QQFSHVFRLLFQFSFSCQEPSPSHIQPG VCTRNTKVSQAW*CVPVIPANREAEETGE SLEPGRRSTRP
7727	21628	A	7787	270	1	RPRRHVPCVLMGLPKCPGLPHTLTTLTLP YTLTPSPTRSLGPPECK*SFHLSFPSS WDYRRMPQRLANFCRGRILLCPDWSSS PGLQOS
7728	21629	A	7788	229	2	DGWVRINWAQPGTVAHAYNISNLGGRGR RIT*QGEFKTSLTNMEKPCLYSDHEVRS LRPARPTWRNPISKNTKM
7729	21630	A	7789	118	263	CSKSYWPDVAVVHTCNFSTLGGQDGIWA *AQEFKTSIGNIARPPISVF
7730	21631	A	7790	246	359	TFIFSETRSHSVTQAGV*WHDHGSLLQ* PPWAQVILSC
7731	21632	A	7791	70	102	AA*SRLTATSLSRVQAIPLPQPPEQLGG QGGRI
7732	21633	A	7792	7	312	FLDFQLRLHSNSYCEDKGVDFDSEIYEIC IVLICKK*RKFLNQKKKKKKKPKGLI* KKKKNSQKKWDFPWLPPNPETKNSLFL PKEFLWLKTKPPFPLTLT
7733	21634	A	7793	1	341	IKPE*YLLFAYTLRSVFNKLGVLALL LSILILAIPIILHISKRRSIIFRPLSRS LY*LLAADLLILT*IGGQPARYPFTIIG QVASVLYFTTILILIPTISLSENKVLW A
7734	21635	A	7794	1	143	YGSTFFVATGFHGLHVIIGSTFLTICFI RQLIFHFTSKHHFGFEAAA*YWHFVDVV *LFLYVSIY**GSTFFVATGFHGLHVI GSTFLTICFIQRLIFHFTSKHHFGFEAA A
7735	21636	A	7795	2	257	KWAIIEEFTKNNSLIPTIATITLLNL YFYLRLIYSTSITLLPISNNVKK*QFE HTKPTPFLPTLIALTTLLPISPFIIL L
7736	21637	A	7796	22	326	RDASDCSFQNLFPVPLWVEK*MVFLTKK KKKKKKKKKKKKKKKKGGGPKKNSWG AKIIPGKKKIIFFFLEGQKKLWGFKK KPLFWGKKRPNPPKKN
7737	21638	A	7797	506	281	RGAN*NRSGCGKRHEERERERERERE RERERERERESRPPKQRERETEIQ TSLTSLAPPPTCVF
7738	21639	A	7798	435	336	MRSNIHFFSHTHTHTHTHTF*ILKQH TFSK
7739	21640	A	7799	411	106	RNPPLFFSPPLQRGGFPIYWGPFRPF PPPL*KTPEKLKIGAPKKKKPPPPG EKMVSF*PPPPPPPPFLRRPPLPSP GGGFWGHFRGPPPPPGV
7740	21641	A	7800	2	296	FVPSTANWCFFLWSVF*IGGSNYFFVHR SYSQAGVDLIFIRLANTISNLSFI**RG GLAMLPRVLLETRAQTILHSWPPKVLGL QVWATVPSFQFLKN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7741	21642	A	7801	344	105	PGFFFFPPPGKRGFFPKPFFLGTGPGFFP PPLF*NPAP*FFFWAPKKKIFSPPPPGK KIFLLKGPPLPFFFFFFFFFFFFF
7742	21643	A	7802	68	216	VHTIAKIWKQPQCPSMDD*IKNMYLYT VE*YSVLKEREILLYWGHYAM
7743	21644	A	7803	407	3	GFIH*FPLFSGYTLDTYAKIHFTIIFI GVNLAFFPQHFLGLSGMPRRYSYDPDAY PT*NILSSVGSFISLTAVILIIIFI*BA FASKRKVLIVEEPSINLEWLYGCPPPYH TFEEAVYIKSRQKRKESNPPMY
7744	21645	A	7804	2	156	THRRITILSQGL*TLPLIAF**LLASL ANKKKKKKKRGPGPKKFPWGAKE
7745	21646	A	7805	2	309	THSRITILSQGL*TLPLIAF**LLASL ANKKKKKKKKGAPLKKIPGGAKIKRGME IKNFSQKGGEKKTQRGIFGKKPYLGGGQ NWEKLPKKFKGLGKKNF
7746	21647	A	7806	110	362	TLSDLERLMLKAVSHFLMIDLEK*CV LKNQSSKKKKKKKKKKKKKKKKKKKK KKKKKGGLLKNWGGPNFPGGEKIFFF FFRGGF
7747	21648	A	7807	295	108	KQRGFVFFFFEMESRSVVQARVQWCNL SSL*PPPLGFKQFSCLRIVYRKDSLSPN KPRLLP
7748	21649	A	7808	2	142	GSTFFVATGFHGLHVIIGSTFLTICFIR QLIFHTSKHHFGFEAAA*YWHFVDVV* LFLYVSIY**GSTFFVATGFHGLHVIIG STFLTICFIRQLIFHTSKHHFGFEAAA
7749	21650	A	7809	390	2	PASLLHCG*ISDCCASNE*GSVGLGPSE PGAGYNLLVCHLLRPLEKCSIRVGVTRF SRCCLSPLPLDRKGNLTPCTSQVRQCL ALLQLTLGALHPVSCCTHCPTISGEMNPV SQLEMOKSPIFCVTHAG
7750	21651	A	7810	1	157	FLHFGQAALLLTSGDPPASAS*SAGIT GVSHRAQLVCTFITIYVFLKNSSY
7751	21652	A	7811	368	44	QNFPFPKKRLPPQPPLFFFLVPSFKGEG FFFFLGRGFFFSQAQRALL*FIYFIFFF FFFSFFFFLYFSISPDCKGDTHTDLLL GVSWWTRSLPLWIARHNMHKVVGW
7752	21653	A	7812	400	80	PQNSFSPPGIGGFFPPPL*NFFFSPKA FFFLGGFSPPFPKPSFFFKIPPGFPP SPPLKKKIFFFPFPFLAPPRFFFKAPP PPPPPPPPPPPPPPFFKYFRHI
7753	21654	A	7813	119	230	SEEFETSLRCIVIPSL*KKKKKKKKKKK KKKKKKKKKKKK
7754	21655	A	7814	3	412	HEQEH*LLLP**PLAIT*VISTLAETN RTPFDLAEGETELDSGFNIEYAAGPFAL LFIGEYTDIIIRNTLTITIFLGTIDYDAL SPELYTTYFVTKTLLTSLFL*MRTGY RFRYDQLIHLL*KNFLPLSLALLI
7755	21656	A	7815	1	183	LRRLERLSEFSTRRERERERERERERERD TRIDIYIVSQKRKKYIV*IRNIFVYHA EFSKR
7756	21657	A	7816	484	97	QPRTPDLK*FACGLPKCWDYRHKPPCL ASDGNHS*SSPGLLVLSASVSPGHMS PSQQTSPWVSEESLLGRVPGFLYFPV DAPGPGAWLAHVQAVLKLGSSDPPVL PSQSAGFAGLSNCAWPW
7757	21658	A	7817	2	219	ADRLRNS*EA*EREREREREREREREPEY

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						PPSHIYTDNRH*MRHEERTLFLWGSGE VRDAAPWVSHIPNTAL
7758	21659	A	7818	190	292	NSHLIFPWTKVFFMS*CTYNLVLPSEK KFYSHA
7759	21660	A	7819	498	139	RRAATPAPAAAEPFPLQRP*PFSEPPD TQDARGRRRGEDPGNSPFHPNDRQPS RALCSTPRMHLRWIGPAFFLMTSLSVSG AVIPRNGGPGGVSSGPCLLQLLQCGAGS STIRKIPS
7760	21661	A	7820	489	330	ELGFLHVPQAGLELLS*SNPPASASLPT SWDYRHDHRTGHHPGIYDSKMCIF
7761	21662	A	7821	490	260	FFLXNXFXFFFXFXFXFXFXFXFXFXFX FFXXFFFFFXFFFXFFFXFFFXFFFXFF FFFFFFFFFFFFFFFFFLY
7762	21663	A	7822	493	482	VGQAGLKRLTSGDLPASASQSAVITGVS HRARPIMYFRYVQ*AKGSHV*RWY
7763	21664	A	7823	456	121	ASFFPIQYKGLGGATPPQEGGCG*GIPY KWGYKRRPGGPHGSGKRPTQ*KKSYFI NVLVLFYLRDKGLAIPTLVSNWAQVIL PPWPPKVLGLQTRVTVPGONILKENMFF
7764	21665	A	7824	294	457	LCIGFVILISYFNIMENWYCRPGTVAHT CNPSTLGG*GRQITRSRDRDHPGQHG
7765	21666	A	7825	26	235	SVVWNSQTGNKVKFTISW*IDKQRCIH LMEYSAIKRNEVLINATTWINLNTIK LSKRSQTLKSNTL
7766	21667	A	7826	30	303	SYVSVEFFPGSSGPTLPSPWHQTPRTYL NSVASAINLTQCPH*PEKKKKKKKKKKK KKKKKKKKKKKKKGAPKKKG*KTPK KTPGGF
7767	21668	A	7827	464	21	REPPHPAPADILILHFWPLEL*ELISVV LNTRCVVICDDTPRKLTCQMPRLLLQT EPL*VLFSNLGSPGSLSKS*MGLVNFPC KGTDSRSFSLFVAVFCLEL*RWGLAMLH RLVLNCWPQVILPPPPPKLLGLQVEATT HEFHGTE
7768	21669	A	7828	372	205	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFKKFFI
7769	21670	A	7829	463	313	DIYPERNSKIMSFAATWMKLEAIIK* LKNRKPNIVCTHL
7770	21671	A	7830	449	266	VVQMRFLHVGQAGL*LLPSGDPRASVQ SAWITGVSHHAQRSIFFKRNNDCDRPD NTECT
7771	21672	A	7831	480	148	IELRLSHGAAEFHPRPREWYGFVKLKER DFYPRIIYPAKIIIRHEGEMKTFPDKQT LRHFINTRPVLQEMLKVKVHQSEIKGC** ATNNHLKVKKKKNSLGN
7772	21673	A	7832	23	131	QRGNSKGYHLKMIQEEIRKLEEEKNQ EGEIIHFYKMAASEALQTLSTDTKKD KHGKKQ*FL
7773	21674	A	7833	16	339	NTDTLGSLMAFCRDGLAMLPRFLNTGL KRSSCPDLPNCWDYRHGPPYLASFVLLK *TSLILLPPYHKMHTCFMVLCINFCG GVCPCMELLCCLKVGYLSLKHTFH
7774	21675	A	7834	355	70	KKTPRGFSGVFLGPFYKKGPLFFFFFF FFFFFFFFFFFFFFFFFLQFFILCQQFL S*STEKTVHVKYILSFPHCLIFCPFIL LCSTFCNGAHY
7775	21676	A	7835	494	282	PENGMIQGGGACSEPR**HCTPAWAKER

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						DSVSNAKTIQNKKNLGN*HSISTAKAKN IIIS*YKSELRKMM
7776	21677	A	7836	305	185	LVITCLTVRPLSPS*AIISPVTCTYTF RWPEVTEESQKK
7777	21678	A	7837	179	191	LGCRKYLFLYLNGLKCLYIKVCVCVCI YIGVYIGMCVYICIVYILMAS*NQVTSF LSFYVFLNLYR*IPVKVITVLFNLMTG LP
7778	21679	A	7838	466	343	LGRLRQENHLPPEGRGCSEPRSRPCTPA WETEEDAVSKINK*INK
7779	21680	A	7839	451	89	LRDTR*SGVICLPKQAWAMVGAPPPASL PPCSLISDCASNORDSVGVGPSQPGGG YNLLVRRFLSLSEKRSIRGVNRFSCRH LSPLSLTRKGNSLTPCASVRQCLALLR LAHGARTH
7780	21681	A	7840	442	164	AHTNQFSQCIKKSVPDLMEMYKKAHA AI*BNPVYEKRPKKEVKKNRWNCPKMSL AQKHQVA*KKASSLRAQBQAAES
7781	21682	A	7841	494	359	ICMLPRLVLNS*PQVILLPWPVKVLGLQ A
7782	21683	A	7842	577	224	IFFFFNKIFLFRPGLNLMGDIWVPSTPP LQG*TNFPPOPSQEVGLQKAPPPGLIL VFLSRQGFPPQLGRVGFHPPPGDPPPRP FKKIWSHPGGGKSPPKKKKKKEIAEVLG AFRLR
7783	21684	A	7843	404	56	HTLSTNVCSSYLNLDFFSLRGRGLIMLP RLALNSWAQEILLPQPPE*LQLLRRLRQ ENLLSPGVQGPQGHNETPTS
7784	21685	A	7844	1	323	INTLLALLLIITF*LPQIGYINNSTP YEGGFDPISARVPFCIKFFLEAITFL FDLEIALLLPLP*ALQTTNPLIAMASL LLIIILALSLAYE*LQKGLD*AE
7785	21686	A	7845	419	159	FLFFFFXFXXYVLSGCIY*YWCNLFSS* QYFFFYVMAFRIFLTFLFLHYNNMF* CTYFYLSC*PEYICSHIIHYFIYFLHL ENF
7786	21687	A	7846	475	124	FFFFFQPPQKEGGPPPPKNNFFFFTRI FFFGVFFFFFPQKNFFFF*KTGCVFFF PFF**KIFFFPVGVFFFPVFFLSPPP SSSFFFFFFFFFFF
7787	21688	A	7847	6	189	LIDTVSPSVALAGVQWCNHSPPQ*PPS LKRSSRLALPRFWDYRCAPLCKAHSFNS NHEK
7788	21689	A	7848	20	249	KINFIVVELTCSNTVHTFYVYGFDKCIL PTTQLFFFL*ETGFHSVARLECSGVIMA HCSLDILGSSWRPANFLNFL
7789	21690	A	7849	101	398	LFQKKKKKKKKKKKKGGPLKKKPGGGK NKGGEKKKIFFLKGGEKNPRGNFKKKT FFGGGKKGEKPPKKKKSPEKKKF*RGK GGKSLICWVEKNLG
7790	21691	A	7850	87	226	GSLSPIMLVLPFLIHL*KNFLPLTLAL LI*YVSIPITISSIPPQT
7791	21692	A	7851	2	440	GATIRRLH*FPLFSGYTLHQTYAKRHF TIIFIGVNLTFLPQHFLGLSGMPRRYS YDAYTT*NILSSVGSFISLTA AVLITL MS*EAFASKRKVLLVEEPSIDLERLYGC PPPYHTFEFPVYIISRPRRKESNPAKLV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SSQPHG
7792	21693	A	7852	1	80	SSLILITILALSLAYE*LQKGLD*AE
7793	21694	A	7853	5	135	ATFLYFS*K*SLSMLPRLVLNSWTQAIL PPWTLKVGLCFFDPL
7794	21695	A	7854	38	419	FVMPLHSSLGEVVRPYLKKKKKKPPWE GGSPPKPNFKNQIFA*NQKPPFFFIIPN KKWGSPPGGGASPL*SHPSGGPGGPNNK VKLSKPPCPPGGTPVFTKTPTPT*PWGP IPEKEGRKTVCPRTH
7795	21696	A	7855	398	61	FFSFRPRGGGFPPPPKNNFFSPPTIFF GGGVWNFFPPPKMVFFLKISPVVFFPFL IRKKIFNLSPGSPWSPQGGFF*GPPPKF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFF
7796	21697	A	7856	1	121	LDASGRLPSPSPKPIKIKYNNRP*EPR*T KICSLHSLPPQS
7797	21698	A	7857	1	332	TPPIARPAENSARGAEGRRR*YIALQVC NKKWPPTKLHCIKKKKKKKKKKKKKKK KKKKKKKKKKLWGGGGGKNFFKGGGKK KLGGGFKRGRKKKK
7798	21699	A	7858	3	191	SPRHLTRAAGIRHEGQTGLKLLTSGNLP ASAS*SAGITGMSHRIGPRMLDLLTLVS WKOHL
7799	21700	A	7859	503	62	FFFFLNCCLSGLRHLIKLFEPQFLHL*N GGMVLSIILSIKSPLRSPSLYSWL**P REKIKWGGQVRWFMPINPRTLGGGGGQ IA*SQEFKSSLDNMVRPYLSEPP
7800	21701	A	7860	355	86	YIKG*QMVGNRGASQAGMTGYGMPRLIL
7801	21702	A	7861	336	225	PQLAGPVKTVRKVKYKKEKARVPEEKK FKAFASFRKGRANRVRGIRAKKAKEAA KQDV*KKPPPLAGGSPTREPPSQAHLF PQNPPRGNPP
7802	21703	A	7862	465	170	GGPPPKTHPFGGERGGKYHRGKKKPPGH QRVNPSPPKKKKNWGRGKNPFTPLIGG GOAKKPPQGRGEC*KKVPPNNSVLGK KNFFPKKKKKKK
7803	21704	A	7863	495	275	RSFFFFFFFFFFFFFFFFFLVARK*YFYL ATKKKKKKKKKKKKKK
7804	21705	A	7864	493	70	PLTASISLPVNWRYIAPHRVVKIK*KSV Y*KYLA*CLAQSKCPKSVCSHLSSP*LH FVPPPNPAEAMWTARQC*CIRGLGGKGT LCVAHTYNPSCSGG*GRRIV*AQEFKAS LGNSEPLILKKERKKESQAWWLIPITPA F
7805	21706	A	7865	67	385	VARTTGMQHHAWLIFIFIIFVETGSHY VAQTSLEFLASSDPFTSVFQSTWITGVS YSWS*PGIAHTCNPSALGDRGERIT*GQ EFKRSILGNIVRPCLYKNNKNN
7806	21707	A	7866	454	0	LSFFFFPLGDRVTLCCPG*SAVARSQLT VALNSWAQAILLPQLHKKHVPCLANF*N FF*RQRYTMLHRLVLNSWAQVILQPWPT CPTAAQA
7807	21708	A	7867	1619	698	PATSSSSSSSSSSSSSSSSSSSSSSSSSS PPCRPPLRPPLAPHEVATLAPWRG*K PSFTSSGKRWLTSEPQTSGSCASCL*SM RASSPSSG*SKKKPLPAEAAAASVAACA VCWRVRAPPYVAATTAYTMAVMGMAFP WEVIWTRWRMMSQAIRPLQTWINSVTAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7808	21709	A	7868	52	187	LDNF*RRCLTKLPRLVLNSWAQVILPPWPPKLLGLQV
7809	21710	A	7869	33	373	AGVQWRDLGLLQPPPPGKRFSCSLSPS GWDYRHAPPHLANFVVLVEMGFHHVGOA GLKLPT*GDPFTLAYQSAGITGMSHRAR PGISVFHLKLHSFDPFKIIFRPGAETMP S
7810	21711	A	7870	100	119	VFVEIVFPBGLLFSPCSFHLGCFRIHLK AEF*FFVETGSMLPRLVNSWAQVILPP WPPVVL*LQA
7811	21712	A	7871	471	446	LLMLPRLVLNSWAQVILPPQPPKVLGL* AYI
7812	21713	A	7872	449	33	FSFFFFFLGKKDLFFSPRGGGGGANSA FFPPNFGKKSAPPPLKSV*NPAAP TGVFFFFCGGA
7813	21714	A	7873	334	41	PCPSLFFFFLRLQSLTLWRLECSGVIS AHCNLCPLSSWDYK*HCPYLATGAPGLL SQSELSVYTL*LQESRPLCIPVDFMTFL PSLCFQSPNSTTL
7814	21715	A	7874	342	716	STGIFLFVCF*DGVSTLAQAGVQWPDLG SLQSPPRLK*FSCSLASSWDCRHVPP LLANYLYF**REGFTVLAMMVFS*PCD PPTSASQSAGITGVSHCAHPGMFTLNWP LKSCPSSEGAHV
7815	21716	A	7875	454	215	PPPARCH*PP**TLVHAVEFKSHHYSLI SSTQGHKHCGRPQGPLPRKTRDLCSLVY LLTFPSLLSYDPAKSLSARNTQE
7816	21717	A	7876	492	176	PCGGRGAGNNGWPPWHLRASASSRWAW ALQPHTRSSQAPGTGPRQ*GAQHLGQQ LLCSISHQALAAPPGRAQDLQAMPPEP SPRPPLPWAQ
7817	21718	A	7877	281	439	TWSIDL*HMAYFLFFSFLFPAPLSFSL SFSLFFFAFLFL*VPSFSLFQRQSL
7818	21719	A	7878	507	338	LLRRLK*EGHLSPGGRGCSKPRLHHCIP HWATE*EPFSKTINK*N*S*MKMKMKIN
7819	21720	A	7879	55	298	PPCLANFLKFFL*RQSLPMLSLFNSW PQAVPLPRPPKRNQLYLYFGCCSQCNP QHLCCKQHTFKILFDIEKHFRLEH
7820	21721	A	7880	145	292	YFGGKQIYFIFCRDRISLC*PVLLTSLV SNSWPEAILPSQPPKVLGLQA
7821	21722	A	7881	3	203	LSLLPRLECSGTFTAH*SFKLIGSRDSP TSAS*IARTGMRHHAQLRFFFPVPGGV CVCVCGCVYV
7822	21723	A	7882	324	211	AWWLMFVIPTL*EAKMGGSLRSLRPV WAHNETPFLF
7823	21724	A	7883	2	124	QHFGRLRQVDHLRLGVHYQRQGHGETPS LLK*INVYIYMT
7824	21725	A	7884	367	141	KCWDYRREPRLAQGLEFLNFCFEIVT EPPCPALAYF*NFL*RWSLATLPRLVLN SWPQAILPRWPPKALGLQE
7825	21726	A	7885	471	215	RGMCVSHIFLCVGARYNISSARESLLKE FTECTERKHTHTRAHHTHARTHTHT HTHTHTRV*NSRSQPYCRVHACSPAYLG G
7826	21727	A	7886	462	204	RHSS*LGLPKCWDYRHEPPHLACISSF* RKSDISLSDELGTCKHKWPPQVVKSRAG SVGRDPCSGHIFLAGFGQLGA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7827	21728	A	7887	409	152	PVFLALERPNQDQLRPGVLDQP*QNNK ISFFFFFKKKKKYIYICMVVHAYNPSY SGG*GGRIT*AQKFKTSLNNTVRPHLYK K
7828	21729	A	7888	1	152	GVHVCCDCKCICVCLCVGVGHECLCVCV SK*VHMCHREGTIFGNISWEGD
7829	21730	A	7889	101	399	EIINIVFFFFYFLLPLFFFWGGRPKKQ LNPEFLTNSWKKNHKTIGGKNPMGG*KK AITNPQKKGRKRSFSF*NKAQPTQGNK QNSQGSKAVGALTAH
7830	21731	A	7890	478	142	KFSKKKKRGVNLNFYKKKAFPSKPPKPVF KKKLLKNFFFKAKKQFFFTPTIRPLFR EKFFPGPPKKKKKRPPGLFKNN*KGPPW PREKKRVKKKKKKVKSHYNNHMPISVH
7831	21732	A	7891	497	320	PPWKFEFEFWFSP*LHKYPPYVCVCVC VCVCVCVDFRFFKPAPSPQSHFGINLS FLL
7832	21733	A	7892	217	23	IPPFKKFF*EMGSHAVT*ARVQVWHNHA SLQPETCGLKGFSLTLTNSWDCRSVPS SSARRQSH
7833	21734	A	7893	652	470	SSSSSSSSSSSSSSSSSSSSSQFERK TRSA PQVEGKGNFCSLEAPPGLSLFS CLNF*RSWDPGPP*PHATPKTRAGGDL LCATHRRARHCTPGLRFELFLAL
7834	21735	A	7894	25	178	GILFFWRDGGVLILHRLVSNFPVSSDSP ISASQSWDYRCDDPCPACPLIFW*LLKH SF*FFWRDGGVLILHRLVSNFPVSSDSP ISASQSWDYRCDDPCPACPLIFW
7835	21736	A	7895	104	451	ILSFMTTWMEADIMLSEISQTQTDTRYC MILLVESKNVNLRPGMMAHAYNPSTLGG *GERIS*GQEFETSLVNIARHYFYKRN KIKSKFKKIVRKSQKKNVRRWLLEARNK GRYG
7836	21737	A	7896	510	335	SCIVSLHRSWDLWHVPFLANF*IFRKG GVLPCCPGWQIYTFQLQIPFLSITPVAF SG
7837	21738	A	7897	37	260	AGNSQNQGGGACSEPRWRHCTPA*ATER ESVSKNKQTKFLCSVPYFESTHFHCTNE ATGAWGVEKVALGHAASW
7838	21739	A	7898	35	466	THTCGGIRKKLTNKRNOK*SQOKPSAP KEPEVRNKQKTKNPKKKKKTPQIQPT KKFFRNPNLRVFTFFVITQNKTPTRGRK TFQKVKLFPPNPCLGNKPKQTLPRGGLQ KKKKKIPFFYSHPPPLAQKKKATPWQNG LGFT
7839	21740	A	7899	494	149	PARLLSLHSYEVKSVLPKEEGLNFFVQ SVTAHPTSCIGLEEI*LLD
7840	21741	A	7900	494	114	GAEGGPLSKKKKNLDPDHTGPMLSL YLWPFSLNGHTLTLMCAHTHTHTHTN H*LSRVGLPVLKPGQYQANGNRWSP*YN IKE*PRKTRVMPVTPQLRNDGPMLTFWC SSRNSFAMHVLGKL
7841	21742	A	7901	19	454	VVCNSSVSIHTHTHTHTHTHTHTRSW VGWHMPIVLSTQAEAGRLLGSGSLRIQ RAMIVPLHSSLGNAARPCV*HTGSCCVS QAGVQWHNHSSLYPQTPGPKQSSSLSL SR*DYRHVPPHPASCVCVRVCVCVCV CVYGDRGITPH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7842	21743	A	7902	3	393	DAWDPLNPLVNLVSPKRNSSLDTRKKP CRESKKFNTHSRPKSSHQLRKSSSTPT T*KIPNT*LNSTSPSRKKRKKKPKKK KK*KNSQKKKKPMRKTKKKGGGLKKI LGGAKFFGGRKEKIFFF
7843	21744	A	7903	424	139	LLLLLLLL*G*GFVIFCYVGQVGL*LL TSGDLHISASQSABIRGVSHHAPLSLI VVFISQCVGILNHTVHLQYIQCSFVHHF LINQEKIDIIK
7844	21745	A	7904	1	181	SQ*LY*LLAANLFILT*IGGQPGSYPT IIGQGASGLYLTITLILIPTICLIESKI LKWA
7845	21746	A	7905	3	281	HAYAHASATFFVSTCFHGLHDMGSAFL TMCFIRQLIFHFTSKHHFGFQAAA*YWH FVDVV*LFLYVSIY*GAVLKEPWGGQS
7846	21747	A	7906	1	84	PTRLTMLPRLVSTPGLKQSSQLSLPKC *DYRCEPACTAYSF*LTMLPRLVSTPGL KQSSQLSLPKC
7847	21748	A	7907	3	392	DPDNYTLANPLITLPHIKPE*YFLFAYT ILRSVPNKLGGRLALLLSILILAIPIIL HISKQSIIFRPLSQSLY*LLAADLLFL T*IGGPRSPYFFILIGQVAFVLYFTTIL ILIPTISLIGDRILKWA
7848	21749	A	7908	2	231	GCVEKGTLSHC*WECKLVQPLWKTVMGF LKELKIDLPFDPAIPLLIYPEENKFTL GPLHSVGRSSRKLPGYSPRV
7849	21750	A	7909	529	297	KIFIGAPVFCPPPHFFFLIPPF*GVSKI FFSFFVLLPFGFFFLFLGLFFFFFKLFF FFFFFFFFKIPFFFSKKVGVGK
7850	21751	A	7910	410	61	FNNQAMQVFPFPPLKIFFFP*RV*FLE GGWSNLSPPK*GPSKPFTRVL*GPP* GKN*NFGFPG*NWAPHRFF*RAAPFFFF C*DRVLLPRLVSNS*AQVIHPPWPPKVL GLQA
7851	21752	A	7911	512	314	ANFC*LFITGFPFHIGQAGLELLTSNP PALASQIAGTTGVNLRPGQDFSSYHSEN PLVYGSLYIA
7852	21753	A	7912	1	264	SSTTTLLSRT*NKLT*LTPLIPSTLLS LRGLPPLTGFLPKWAKKKKKKKKKKK KRGGGGWKKPKKGGGGGETSSKDTFFK KGGP
7853	21754	A	7913	416	129	FFFFFFFFAPPPKIKTPFFFKREVYIY* ALSVFQSVCKALYIHFRIISSQYPC*LG FFFFFFFFFFFFFFFFLKGSLDLLSAYCVPG SVQCALHTLSH
7854	21755	A	7914	397	34	IFSNLFFPPQKKMFFPPPLKYFFFSFT ALFFFLVFPFPFPKPKIFFNNPPKFF FYPS*KKKFFFIIPVYFLAPPEFFF*AP PPFFFFFFFFFFFFFFFFFFFFFFFF FSVSKQPLFCLKI
7855	21756	A	7915	396	86	IFLSPRK*GFFSPPPP*KFFSPKPLIF FGGFPPKFPKPNFFQNPFGVFFYP FKKKKFFFPPLNFGPPRVFF*RPDPFF FFFFFFFFFFFFFFFFFYLWVC
7856	21757	A	7916	351	112	SFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFPI*KYVFIYISLSLIPCKFLK GRECDIHFCDIQHSYSKYLGHFKCSTND RQMNK

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7857	21758	A	7917	445	2	FFFFFFFFFFFFFFFFLSYF*LIHYAEGIG ASPCYIMLGYNFSSFP CGTISTAPGFNF YRLYPISHASADAWDPRLDRYRRGIN
7858	21759	A	7918	2	407	PPPPQVYFNIWRTIFFGEGLLHIFPPQK RFCFYKTYTNYIKTLFKKKNI FSLAHI KMVPPRSIY*TPPPLFFFFFFFFLFFFF FFFFFFFFFFFFFFFF
7859	21760	A	7919	107	11	KMWYIYTLECYSAKKKKKILLPDTTLI NLKDIMLSKISQHRKHTHT*FKT
7860	21761	A	7920	1	70	FFFF*AAESCSRIKCSGTIIAQCNPELP GLSDPPTSAT*VAGTKGVCHHTQLRFIF IV*LSGRILLQDQVQWHNHSV
7861	21762	A	7921	123	260	GIQARKEPGAVAHAYKSLTGG*GGWIT *GQELETSLVNMVKPCL
7862	21763	A	7922	184	399	LHLMRVLKKKKKMGGLYRSRPGAKVN PALQRLDLSLIGSRILSNLGI FGKAPH WGG*AFFAATGLHGLHVIIGSTFLTIGF IRQLIFHTSKHHFGFKADD*YHVFVDV A*LFLYDSIY**GSRILSNLGI FGKAPH SWGGTKWDNPPDMKSS
7863	21764	A	7923	2	407	GRVGM*EAFASRKKVLIVEEPSINLE* LYGCPPHPLHTSNKKPPHTKKKQKKKK KKKKKKKKKKKKKKKKGGLLKKLWGGPK NTGGKKKNFFFFWGGKKKNLGDFLKKNL FWGGGKIGPTPPQKKNP LGEKKF
7864	21765	A	7924	1	398	PTRPPTRTSSRSRAPPPPPPPPPPP FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFVSAALFGKKKNFFFF*FFRG *GFYFFPPLYFFICGGGVVFFFFFAGW NIFIPPKKNGIFKTLRGKGG
7865	21766	A	7925	2	335	NLTFFPQHFLGLSGMPRRYS DYPDAYTT *NILSSVGSFISLTAGILII FMI*EAF SKRKVLIVEEPSINLE*LYGCPPPYHTF EEPSIKKKKKKKKKKKKKKKKKKKK
7866	21767	A	7926	1	328	RTRGRTRGESNPSLRIONS PCHLSHPIL KKKKKKKKKKKKKKKKKKGGPLKKNPG GAKI*PGPKKNLF FKGLKKTPLGNFE KKPFFGGGKKRKKPPQKKKTLKEKKKF
7867	21768	A	7927	27	226	LSR*KM*NKSHIYSFEKKKKKKKKKKK KKKKKKKKKKKKKKKKKKENRPKNGDSEN GHPKSKIFWL
7868	21769	A	7928	398	2	GGGGGPGGRGRP**NPHKCEGRDPHPK KKFFPRRRKNRGGGGRKSPQKKKAPQ KKPGRGFKRAPQKKKTPPPPRKGGPPP KNPKKGAPPPPPPPPPPPPPPPPPPP PFLGILARTTTTINDMKNHR
7869	21770	A	7929	3	156	HASAHASAPV*SVLMTAVLLLLSLPV LAAGVTILLADRILNTTFFDPA
7870	21771	A	7930	405	249	ASAHASAPLV*SVLITAVLLVLSLPVL AAGTITILLDRNLNTTFFDPA
7871	21772	A	7931	921	699	DHPGQHSILSLQKMKMTMSQCGAHL*S QVLRRLREDCLSPGSQSCSEL*SHHCT LACETE*DLVFQKKKKF
7872	21773	A	7932	423	259	HDLGSLQPLPPGFR*SSYLCLPSSWDYR CEPLRPAQRRGI LMAATSRILTRSKGW
7873	21774	A	7933	395	35	PRVKRFSCFWLPSKWGPRPRAPWPGYFC FFC*NGGSPFLPGGSWTLAPNYSPPPAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QNGLVQALRPPGPPTFFPFLIFPTKAPWS WPFPGGKKKKLSPKGHSERHLHHKYIR LLSQHGGM
7874	21775	A	7934	1	118	NF*IFCRDWGLALSPQLSNSWPQVILP PQPPKVLGLQA
7875	21776	A	7935	322	383	KKKTGLIKISTLCFVKNTFKKTKWQAPE RKKKVPIFLSYKRPVFKIYKLFPPCRK KIKKKIPPPGFTSFCLSLPSSWDYRHP PPCPVNFCCIYNKNGVSPG*PG
7876	21777	A	7936	3	131	GFHRVGQVGL*LLTLGDDPASASQSAGI AGLSHRSQPLTWSL
7877	21778	A	7937	334	146	HPQGLNI*NMVSSSGAKHSSRLSLPKW WDCRQEPCCPVIMFLKRGINHALYSPSR KLLHFL
7878	21779	A	7938	2	371	SEPGAGYNLLVGRF*SPSEKCSIIGVGT RFSRCCLSPSLTGGKNSLTPCASRVQ CLALLWLQGVHLPLSCTHCLALPSEM PVPQMEMQKSPIFCIADAGSCRPELFLF GHLGSSPQSKL
7879	21780	A	7939	2	95	RLNLGGGGCCCEP*SCHCTPAWVTKRNSI SKK
7880	21781	A	7940	1	191	PTRPSQTPGLK*FSLSLPKSWDYRCEP PCLAVILSIPQNSSMPSNIFAASYSS*F GLYSSRW
7881	21782	A	7941	127	383	SKDCVRIVLLRAQAKAGSYRTVNWCRPG AVAHTCNHSTLGSRRGRIA*GHEFKTSL GNIVILPLYKKNKKKKRGARLKEPNLT P
7882	21783	A	7942	235	3	KNILPGYFCFFLREKPPPPGLESLFSKK KKKKKLARHGVAPLLGRMR*EDRLRPGV QGCNELWWCHCTPAWATEQNP
7883	21784	A	7943	3	225	EHGSLYPPTPGLKQSSYLSLLSR*DYR* AAPCPANFFIFNPL*REDLTMLRLVSN SWTQAVLLPPKVLGLLV
7884	21785	A	7944	2	232	TLLPDNLSQTIYPNKKKKKKKCKKKKK KRGGPFKKKKF*TRGGGKNFFFRAPKI FFGGRVLKKGKKKPGPEPTN
7885	21786	A	7945	394	41	WCRWLETWGAGGSGAVPPPPPPPHSSS WDLALQGGGASSPSPGAVAHACNPSTL GGQGGWIT*VOEPETSLANMMKPHLFSK KGPVTAVAHPAKAHRAWCTPTHMTQH VLHVL
7886	21787	A	7946	405	100	FFFFSFRSSSLFLFLSSFFFFFFFFFFF FFFFFSTGLFVYWSPTH*SLPVPRIFFF SYLWQTEVETMLGTE
7887	21788	A	7947	391	212	KEMQIMPAMR*HLTPVRMVITKSKAKC WQCEBKGTLAHSWWCKGTAETGKLAG F
7888	21789	A	7948	106	301	LQLPITQLVWHSIYFMKKIRYRLGVVAH TYPSTLGGQGGRIA*GQVFKTSLSNTA RQKKKKKK
7889	21790	A	7949	342	208	GLGAGHTYNPSTLDN*GGWITSGQEPD TSLANMVKHHVVQTGF
7890	21791	A	7950	391	21	RQGFPMPLRLISNS*PKGSAHLSLPKCW EYRSEPPSLATWYVTLRHFCS*TLLLGQ GRSKFHMKWESEGLLAKVSSLRSSYC SSLRILGLEILLSPLLPLETSGSGSVSQ AGVQPLCPGLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7891	21792	A	7951	146	355	ENIRQTONEVDVVKSSNETVFCKNIITS LGVVAHACNPSP*GQGRIT*AMEF* TSLDNIARPCLYQK
7892	21793	A	7952	289	327	KGIPPLPRLKDKGPPFFFFFLKRESLF LP*FWKNGCRGPPLFFFLRDSVSLLP RLVSNWP*VILLPQPPKVLRLQA
7893	21794	A	7953	861	586	DRVSVAQARLQWHDLSLQPPPGF*Q FSCSLSSWDYRMTWPFVF*WRWGF TCVAQAGLDLLSSDNPALASQSAIIG ESCCVLLK
7894	21795	A	7954	402	52	PRKVSIS*PHDLPASASQAGITGVSHR TRPSFNFSYIETAITETRSLQSPGMN *SLPSGMVGFKPHSFHISANFCEALAVQ QTLGEVPGHAPLSPPRQBRVCPKVKCL KTALK
7895	21796	A	7955	259	3	YNTKVLSPFILL*TFLKHLWLGAVARAF NPSTLGGGGRIA*GQEFKTSLGNIERC RLYKNLKLFLSGLFLMAWRGAKVRTR G
7896	21797	A	7956	171	386	LPIRLFSLVFTTIEKSRPGMVAHTCNLS TLEG*SGWIT*AQEFETSLGNMAKLSLP KIQESASLITRSQNK
7897	21798	A	7957	397	283	PQPLPGLKQFSCSLPKC*DYRDSAR PAKKNPTFNK
7898	21799	A	7958	169	324	GTHRVEMCSQWLGVVAHADPSPLGGQV RKIT*AQEFGTSLGNIGRPCLYIK
7899	21800	A	7959	290	397	DCSSCCSPLKGR*RG*AQWLTVPVIALW EAEAGGS
7900	21801	A	7960	496	298	LSKTGSLVVAQSVVYWLFTGTMVHDSL KLLCSSSPVVSAS*VAGTTGAHRCCEVL TTFQPDVYRL
7901	21802	A	7961	404	174	PGPQKGSFF*KKKKKKKIDHILSHKAN LNKC*RIKII*TMLSQNEIKLEIIIR QLLKETLFLEMKRYTIRKLS
7902	21803	A	7962	25	99	PGLFLSS*HQVILLPWPPKVLGLQL
7903	21804	A	7963	436	106	GGGKSPPGNWAPPNGEPLFF*KKKK KNPGGGGGRFPFPPCGRKKKGVPYGGG GFYLTNFPFPPPPWGKKKNFFKKKKK KKKGRIAICYIILFITSINFKAFF
7904	21805	A	7964	212	395	ERERKERDRGEREREREEREGRKKHG GR*GGERGERHRPRGAEDFDRAGRATDK RTGAL
7905	21806	A	7965	344	345	FSDCYKRSSCASWTWYTRLAHQPPARP GAAPSPKRWVDFAVNRNFPSSRRHPCAT PRPAPGATGRPSRVPKSTAFTQMLTQPR DPLPLPIPLPSQPPSP*PAPLVMR
7906	21807	A	7966	397	298	RGFTMLPRLVLNRTQVI*LPWPPTVLG SLSIF
7907	21808	A	7967	92	268	IKMSLCPNFFFFFKQNVGPRAGAYPCN PTILGGQGRKIT*GQDLKTTLVNMGKPH FY
7908	21809	A	7968	257	107	RTHTHTHTHTHTHTHTHTHTCENSKT TKNIANNCS*LESQRNNGKCTYAKF
7909	21810	A	7969	413	12	PPPPPLLPWPCFPQIL*PVGHSAPPL FK*LKIPRPPPPPPPKGIGAPPPKIPF PPGFSLPFVKLPGEKILFPFKKKKY PPPPQS*SF*PPPPPPPPPPFFSTSAK KSKKNFLFIFSPFFNPKYNT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7910	21811	A	7970	399	212	TGVQWSNHSSLSQSTPGLKRLFLILLS IWDYGCMPYPYLSFKN*FCTKGGSCYVAE ADVNIL
7911	21812	A	7971	584	424	RPRRENRLNPGGGGCSEPRSRCTPAWV TE*NSVSNRNKTNQNPFFSCKQFD
7912	21813	A	7972	105	1	PSMPQLSHL*NGILGRVRLTPVIPALW EAETGRS
7913	21814	A	7973	363	28	SSSLGCHPQLWPHLTKLRPVTVSYA*NK LCDKIEKKLFFTIALHNKFLRKLTRDV KILFNKK*IKKEGPNF*NILCLWIERI NINKVPYPSKVMYRSNTLPFVAVFKSQ
7914	21815	A	7974	404	250	FFFFW*R*GFTMLPRLVLNSWTQAIHPP ALASQSAGITGMSHHAQPLSIIF
7915	21816	A	7975	2	60	FSCLGLPFCWDYRHAPPHLANFCRDGVL NY*PQVIHLQPLPKVLGL*ACTTTPG
7916	21817	A	7976	325	81	KTIHSLFLGQFFLLQPLLPSPPIHAPP TPHLIFLLLLFCF*PFK*RQKQGLTTL PKLISNSYSQVTLQPQPKVLGFOA
7917	21818	A	7977	406	282	QWRDLGSLQPPTPWFK*FSSLSLPSWE TKAGRSREPGGD
7918	21819	A	7978	382	221	DCIISASYLQKNFFFLGDKVLLCHPGW SAVA*S*LTVTSKRVHFYSSEISLY
7919	21820	A	7979	423	29	FLW*RRGFTSLPRLVSNFWAQQICLPWL PKVLGLQA
7920	21821	A	7980	3	238	SLAFFVETGSHFVA*AGLELLSSNSPA LASQSAEITGVSHHTQPE*GYSHM*PQY PYQLRFNSDTIILSNVLFVFN
7921	21822	A	7981	324	128	WLSVSPYTFELSLLVGYEFVIHDVI*TL IFVVVVVSLFCFLWFFLVCMVVFVFFC CCFLSVFCI
7922	21823	A	7982	1	86	NLTMLPRLVSNWSWAQAICLSWPPKVLGL *AQAICLSWPPKVLGL
7923	21824	A	7983	1	137	RPANFCIFFVTEFCHVAQAGLELLGSG DPPTSASQGAGTTGMSH*D*PANFCIFF VTEFCHVAQAGLELLGSGDPPTSASQG AGTTGMSH
7924	21825	A	7984	2	277	PRRSVQRVIYQYV*NLQIHVPFDSTNL GIYLTDLPHVWVNDNMVKFAAVSFVIA KY*NPCLTRRQCCKLWPIHAMEYYVTIK KNEDGRA
7925	21826	A	7985	211	42	GPQKWPRGPGENLGGFFFFFRCDDGL TMLPRLALNS*VHAILPPQPRKVPGLWV
7926	21827	A	7986	409	183	LLRLK*SSHLSPKWDYRCEPPCPAIF FKRKQILKESFPGENTCCHLNSLEVLLK NKRRTCYNFENTLAVLKNM
7927	21828	A	7987	2	194	RFFETQSRLQLPPPPQLK*SSHLSQLSS WDYRHVPPCLANFFLFWYFLQGQGFAPL LKLKFLFK
7928	21829	A	7988	483	209	SSPSLGNFCIPSSGGVSPCWPGWPOTPD LVIWPPGPPSLVFFFFFRDEGLSMLLR LTLNF*AQVILLPLPE*LGLQADRQVP LYPAEVF
7929	21830	A	7989	164	29	KFWFWLGTVAHACNPSILGSQGRRIA*A QELEPSLGNBGRPCLYK
7930	21831	A	7990	3	474	PTRAPLRAPFETIVQEEEFKHHFGFEA AA*YWHFVDVV*LFLYVSIY**GSPPPP PKILIKNGAETKFFF
7931	21832	A	7991	469	323	VETGLHHVAQDGLLELPTSGDSPASASQN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IGITGVSHHA*PDFTFLEQF
7932	21833	A	7992	469	13	KGDTVSSSDSSPSCGGLFPVGAS*LLCL FTQALAMVGARRPFSMLPCSLISDCCAS NERGSGVMGSPKPGVGYSLVCRWLRLP EKRTIKVGVTFRSRCLSQLPLARKGNS LTPCVFWVRHCFGSHSVGCTHCPAPAVR QAPVK
7933	21834	A	7993	15	439	IASGRPFSSIKFFLVAITFLFDLEIALL LPLP*ALQTTNLP LIVMSSLLIIILAL SLAYE*LQGLD*TEPNKKKKKKKKQOE KKKKKKKTKTKGGGLLKKILGAPILW GGKNMFFFFWGGEKKTGGFLGENLFLG GGK
7934	21835	A	7994	392	186	YFYIINNFFFKKIFI**IIFFFLKKFL *YSPKKVFFLFF*IFFFFPSSSLFLFF SSSSPFFFFFFFFFFFPLRG
7935	21836	A	7995	11	386	TWEVEVAVS*DHAIALQPGQOE*NAISK KKMTGRMFIEVSFIASSWKQLKCS*TG E*MKSLWYTHIEYLTIKENKVLHEV SRLTLIDTGRERSKTEYTLNDIYTNL RIAKLSGCCGSHL
7936	21837	A	7996	3	186	DSFCF*RQSCSITQAGVQWGDGSL*PQ SPGLKRSSCFSLPKHWDHRDEPLHPAGV AVLN
7937	21838	A	7997	316	649	RDHSFFFEMESRSVAQAGVQWHDLGSLQ ALSSGFMFPSCSLPSSWDYRHPPPCPA NFLYFLVEMGFQHVQNGLDLLTS*STR LGLPKWLGITGVSHWHPAQDGGFHHVG
7938	21839	A	7998	468	336	RRGFTMLARMVIS*PSDMPASASQSAG TTGVNHHIRIHRSL
7939	21840	A	7999	464	283	TLCGGIRPTNIMKGNLLYSKISGLNVSL LPKNPRRNQNNV*PNIWALQPSHVDI
7940	21841	A	8000	46	487	RQGRLSLQKFLLPFVQLCPAHRGGVYRG RQASLSGGLHPVRVSQPLCLPT*VSAM AAAPHPASLLPCSLISDCCASSEQGSVG VGPSKPGAGYNLLVCHLLRLLEKRSIRV GVSQFSRCHLSWLPLARKGNSRTPCTFR VRRCLAL
7941	21842	A	8001	295	1	TQPWGTRKRLPLKKKKKNSGDREWRWLC NSVTILNATMYTSEWLRPGTVHTCNP KTSGG*GGEIA*QEFKASLGNTA*SWL YKKILKISPLWWQT
7942	21843	A	8002	144	317	ELFYLKEMV*RPGPVAYACFPSTLGDRG GRIT*AQEFRTDLGNIARPCVYLRKKKK RG
7943	21844	A	8003	69	291	HCVWTMIFIVIKYFYLNPONNSMRYYS HFMDKETDVQSD*MTCLRGAVAHACNP STLGRIA*QEFKTS
7944	21845	A	8004	3	176	IVAHSSLTPGLKQFSCFSLPSS*VYRNM LPRLANY*FFGTNRVSLSCQGW*TLAS LLGSSSSPASACQVAKSTGTCTYHAWLII DFLVQTGSRCLAKAGHELCSCL
7945	21846	A	8005	419	178	NPPPKKFLSSSSSSPLPHLNWGTGPGFF PPPPF*NPPPEFNFAGPKKKKLSPPRA EKLVEFKGPPPPPPPP
7946	21847	A	8006	429	225	QPLPFRFK*FFCLSLPRR*GHRHRPPHP FNFFFF*YFLRWSFVLVAQAGVQCMDLS IYLNFEFWLLDF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7947	21848	A	8007	756	224	PPRHQPQHVPPLLHFSTPSPAPPKSHA AAPNSNPPQAHAPPAPPAPRAHSPSPPP RGATPPPPPPFFSFLAAVGRAPIFPREP LLPSSSSPPPPP*IGEPGFSPPPLLKT RPPK*N*GPPKKKNNFFPPRPKNWFL*K GPPPPFFFFFLLRQSFTLVAQAGVHKT RLHLKKKSN
7948	21849	A	8008	170	559	SSHLSPOSSWDYRSGMVAHTCNPSMLGG QDGRIT*AQKFQTSIGNIVRCHFYFKKY FKNKIFFYSPFFINTNPKKKKKGGAVLK NQSLRPRAGKVLVFLWGHLLQFRGPRFK NGGTGKPGGLPNLLAPR
7949	21850	A	8009	1	662	RTRTRSWWYMPVLPPLSHYGEAGESLGP *KMWVD*APIAPLHSTLGDKMTLPDIKK KNGETVANTSPLSTTAKPAKFLKAKKD QLMRDLFLPKTPKPKQMSGTGLDARSKRW LKIWRRHGIWPLKNIGPTEDVQASAHG GVEENMTSDIEIPEAKHHRPTEDVQVS AHGGVEENITSDIEISEAKHDDLVEDL SESLSVCLEDFMTIGSQWKPICLS
7950	21851	A	8010	377	2	NFFFFFFPFWGFFFLGPGFFKVF*IF PFFFFERNPPFF*FFLGVLFFKK*IFFF PFSIRFCFFPKKFFFLILFFFF*PFFF FFFVYVDFFFSFILYIFFVYFSLPPT VLIISLIYHFAPA
7951	21852	A	8011	1	363	PTPLF**RGCFTMLPRLILNSWPQVIC PPRPPKVLGLQT
7952	21853	A	8012	278	39	FXKXFFLSPPXFLIFFFFFFFFFNFNF FFFFFFF FH*DQ*FSNEDFTPTFTLISNII
7953	21854	A	8013	79	412	MNECILGKGGKDGFFEQECENLGLC*FL KVP*DSDIWLGAHAHAYNPSTLEGQGER ST*AQEFKTRIGNMTRPCLYQKHTHKKK TKKKPHPGGLGWGANGPTYLGGVGTKIT
7954	21855	A	8014	277	19	FGNIHNFFLIGSRSVTQAGQWCNHS *PQTPVLKQSSHLSPSSWIEAAVSQV RITALQPGRQSKTLPGNSGPVLRADARR SI
7955	21856	A	8015	1	130	ARIVSIS*PCDLPASASQSAGITGISHH TQLAHNTLKASPTLF
7956	21857	A	8016	4	417	RLMPPHLANFLFF*RHGFYVAQVGLKL LGNDPSASTSQSTGITDVSHCTQPHLL KSSHSTFPLKTLDSMAINCSDKVHYLP TACRALLPCPLPSACFPPLSQVPSVFTC CVPATLTITLLPLLRAFEHVTLCPLF
7957	21858	A	8017	388	158	CVTWASNCINWICFPLS*INSHLCNEII VLI*GEIYNVCISYLCIYMCVCIIYSV CVCVCIIYH*TPYLIHKCLI
7958	21859	A	8018	154	382	GIKRPGAVAHNCNPSTLGG*GKWIG*AQ EFKTSPGNMVKPQIYLKKKKKKGGAVLK DPSLRPRAGKVIVFWGPLI
7959	21860	A	8019	396	237	FFFFFFW*G*GFTMLPRLVSNWAQVIH LPWPPKALGLQVRTMVPLRLANF
7960	21861	A	8020	412	168	GNLGSPPLPGNVCKNKPFLF*KKK*SL AVLPKLVSNFWP*MILPPWPKI*GVQA RAPPPSQILKKKKSHFYNSHNSL
7961	21862	A	8021	1	124	TRFLHVSQAGL*LLTSGDLPASASQSAD YIFIISPAKIIFL

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7962	21863	A	8022	3	200	HLSPYFYFFKDRVALCHPGWSAVVQ*PI VTSIFWSSC*KLTSVVRWRPSWLTR*N PVSTKNTKN
7963	21864	A	8023	3	132	FLFFQF*FMRLGLAMLPLMGMNSA*V ILLPQPPEWLGLQA
7964	21865	A	8024	3	187	VGOAGLEPPTSGDLLPASASQSAEITRMS HRAQTK*DFIGSFSEFS
7965	21866	A	8025	405	231	SDKWIKRMRYIHTTEYY*ALKRKEILTH ATTWLNLENILLSEISQSPKHYVYIPL T
7966	21867	A	8026	175	382	GKRIFPPYPPEGGKTPGPPTGLFFFF LKKK*PGGLGGARFSPLLGGVGRKNSFT LKGGGAINLKGPPLPPGGKRWAPPQKK KKKGOAWWLMPIPALWEAEAGRS
7967	21868	A	8027	83	374	GDQVWVLMHACNPSTLGGQCGRITWDRE FETSLANIFFPISTKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKASSGGGVS*K KNFSPRAGKEIFF
7968	21869	A	8028	382	148	SPHCSDLVLGLKQSSHLSLPST*DHRCV PRLAIFSFAPLFFWEATTTTKATMLP RLVLNS*AQAILLPQLKVLRL
7969	21870	A	8029	88	208	SGSV*ENNPLSWAWLQSIIPATQAEV GRLLERSSRSA
7970	21871	A	8030	1	283	NKSRIKKAIKMTEKMEKIEMMKLMNQL PNGEHAMIQMMKIEKGRMKIKE*DK ESDKDDRDEDEDRDDEDEPTPERRTS RDDSDDEDRDEGNEDKRKDDSKDDDE ADEDTQDDYDPMDAHKADEDDDEDED EVAEQMTKKKKKKKKKKKKKK**KDRK DEREDRDEDEPTPERRTSRDDSDDE DRDEGNEDKRKDDSKDDDEADEDTQD DYDPMDAHKADEDDDEDEDEVAE
7971	21872	A	8031	2	139	LQTLLELIAP**LLASLANLALPPTINL LGELSAQFAVIGMYILY
7972	21873	A	8032	80	324	YLHFYFFVR*KLMGLDTVAHTYNPSTLG DPERRIA*A*EFKTSLGNMVKPCIYKKK KKKKKKKKKKKKKKKKKKKKKKK
7973	21874	A	8033	299	158	GNQPGASAHTCNPSTLVGGGRII*AQE FKASLGNMVKHYLYQKHKN
7974	21875	A	8034	416	60	AQWLTSIIPPL*EAEVGGFFEPRLSPA WATE
7975	21876	A	8035	398	271	FYFL*DEVSLLPRLVSNWTPAILPPWP PKVPGLRHEPPRPA
7976	21877	A	8036	385	151	FLYFL*RLGLTLLPQLVSNISSDPPT* ASESAGITGVSNHAHLRICILTRLPGNS SH*NVRAGLQDTQSSALIPPG
7977	21878	A	8037	3	406	PASAS*VAGITGTHHAQLIFVFLVETG FLFFFWAVFLFFKT*KNGPFGGLFFFA APPALGGGDFGGGATFSPKGLVLGET RGGAPAPKKLGAKKEPSHLLGGGAQNL P KPRGQKGFYFYFLARDFFLG
7978	21879	A	8038	428	20	LANQ*WKPPSNPWETKISPKKKKGPFGQ GPPPLTPPLWEAPKARKLGSPLPR*NP LFPOKPKKFFGFGGPPYSPLPQKLSPK NGVTPEVGPSHKPKFPSPPLGQK*TP FPQKKPKRLKRGMLHGSTFQSL
7979	21880	A	8039	3	194	QNKISQVWYTPVILATWEAEGGESVBP GRQLW*AKTAPLHYSQDEKYLKASVDS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YCLISCH
7980	21881	A	8040	415	96	LEPL*KYFPILDAIKNICDSWEEVKIST LTGV*KKLIPMLMDNFAPKTSMEKVTA DVVEIGELELEVEPADVTELLQSCAKLE GMRSCFLWMSKESGFLRWIYSW
7981	21882	A	8041	413	254	PGFKQFSCLGFPKR*DYRHKPPCPASKY FKINYLRTIYRSLILKN
7982	21883	A	8042	409	102	GFFPFGPFFF*PPPPGVFPFPPPPNFWF *GFGPPPPPLF*FFRGGPKKIWFPPFF LWPPPLFFFFFPPWPKTTPKKARSLKIF FFLGPKKIPNPPFFFFFF
7983	21884	A	8043	414	153	GRGWATNFYFLIILK*FFFIKKFFFF HLFFFFFFFPPPPPPPPPPPPPPPPPP LFTLVLTCPQTSCEBAEPDHHKVCVSLK ML
7984	21885	A	8044	401	292	NYLPPQ*KKKYYPQGFRKPIKKSPPPC FFFFFFFPPPPFLNIPPPQKGFPPK KYFFNPPLPPLFLKPPPLFFF*GPKK KNLIFHPPSKKICPFKRGPP*FFFFFFF F
7985	21886	A	8045	370	14	TPPPTKTTPFFFLYPPPWREKREGFF*KA NMSPVWKKKIPPLPPIYL*KGGSRYL AKLSLNLKGSIIYLSFCFPLPPSLPLSL FERWGLTILPKLVLSWAQMILLPWLPK VLGLKV
7986	21887	A	8046	395	268	PPFFFF*ETGSCSIVQGVQWLFQTGTLV LISVGLTCSISDL
7987	21888	A	8047	379	98	GPAHNSPPLGGESETPLGYPGKPRFF*K NKKINPARGPGPVVPPPPQG*AGKRPLP PRRGQLTQNGPPPPPPGGKKKPPFQKK KKKREPAIC
7988	21889	A	8048	369	177	RNTRGGPTFFFFFFFK*NLARLSRIEC HGTISAHCNFRLLGSSDSLPLTNDIGQ INKSLFA
7989	21890	A	8049	1	128	ALGLVAHAYNPSTLGSQRGKIA*GREFG TSLGHRARPCLYKK
7990	21891	A	8050	166	163	PVHGGEQTTQDKCLR*STHLGLPKC*DY RREPPCQASKLVPTGILADSKHSCQTM DSCFSNQLYKQR
7991	21892	A	8051	402	245	YFKSVCQAQWLNTYNPSTLGG*DGWITC QGEFRLPWPSGITGASHHAQPHFF
7992	21893	A	8052	404	268	QQLWRLRQRDCLNLGCGGCSEPRSCYCT PA*ATEPDPVSNKQINK
7993	21894	A	8053	1	154	GFLRVGQAGLELLTLRDLPTSASHSAGI AGVIYRAWPGEAYLFGS*WLRF
7994	21895	A	8054	406	150	PKKKKNPCPPPEVKFDSLKRAPLFFFFL EESCFVTQAGLECSGAILAHCNLCVGS SDSPLSL*RWVGNSHFIFTSLLSVSPRS N
7995	21896	A	8055	1	125	TAVILIIIFI*EAFASKRKVLIVEEESI NLE*LYGCPPTH
7996	21897	A	8056	400	260	HMSPHLAFFFSFLFL*RLDMLPRLVSNS WPOAFLQLLLPQVLGLQV
7997	21898	A	8057	396	263	FLQPGTVAHACNESTFRGGLIT*AQEFK TSLGNKVRPCLYKKQY
7998	21899	A	8058	402	211	FSCWACTKPKAAG*FPAPWGPPFLNNPP GAGTNFPGPFRSGGFGSPPPWGPRRP CPNGIFFC

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7999	21900	A	8059	1	279	VLLYHPGWSAVVQSWLMQ*TPSNADIWR IARGFKRSSHFSLLSSWDHRHVTPCLAN FFLIL*IWGLAMLSRLPLRLRPVLLD *APSPCGLI
8000	21901	A	8060	408	315	SLTMLPRIVFNS*AQAILLPNPPKVLGL QV
8001	21902	A	8061	198	2	RIQHVESNCHLEVEGGWAQWLTPTSLGG RGRMIS*AQEFETRLGNTVRPCFYKNLK SQPGMVVRI
8002	21903	A	8062	3	294	GLSPTAHPITAFTSQPLPSGLSVCRPL WAMCEQCPLPIRPPCPRIIGPECALYT TSCLLHQLKKREGF*KKKKKKKKKKKK KKKIF*WGGGKK
8003	21904	A	8063	197	184	IHDPLFFF*GRVSLCCPGWSAAQSRIT AL*PGEKETFYL*IRRSWDHKKAPPLP APF*LFWVTLIITPSTHEVSSAVCSLLY VKSEQKCQ
8004	21905	A	8064	3	373	TSGSLAKRPADCLSAQPTTPSSLCGCSP VRVCITVPRCTHARAHTHTHTHTHTH SNHG*APGALYIQELQRGKVSHVPEKEK SDPETA*TKGG*HVTNPHGRQSRGQEE HRCVGRCCSG
8005	21906	A	8065	532	106	ENKPIHNLSINKYIGKILRDKALLYCPG WRAVMQS*LPVANSWAPAILLCFGFLS TWDYKRVPPQLVKIFSKKKKNKPTNILR PKCHTRNQDIYKRKVGFLCSYCPALL LLLSLLLLLLLLFSFSTRDSASGAGCSS LP
8006	21907	A	8066	411	130	PHAQLIFLRR*SLTVFPRVVSNSWPQAI LPPWPPKVLGPQARAMVSPKLVLESIL RIPTSVIFFPLNLCNKLAEIKEGCSA AFLNORFAN
8007	21908	A	8067	3	32	DAWADAWGSLTDEWVEKIWIYHAMQYYS SFEKREIL*YVRTCMNLEDTMVSEIRQS QRDDYCMIPHI*GRTRGVH
8008	21909	A	8068	410	116	STFNIQTWPGTVAHTYNPTLEGQAGRI T*GQELTSLGNITRPNFLFCQACPGQ GLSTVRMCGSLHYFVLPLRPLLKCLDNR KSPFYHPVILPCYE
8009	21910	A	8069	158	289	DLCSLRNIVRPQLYKK*KISQVRKKKK KKKKKKKKKKKKKKKKKKKK
8010	21911	A	8070	388	1	APTFFCFLFKPFLVGGPFGKAFQKFP GGGFFPSISGPKPPPPRNPISLISKGRV PSPQSPIMVFPAGF*RPFFPLMVG*KI KIFLPPPPPFKTPPALSPPFFFEAEFRS CWPGWNAVMSRLSATS
8011	21912	A	8071	15	336	KLDKRYDRTGSPGTHASGYLIEPLVAE ASYELILSLAFFFFERRGLALPRLEGS GVIVAHCTLKLLGSGGPPASAS*VAGTA GMNHHEGHEPGLFEKQNSGFIF
8012	21913	A	8072	396	274	PHLHTWESSL*RQGLAMLSRLVSNWPQ VILSPWPPKVVVL
8013	21914	A	8073	189	54	NKPLGPGMVVQACNPTPLGGQGWIP*A PEFKISLGNLAKPCFY
8014	21915	A	8074	3	257	HAFVLLFETRSCLSRLLESSGAMIAYCR LELLGSGDPLTSASQVAGTKGM*DDAWL RQVSNWPQVILRLSHPHMFLQFSLET
8015	21916	A	8075	1	119	TLPATWEAGAGGLEPKSLRV*CVFTAT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VNSSRTPAWAA
8016	21917	A	8076	232	266	LPYCSGQWCLGLPIIQGVQWHDHGS LQP RLPGLNQSSCLSLPKCWDYGREP*YLA* YQARYHGSLARQNVFNIRPGIMVHARSP STLGG
8017	21918	A	8077	390	143	LGGFLVFCPPAKKGFFPNPINLGTBRFF PPPPF*KPAPEINFGGPKKKKIPSPPPG VKFDPLKRPPPPPPPPPPPPPIRLLV
8018	21919	A	8078	424	144	LKNYIFFTFL*NRDRVSLCCPRLVLFNW AQEILLPWPPKVLGLQA
8019	21920	A	8079	182	45	VHKAGMVAHAYNPSTLRGRGGWIT*GOE FETSLASLDNMVKPLRC
8020	21921	A	8080	405	163	YFLEEMGFHHADQAGLELLTIGDPGGM SHCTWLNVLNLIQKHPHRIQNNV*PH ISGPVKLTHEGNHNNHMS TQKHSP
8021	21922	A	8081	39	240	QSKTVSKKKRKIIFCRYRVS*SPGPKQS SHLGLPKGWNRYRREPPHPASTFSQSFPV KDHFCSGVSS
8022	21923	A	8082	2	263	DCCVSS*GSVGVGLSEPGAGYNLLVFR LLRPLEKRSIRVGGSRFSRYLSWLPLA RKGNSTPTCTSQVRQCPTLLGLHPLCD KPO
8023	21924	A	8083	1	248	SVGVGPSEPGA*YNLLVCCLLRPLEQHS IRGGVSQFSKYRQSWLPLARKGNSTPT* ASCGMRGPALLWLTLLGLHPLSNKPO
8024	21925	A	8084	3	255	HLSLPSSWDYKRMPPHLANFFFFLGKK GVLP*GQTGLEL*N*KNPPA*PPKGAGV KGVTHRPKP*NGGKGRFEDTDPGGPFL
8025	21926	A	8085	409	145	LRGPYKKNFSQAPGRKIGSFKKAPPPF FFFFF*GQSLCCPVGLSTGVI IAHCSLE LLTSSDPASSASRVAGTTGACHCS*VLQ TFTF
8026	21927	A	8086	199	26	GFPFPPNKTEIF*RPDFFLNFFFLVBMN LTSLSRLVSNPWAQAVLLPWP PKALGPQ A
8027	21928	A	8087	222	3	SVGITGVSHVWLWYFTLKGFLGRGAHSC NNSALGGRGGWIT*AEFEFSLGVARH HLYKKYKNYPVAVVRL
8028	21929	A	8088	415	197	TILCFYHQNNVSFSSNPFSL*IFIF*D RVSFCHPGWSAVVQSWLTVFPILCATVK YFTCQQYIIMIFALNS
8029	21930	A	8089	297	71	FIFPENKNRPEVVAHACNTLRGRGRIT *GQFEKSLNIARPHLYKTKTONILSK YIQYLGFLTLQIDLANIY
8030	21931	A	8090	185	415	PFGLKQSPHLTLLSS*DYKHTPPCRVNF FFFLGGFGFPKAGFNIGN*RNFLASPS KRAGMAGINNLAGPIFRFFKK
8031	21932	A	8091	2	125	RKQASKKERKE*KK*KKKERKKERKER KKERKEKERKEP
8032	21933	A	8092	8	412	KGPQGTTLTCIFDLSYSSSLSHWSQSLC VAFPLPECIFPHKPLCPACHFFFQSWG LALLPKREYRGKIGVNGNLELLG*NNPP SGTSKIAEPAELFHHTHARPFNWIIKTD FPYIAQTGF*LRPSRNPSTLEV
8033	21934	A	8093	249	143	NIFAATWMRLBTIILSEVTQG*KTKHQM FSLICGS
8034	21935	A	8094	3	280	PERWDYRHEFPGPASFT*LLLFVFNLR KGLYVGQRGRQLLASSSLPAPASISAGI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IRMSHCTPAWVTVRACY*INK*INGKDT IRQNLKKM
8035	21936	A	8095	404	16	QMGFCLFFLFSSKEVFFPPIFFFYRESF FLPHFFLDPRQY*LYFIIKKNIPLSPF IFFLIRVSPYIFFFFIFFFIFFFIFFFI FFFIFFFIFFFIFFFIFFFIFFFIFFFI FFFIFFFIFFFIFFFIFFFIFFFIFFFI FFFIFFFIFFFIFFFIFFFIFFFIFFFI LSKAHQCISSHGSG
8036	21937	A	8096	358	200	KSYFIFSLIIFSHYFLLFLKHLLATYY CFLIDCTLFSSFYCPFCCLFVLLSGRFP RSCL*TFH*RLYFSFPIFNQKLF*LS ICFCCIYLFYIFETVFCSCCLGWS MMA*FNGMFKDRI
8037	21938	A	8097	2	132	KEEKKERKE*KKKKKERKEKREKKR EGGRKEGKEGKNSST
8038	21939	A	8098	48	331	PGTWHACLGGEDILKWQTKGRGRAGSH RTSWLEPLETVFLELEAGGRLESPGK SRLGAVAHICIASTLGGGRQIT*QGEF DTSLADFCST
8039	21940	A	8099	7	373	NGRLRRGFAMLARLVNLF*PRDPPT*AS QSAGITGMSHHARPITBSFIHYCWECK E*PLCKLILYFHLFIKQKQLGVHWHCH SLLQPPTPGLQRSFRLTPPSGWDYRRGP PCPANI*LII
8040	21941	A	8100	116	432	YLRNLFYQQAQFSPAILNLMCSAL*BSH TVAQAGVQWHNLGSLQPLPRFKRFSCL SLPSSNIFAPLSYFFRNSSFTNISPS GPQITDPLFIKKKI KVSVMVE
8041	21942	A	8101	361	138	FNLLGRKKKNFGGLKEGESRRPPNPGPQ FFFFFLFFFFFSG*RWGLTMLPRLVLNS WAQVILLPWPPKSLGLEV
8042	21943	A	8102	1	199	PTRPFVFLMEMEFYHIGQTALELLTSGN LPASASQSAGITGVSDR*LA*YLEFFHE LFCYFALLLI
8043	21944	A	8103	412	46	KGGSPPPPPPKIGRKGPPNPGDPFFFF SPFFFRGF*GSPFFPK*KVLLVGLKPK PPFPLGWGNPPPPVGGFSPQSLQFFF FKKVEGWVFFFLFFFFFSPFFLFFS ETESHIIAQA
8044	21945	A	8104	192	2	EETELSFIIKYYLPRNQKVKRRL*RR GPVAHACTPSPLGGQREWITRSGVQDQ GQDGETP
8045	21946	A	8105	373	183	GGPF*FQYILILFDNFFFLSFFFSQD FFFLSSFFFIFFFIFFFIFFFIFFFI FFFIFFFIFFFIFFFIFFFIFFFIFFFI
8046	21947	A	8106	373	281	SFKTAPPPFFFW*RLSLTMLPRMVS SWAQVLLPQPPKVLRL*ATQRKKHFRQ EQI
8047	21948	A	8107	3	114	FLIFVHIGPNYVAQAGLELLSSDDPPAL ASQAGITGMNHARPYYLL*TLNIP YDPEIFLLGIYPR*MKTYVHTKACT*FF ITPLEVIAKTWKQPK*PSVLGLQA
8048	21949	A	8108	416	243	PGVFPFPPF*NPPPEIIFWAPKKKYFP PPPLNLFVFFKGPFFFIFFFIFFFIFF L
8049	21950	A	8109	2	211	SVTQAGVQWHVSLQPRLEGLEQSSCLG L**CWDGCGHEPWHLALVTTSKHTESCS LCIPTATFLGLVT
8050	21951	A	8110	172	28	HVVCFITSFSGFYFL*RQGLTKSPRLVP

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						NSWV*VILLEWPPKVLGLQA
8051	21952	A	8111	2	225	QKSAKNFVHLSIYLSIYLSIYPSIYHLS IYLSIIYLSSTYE*VIILEQKWSIKKG CL*CTIQTNCL*QLKE*VIRLIPKL*YK IKLPTCWSVHLNWFTLCNISWYLYLAM **RKLVCFA*FVVVNSNKLITIKRIGH
8052	21953	A	8112	392	221	PPFKRESPPDKVNPPPDIFGGKTKKK TLANN*FPPKEKEFFVFFFKKEDFF*NI VGNFKTPSKI*AVCF*NPVFKKKGAPK KKSSFKNF
8053	21954	A	8113	369	112	IFFSTIIYFXHPFFPPPLFFTPPPLFF FFLKKKKFFFFFFFXKXFFFFFXKXFF FFFFFFFFFFFFFFFFFFFFLAF*HVSF
8054	21955	A	8114	418	248	KYYLPTPGY*NLILLNGPPFFFFFF*D RVSPCCPRLP*TPRLTQSSCLSPRSWD HRCMLRLVTF*FTFKLSHQSLRTLTY TLAGTTLG
8055	21956	A	8115	229	78	SFKGAAPFFFFF*RQNLTMSPKLVNS RPQAVLPWPWKVGLHRRGWIT
8056	21957	A	8116	356	66	PLFPFFYIKNFKKKFFFFQYFFFPFF PKHYSHKDIFFFFIIFKFPSSSFSFPFF FALSFFFFFFFFFFFFFFFFFHA*FPVF FLYKIPMLYPQL
8057	21958	A	8117	212	81	ERLSHCSLNLDPSSNPPASAS*VAGTSG THQLVMVHAGSPRF
8058	21959	A	8118	367	2	GVFFFFFSPAKKGVFFHPFFLGRPFPP PPPPFFPLWFFYPWGP*KKY*FPHPRGY EFFFF*GGPPHFFFFFFFFFFFFFFFF FFFYAEGIGVSPCYIMLGYNFSSFCGT ISPRVRPRV
8059	21960	A	8119	38	215	FFKSAFHHTRLIFNFFFLEKTGSHYVA QAGVBLLG*SSPTTSAFEIGGITGLPLS FKN
8060	21961	A	8120	266	2	PQIFLFIETRSHSITQGVQWCDHSSL QPQNPGLKQSSLSS*DYRHTLTAP*PC FL*RCGLAMFPMLVLSSWPQAVLKIHPC CGMC
8061	21962	A	8121	3	332	DANADAWGHVPPPCPANFVLV*TGFLHI GQAGLELPTLSDPPASASQSVFIYFLET ESHSPAWEATERDSVSQKKKRGGRFKGS NFTSAGLQRFIFPMGPPLISRAGV
8062	21963	A	8122	378	66	LFIFLPPIREEVFPCIPG*NWAPPVGLYN GRPFFFFLLETVPLHAGQAGLELLGSSD LPVSASQSVGITGMSHRVQPKLRIFVNI SFPFEIFCEIMLLVPLAQF
8063	21964	A	8123	2	316	ISMALLALLRIITFRLPQLNGYVEEFTF YECGFNPISPGRAPLFIEHFLVDITFL FDVQIALLLPLP*ALQTNLPLIVMPSL LLIIILALRLDYERLQNGSD
8064	21965	A	8124	331	14	ITSILLIITTF*LPQLNGYI*KSTPYEC GFDPIPARVPFSIKFFLVAITFLFLDL EIALLLPLP*ALQTNLPLIGMSSLLLI IILALSLAYE*LQKGLD*AE
8065	21966	A	8125	2	228	IIITF*LPQLNGYIEKSTPYECGFDPI PARVPFSIKFFLVAITFLFLDLIALLL PLP*ALQTNLPLIVMSSL
8066	21967	A	8126	451	200	KA*WNRFAILNVTKYTCEQBVKIPTF

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						AGVWKKLI PAHTDDFVHFKTSVQEVATD VAKIASLLELEVESEDVTE* LQSDKT
8067	21968	A	8127	2	396	LIVIINTLLALLLIITF*LPQLSGYIE KSTPYECGFDPI SPARVFFS IKFFLVAI TFLLSDLEIALLLPLP*ALQTTNLP LIG MSSLLI I I LALSLAYE* LQKGLD* TBS GWEKLVKKEKADKLKGGRP
8068	21969	A	8128	1	350	GTRGLQTLPLIAF* * L IASLANLALPP TINLLGELSVLVTTFS*SNITLLLTGLN ILVTALYSLYIFTTQ*GSLTHHINN I K PSFTRENTLMFIHLSPIILLSLNPDIIT GFSS
8069	21970	A	8129	375	1	LTCFSEHRPPPRANFFFSRKTRAPFFLP GGFQIPGNFFAPP I FPNGGPI PGLDPQ PGPLNFF*KSFFPDPKFFFLPPPPI *N SGVFLPRNPVFPKTPNLFPPFPFPFGD GVLLCHPGRLPRA
8070	21971	A	8130	32	211	GIRHGFAMLPRLVLSWPOAILLPWPPK LLG*QAGVELLASSNPALASQTAGMTG VSTRPPVLLPTLGLTHLCLDACLSSSL
8071	21972	A	8131	396	5	KYRDGPPPPGKFFFFF*DGFSLCCPGW SQTSCPK*SSCLPEG*DYRHEPPHMTLS SSY*CSQMCKCINKNCLGSCVVAHACNL SPLGRRITWGKKFETSLDNIVKNRLKK KKKKIYQGGGDHPCIFTN
8072	21973	A	8132	347	34	KAGFVI PRGPQEFPPFFFPQDGILLCFP GWRVAKS*VTATSNWAQAITGMLPPC PANF*KIS*QSI SMFRLVPSNWPQVI LPPQPPK*LGLHVCLVPSLA
8073	21974	A	8133	102	270	DYRTPPHLANFFYFL* RQILTVPMLV SNSWVQAILLLQDFFSVQLKMGFLSVF
8074	21975	A	8134	338	47	FLSTQKESPLHHTHTHTHTHSHLLTH HHGRGQERGKGR*GG*WRTGTHSPHGP HCVRLRKSRLPSGRLGAAQGGCSLIQPKI EDPGQSGGPREVP
8075	21976	A	8135	68	467	SLNRI PFCLCLNSFDCVFLGLLFEAG FCSVAQAGVWVYEHGSLQP*PRGLK*SF HLSLPKFWDYRNEPPHPPFSCFALNFK DYCDSGTVPCPFMKELSM LFIHALTESF VLFIVMSKLITTKHLTIISNV
8076	21977	A	8136	500	355	FHHVQAGIQLLTSGDPPA*ASQSAKIT GVSHRAPQTSFLNKLPSLR
8077	21978	A	8137	58	222	IYGYEGRGSVAGSLSSL* SATDSDLDY DYLQNWGPRFKKLADLYGSKDTFDDDS
8078	21979	A	8138	345	196	KGDQAQWLRPGMVAHICNLSTLEGQGR IT*AQKFETSLNLTLPPI SFK
8079	21980	A	8139	500	355	FHHVQAGIQLLTSGDPPA*ASQSAKIT GVSHRAPQTSFLNKLPSLR
8080	21981	A	8140	3	231	HASADAWGRNEWPCAVAHANPTTSGG* GGWIA*AQEFETSLCKIVKPHLSKKK KKKKNFSPGWGSPCTPLF
8081	21982	A	8141	416	26	ARIFPNNSFWPGQGGFFPPRPLEGPGG VIP*CGVQARPA PPGEPRLFPKPKIV GGGGEPLFPFPERAGPKCRPFEGGGF N*PKPRPCPPGWAQGGFVSKKKKKRNE DSKIPLIGKYPVGIRNMA
8082	21983	A	8142	413	35	RGAGGGGSPGPRYPSPQHLRARTPTP FARSRGSPGVRGSGWRGGLGG*SRERP

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						LPSLPFRALFRSGASSGFLDGGAGQGPGR RERWAFLLGGIRADARGCRAVTSPEPYRL PGAGAARARR
8083	21984	A	8143	166	368	ENILWAAAMVVLDCHPSTLGG*GGRIT*G QEFKTNLANIERPHLFFFFFKRDSLFA PRAEGGGPILF
8084	21985	A	8144	1700	621	DLRDHSVLQGGPACLRGCEPILSHSEG SKIGSERESGHSRHPAPPPSVEVGS RS*GQDS*GFGPGNGQDTRGPLSHAAPN WTPDPAAAVAAGGTSLEPPRGGGGI*RG SHTARSGARVGSANAHARGSGFSRHS SHGCLRNQSPRLGKAGALCGSAWVSL* GSGLTSPRGRRERLRMPGVAKGRPR*GN PRRGKQKHGIPASGLPGRCNLGIKNT LQPRTRAPERLFPVQESSGSTPEKMLVS FHGSSLRNEATPRYSQQEAGNGRWQOS LSLERWPPWTSHPGLTPPLMPVAVARCC ILPGLWPLLSPPSGASFPVSGPGLSL WPNFAKKDDFPVRQGDTSWRSVS
8085	21986	A	8145	390	38	NTTTFNIYFFFFFSLFIYFFFFF FFFFFFFFFFFIFILFIYSLLVGVWVLGL GLALALLAKLFLVNSLCRRYRG*SLLY AWL*FFIFPLRYIYICARFQFLSPILYL GKWFG
8086	21987	A	8146	20	187	KLTTSTGRNPGRPTRPNF*VF*RDGLI MLPRLVSNWSWPLVNLLEWPPKILGLQM
8087	21988	A	8147	417	64	VRPRVRPRVRPRIRKKKKKKKKKKKK KKKKKWGGGF*DFWGGEKGPPLQKND LLFWGFFLKSTFFFCGGLFFWGGPFFFP PPPNFLGVGGKKKTFRLLCGPFSAPFGG EKN
8088	21989	A	8148	351	187	RLGTFYLSNILRFYLSITHGPIPIYGR TSQNLPLLLDLT*LEKLLPKKSQTYN
8089	21990	A	8149	465	60	PPHFWGNPKKNSQFFWAKKKKIFLGP *KMVAKKGVVFWGRKKGFQRRGKK*KG GOLFYPVLSQVLGGQNHGPPGKAGFGE NFFFGQGLGWAISRWLRTPLFLAGGGE DPKKNFKPPPKIKITLGAGVKKK
8090	21991	A	8150	1	175	WDYRHVPPYLANVFFVIFRGDKVSLCCP V*GPTTELKRSSCLGFP*GWDYRREP LA
8091	21992	A	8151	59	35	RWNSRRRPGKFLTSGDLFASAGSAV ITDVSHHAWPETFFR*RA
8092	21993	A	8152	269	159	ARVEVSKKYIYIHTHTHTHTHTHTHT HTYTTKKLPS*LFQVCKMEKFGRLVVQ
8093	21994	A	8153	1	256	PGPPPRFFFFFFFFFFFFFFFF*TLKI RFIWRKQKTHNPKDGILHQDISQVISLQ ITNHFHRRYFCTNFTCIQERDINQSLF F
8094	21995	A	8154	252	41	LIIPVLICIVFIVLQKIFSVISLNKGL FRNHFFIF**RWGLTMLPRLVSNKAQV ILPPWPPKVLGLQV
8095	21996	A	8155	21	443	HELALI*FISTLAETNRTPPDLVDGESE LVSGFSIEYAAGPPALFFIGEYTNIIII NTLTITIFLGTTYDALSPELYTTYFVTK TLLLTCLVL*IRTAYPRFRYDQLIHL* KNFLPLTLALLI*YVSIPITISSIPFQT
8096	21997	A	8156	2	205	LLHLMKHFNLEIQKAQ*TRINLKRISR

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						HVIINLSKAKHKG*ILKAVREKMLIMYK KPLVKLQVISN
8097	21998	A	8157	2	205	LLHLMKHFNLEIQKAQ*TRINLKRISIR HVIINLSKAKHKG*ILKAVREKMLIMYK KPLVKLQVISN
8098	21999	A	8158	2	222	VYTWGTGKARVFPGEF*LPVWIPTRHLK FYNEPIRDANESASAETENPQSSIHPQ DEQNGDIRRTDKVTIHQ
8099	22000	A	8159	1	297	GFHHVQSGLELLTSGDPLASTS*SAGI TGMSSHAWPLNCSYGDSFSLKCPCLTV ACWWEEGWRKLLMENEQGREAHQKLSV INFYIKDSMTKRKYK
8100	22001	A	8160	138	437	NEYDHFSTIKERRDFIVCVFFFFSKKS LTVGTQGGPSYLEPFFLGNKEFSLTFL GSWDNGGATRLG*FFVFRKKGVSPCG PGWS*TPDLRKTPPSA
8101	22002	A	8161	330	148	QQSKTFFFFFCKKKKIYICMVVHAY NPSYSGG*GGRIT*AKKFKTSLNNTVRP HLYK
8102	22003	A	8162	391	255	RPAPADF*FFFFYRLGLAVLPRLVNWSV POATLLPQLRLVGLQI
8103	22004	A	8163	131	3	HKVSLCYPG*SALMQS*LTVASNSWAQA ILQP*PPE*LGLQA
8104	22005	A	8164	97	440	NKGSCLPPGGRPGALSHPTARSRGSPGP TPQKTGNNGPGPPTPVNLBFEKRGFTP VGQGLKLRT*RSPPPSAPQKAGITGGS RRP GPIQKKFLKTLGETKWMALIKTY LK
8105	22006	A	8165	541	295	FSQQKKKIFISTNLSHQESKIYICKEME SHSVIRLLEGGSGAIMNHCSLKLPSSSDP PASVS*SAGIIGVSQHLANYTFKKIF
8106	22007	A	8166	440	259	PPQKFFFFFFVKTGFRHV*AGFRLLD SSDPPPLAPQSVETGMSFSPARPMFGVF HSLR
8107	22008	A	8167	23	405	FRICHLRLVHLLVYFIPSFDTNHLSTS AMFLYSNDVVIAQNVSGPFLGIIFRTFF FFFLKGEFFAPQVGGQGNLG*LNPPP PGLKGFSGLTTPGGGNSGGGPPNKPWF IFKKGGGSTLWPRII
8108	22009	A	8168	23	388	PYFSCALPRHPPPTNLGPHLGMGAPWG QPSVAHHTLLFFFLKRDVCFVPRVEK LWLBESSLNPPLLGLKBFSLTLWRTGN NGGPPPPPVIFCF*KKGGVYPWPGGGGE TPALKETPGL
8109	22010	A	8169	612	498	NIHFSLSFSHTHRMHHTHTHTAHPTYI RTP*DNVPQ
8110	22011	A	8170	2	288	VNLTFPPQHFLGLSGMPRRYSDDPAYT T*NILSSVGSFISLTAVILIIIFI*EAF ASKRKVLIVEEPSINLE*LYIKKKKKKK KKKKKKKKKK
8111	22012	A	8171	381	101	QKSLQQPSNIATILEEVQVIFLGSPYHL QRWEMRLTKWLRGLGAVAHACNPSTLGG MGGWIA*AQLELTSGDPPPSNRQLFTG EHNNDNKLI
8112	22013	A	8172	136	360	TKKHFGLLK**TKKHFGLLKKKKKKKKK KKKKKKKKKKKGGGAFKKKKFFPRGGGK IFFFFGAPKNKFGGGVLKTGGGKPGVT KK

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8113	22014	A	8173	358	58	EKVSVFFFLKMKCSGILLPCRLTLPGST DSPASVCRMPAIAIGPRRHA*LVLVETGF RCVGRAGLQPLTASDPPTSASPGAAIAD GVSTQCSMVPRIRVQ
8114	22015	A	8174	254	370	GLTVLPGLVSNWSAQVILLSWPPE*LRP QAYATGAGLL
8115	22016	A	8175	48	269	FVYVILCLRDVLLCCIGWS*TLGLKISS YLSLLSSWDLQHVPPHSASCLTF*VKAC FFLLKYLKRLKIYAKIM
8116	22017	A	8176	1	338	PTRPINTLLALLLIITTF*LPQLNGYIE KSTPYECGFDPIPARVFPFSIKFFLVAI TFLLFDLEIALLLPLP*ALQTNLPLIA MSSLLLIILALGLAYE*LQKID*ABF
8117	22018	A	8177	426	130	QSLDPPGNMVTLSLQN*KNPPP*GGAVF PPPGRLGGENPPGGSKEQRRPAPQGG* PRQPPSPKKKNADSEFSIFNLQPALCK QYCVLHLENKILF
8118	22019	A	8178	396	244	KIHLLYICMCIYIYVISRHYILR*HTHA HTYTHTHTHTHTHTPKNTKYTLW
8119	22020	A	8179	2	119	TRFGNWPVGVAHFYDPSTLGA*GELIT* QBPETSSSLY
8120	22021	A	8180	2	80	FLPLTLALLI*HVSIPITISSIPPQT
8121	22022	A	8181	438	333	SPLGRLRHYNCLNWGGKGCN*PKSCPCP PAWGTK
8122	22023	A	8182	393	19	IFFFFPFPPSPAKFFFIKPKRPPPLWG GVF*SPPPGFQKTPPPQKVGSRVFPFP PPKFFFGGKGYFFKEPPPPPPIL*K GGAKISPPPPPGKKNPFFLKGGKKKKT PFIFFPFKIKIN
8123	22024	A	8183	24	269	GSQQVLGFCFRDRVLLCHPGWSAVM*S* LTVASTSWA*RILHCSLLGSWEYRHTPP CL*NRNPQLTVKWRVKDHNNKSHR
8124	22025	A	8184	154	361	WHNHDPLOPQTHGLKRSSHGLGPSIWHY RHVPRLANFLNLSFRQGLAMLPSPVC HLLVFLS*HIYWTFGYLS*SVCSHLLNF L**WHNHDPLOPQTHGLKRSSHGLGPSI WHYRHVPRLANFLNLSFRQGLAMLPSP SVCHLLVFLSETLGFK
8125	22026	A	8185	228	337	RPGMVAHACIPGILGGRGGWIT*GEKFE TSLANMVK
8126	22027	A	8186	314	127	DIQPKNEGEGEEBQELWLGMTAHAYTPS TLGD*GGRIA*VQEFETCLGSLARPPSL QKNFKN
8127	22028	A	8187	10	420	TQAEVAVNWDHATALQGRQSETPSPE KKKKKRGPPRWGENFPPTPGGF*KDGGN KKTGFPFPPKRDGPPPPKNWTPWVFQKRG APPEPPPLGGALGREPLGGFFGKGGVET PPPIFKKNPPPEKKPHRGFNFFAF
8128	22029	A	8188	398	1	LKKKRPQTPFSPKIQF*KFFPPFPFKKS PFPKNLLKKRAPGGPIFFFFFYPGLEK NPSPL*MGSPPPPLFNPNK*KKPPLKK GPGF*WFFQKKKPPFFFFFWRQGTIV LPRHTPSCLVNFCIFCRDGI
8129	22030	A	8189	30	153	AWYVRREDHVSLLGG*GCGKPWLCHGTPA WVTEENPKGKIK
8130	22031	A	8190	206	45	HPSONSLSKN*ERVSVCCPGWSAVAGSQ LTAASTSQAQVILLQPPE*LGLQA
8131	22032	A	8191	3	228	TCVCLCVVYICDVCVGCVCVYIDEYIQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to... last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						IYRYIHTYIDYTHI*YIHTYIDTHMW VCVYIYIYRCMGVRET
8132	22033	A	8192	41	416	ICRVKETASRPLLETHSLSLVELS*PCL TAQ*RNDFLALKHLTAVLYNLILHSSGF WSSLKSHFIFLAL*YYL**FI*SN*RRD LAVLPRLVSNVWPQVILPPQPPKVLIR YEPPSLALILFFN
8133	22034	A	8193	2	183	KRLSTWQKKVEGEFGQMDVGPVSVAHA CVSSSLEGQGGKIA*GQEFETILSNIVR PHLY
8134	22035	A	8194	2	465	AGVQWHDLSLQSPFPGFK*FSSLSLPS SWDYRSAPPCPADFCIFRRDWAGWGVGC GFHRVARAGLELLTSGDPPASASPGAGI AGMSHRTQRQDNFASWRRGGPQMSDPS PSCFLQNTFSLKPSWVAPYPHASALGG GEYGGPPSPQPHLE
8135	22036	A	8195	397	149	LICLTDLPFRFLSLALVFTVFNKVKV KDLIKLGVVAHTCNLNTLGG*GGRIA*A HEFETSLGNIVRAVIPCCFVSILSR
8136	22037	A	8196	355	95	KKIMPTLCLKIPS*YRCBIIQLSLQSS CDHRHMPHPPTNPF*RQHLMSLRSLVLN SRPQAVLPHGPPKVEGLQAPATAPGILS LF
8137	22038	A	8197	382	112	KTDGKKGSPSPSPFFFFFKKSFAFSPR GEKKAPLKSQRGLCPPKPKDPPPPGSG* TQDKGPPPPGQPIFFFFLKKGVCLFSRG GSKTFI
8138	22039	A	8198	32	361	ASRIGFILQEFLEPVRVWTTNPSAGADGY NFLEKQKGTETKSCSVAQAGAQWCHRNL L*P*TSELQSSCLSLSSWDYRMVFL LGKQVTLIGKRALSVPYPRDVVSLC
8139	22040	A	8199	1	314	INTLLALLLIITTF*LPQLSGYTEKSTP YECGFDPISPARVPFSIKFFLAATFLL FDLKNALLPLP*ALQTTNPLIGMPSL LLIILALSLEYE*LQKGLY
8140	22041	A	8200	3	109	FTSKHHFGFEAAA*YWHFVDVW*LFLYV SIY**GS
8141	22042	A	8201	3	216	DAWAAGVHHHTRLIF*IFVEIGSLCVSQ AGLEILDSSDPSSASQASGIRGMSHGA QSEHLFHRPIGKIK
8142	22043	A	8202	1	267	RIHTGEKPKYKECGTGPKGPSTLTTHK FFVYCREVAVLLKNCYSHLYPH*IIVNG SEADKREMCLLCIFFHPLAEQENVENK RKYNP
8143	22044	A	8203	422	92	PLVFALPPKIGFAPTPSSSPPPPLFF FGPPVFPFPPFNPFPFFFSPPPKKF PSPPPRGKIFPF*TPPPFFFPFPPFF FFFFFLLFLYLFLC
8144	22045	A	8204	445	260	VCSPLFIWVAPGFSPPPLFKNPPPNFF FGAPKKKNFFPPPPA*NFFFLKGPPLFF FFFFF
8145	22046	A	8205	103	248	GPGVVAHACNPSSLGG*GQWIA*AHBFK TSLSNAVRPISAKKKKGPPF
8146	22047	A	8206	407	197	QLIFKFL*EQASHYVAQAGLELLGSGNP PASTSQSVKVTGMSHGAWLLAPTLRSTS LNYSLSVLLLRP
8147	22048	A	8207	1	142	SCSVAQARV*FRDLGSLQPPPPRFTFPS CTPAWETVRLHLRKKKKKN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
8148	22049	A	8208	2	370	PEVFDYPN*FKNL*LHKTCTQ*L*AALF VITKTWNQGCPLTGEWINKLEYIHTMDY LAIKINELANHKMM*RTLKICLLSERS* SRKATYYMISIIIRHPRKGRKTIBIVQNSS CQGLGERQKGL
8149	22050	A	8209	363	108	KKPRVEACLSFGVGRERAKRER*KRERE RERERERERENEL*KLSLADLCIKNG*R EFFKEKRYVKRYAKILRVSGRKQKYGNV
8150	22051	A	8210	386	254	LNPGGGVCSEPRLCPTPAWVIR*DSVS EKGKKRKGKGPENSLTATNF*ALSCNLDY LRCSMLKMQQRKRKERTEVRFWQLHHN LTLGFV*LIYVQRE*RRTGWFVAKYMLY TFS*PGSFPRLRKCVEHVFGEYEPACSP FPLIHNQLHAKC
8151	22052	A	8211	3	131	AHLFIWFTEYFKPTVITYCSKKRIPFK MLLLIDSAPSYPRALMEMYKGMNVFMH DNLTFILWPMQ*VIFTS*SYLRN*FC TIAAIDSDSDGSGQSNLKIF*KGFTTL DAIKNICDS*EL
8152	22053	A	8212	86	286	WSIWECTVISVQLFHKPKTSFKNTSYWS GVMAYTNLSTLGSQDPQIT*GQEFETS LANMVKSCLY
8153	22054	A	8213	393	344	SFPFSLPSKWGPKNLVPSPGYFLPFLNK GFRYFGQGGFKILNSNYPPPLASQKGGI SGISWPRALVFF*WRNLGPN*RTIVSP NYGLK
8154	22055	A	8214	3	313	OGLVLWHSGLLQ*PPGLRSCFSLP CSWEHRCTPPHLANFLILCVVCVET GSHFVAQAGLELLGSSDPPLSISQKSWD YKV*AIIPRAKQNYLMFY
8155	22056	A	8215	165	348	RPCPLFPEDLLTFSREGPGTMAHACNLS TLGGQGGIA*GQEFETTLGNIVRPHLY FYLKK
8156	22057	A	8216	379	218	VFLVETGFLHVGQAGLKLPTSGDPPASA SVSAGITGVSQKCRF*YNVFIFQKSSLL NALPICSLTMLLGNLFSMFMTPKFTCS
8157	22058	A	8217	32	276	RYLPITAALEFTIARI*KQPKSSLLDKWI KKLWCITYTMEYSSALKVILTVVTWMNL VGFIPGDINHIIQKAKYCMISLICGI
8158	22059	A	8218	171	2	KGVFGLGRLEFFFLDRVWLCPEWSTVVQ SRLSATSAS*IQAILPPQPPEELGPLCP
8159	22060	A	8219	530	73	TKPTVGSNSRSYINQTVFPSTLTFFGGL MRLTIYHFFLLVYNNPRVMVTPAYM*L LILFYSSSIRDLLIAKQCLPNEGFSH AC*TNATLLFPYSI*YGLPSPHLIFFV CFSFYFL*R*GLTMPPMLVLSSNPQVIL PPQPPKVLGLQA
8160	22061	A	8220	350	135	FFFFSQTGVAQNRVQ*RDHNSLQ*PPG LRQSSCLTLPKCWDYRCKPLCLASWIYF KDKVYTSTPVHTQY
8161	22062	A	8221	185	331	PGMVAHAYNPNTLGG*GGKLT*AQEFET SLGNINSVPKRRKRKRM
8162	22063	A	8222	73	232	YCSFKFITLTCLSWLGTVAHTCNPSTVE GGGGRIT*GWEFTTSLGNIVRSCLY
8163	22064	A	8223	418	211	AMPSLLTYLLTFIFCRKKKIFFYWGEP ML*LVLSNWTQVILPPWPAKVLVLPRL ALFYSLLVLPSPF
8164	22065	A	8224	227	33	ESHSTTQAGVQWHDHGSLLQPPPGMSLY

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						CH*CLRFSWRPAEKPGWCSSLRFMELE SWSGASDAF
8165	22066	A	8225	244	287	TDSPTSAFRSAGITSISHHTLPKSTF*I FCRAGGLAMLERLVLNSWPQVILPSQPP KALGSQA
8166	22067	A	8226	53	235	NNKWQGVVAHTCNPTTLGG*GEWIT*GQ EFETSPANMAKIPPLVMFAFCFEETDNK SHTK
8167	22068	A	8227	275	25	GVLMPNFKFCI*QNSPFMLPGVVLNSWI PAILPPQRPKVLGLQAWTILYKWWYGKE MWHKEICEGTHDVLKLLTTRRFKRHL
8168	22069	A	8228	386	211	QLKLFPKLGKGLRPP**KFFFFFFFORQ GLTILPRLVSSSWHQMIFPPQPPEVLGL QA
8169	22070	A	8229	1	117	VFILFYF*DGLAMLPRLATNSWAQAILL PSAPKVQGLQA
8170	22071	A	8230	356	26	WHVHGSQOP*PPGLKQSFCSLPSSWDE RCAPHPINIFYQICRDRVYKRWANMVIS PNPLVLISQASGITSKIPCPGSEISTIF IFSHQLLLVRGVYPDMLVLQGLKTCI
8171	22072	A	8231	3	188	FPSLRPA*IFFYIYFFFLKNKVFCHPG WTQLLDPNWTQAAGLKQSSHLSLLSSLN FRGSA
8172	22073	A	8232	2	253	KLDYINCGTNLAQCLFCLFGSLFFQR* GLTLLRLFMNSWPQAILLP*PLTVLGL QATMLGSQVPVFDLGITLCRCRFGKLE
8173	22074	A	8233	373	65	PEKAGSCLELAFGLQMHPWASTLPAA LTDGLATVFNHVSQFLKSHTHTHTH THHTCTRTLVLFL*EALTTPLRSI CKHRESACSLTWPCC
8174	22075	A	8234	390	46	RVFKPG*NPLVKAPAPLFFGGV*GRS PKKNPQGGGGPPPGFHFFLTFPFF IFLRREPPPPFFRGGLGPPPPFFKTPFF FFFVWKGKFLPQKKKKFFQSISTRSV IHK
8175	22076	A	8235	387	216	OKLGVGLVPPGRVIFFFFFFC*GGGL TMLPRLVSNWPLAILLPQPPKVLGLQV
8176	22077	A	8236	1	201	RFFFTTPQCFFPQFILSF*RRGLAVLPR LVLPWPQAILPPQPELGLQAHPTTL GPVFYSYCVRA
8177	22078	A	8237	399	229	SVGGGGLTMLPSWSQTPGLK*SSHLSLI KCWDYRPEPPHLAHSLLNLQLYCHTKL S
8178	22079	A	8238	192	335	SHTLPHSSNFSYFW*RQGFAMLPRLVLN SWARAVCLPQSPKVLGLHA
8179	22080	A	8239	442	254	GRDRVLLFCPGWSQTLGLKRSSCLGLPK HWDYRHEPPHAEINIKFCVWPTLYFYWP ALVQINLP*QLOGTECVACMC
8180	22081	A	8240	381	180	VLKLFCCSHRGPTMLPRLVSNGLK*SS HLGLPNCWD*RCEPWHPASLCLLTSTFW PPTLICNIHK
8181	22082	A	8241	388	260	NAIPFYITKCCNPSTLGG*GG*IT*GQE FENCLANMVKPCLY
8182	22083	A	8242	1	145	GFTILVRLVLNS*PLDPPALASQAGIT GVSHCAQLIYVFQRLQLLW
8183	22084	A	8243	1	173	GLTVSQAGVQWCDHSSL*SQTLGLKQSS SLSLPSSWDYKCKPQHQRFFLMEFFQ M

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8184	22085	A	8244	202	327	TLFITFIFF*R*GLAVLPRLVLSWPQV ILLWPPRVLGLEH
8185	22086	A	8245	42	289	KEKRSIILFIFFCRDGVLLWLPRDLNS WPKTIFPPWPPK*LALQHTTIPRGGS IILICIRDVKRERKQYAKSKNPEGET
8186	22087	A	8246	592	485	NIVSQAGVQWHNLGSLQPLPLGLKWFSC LSLLSS*DYRHVPPCPANFCISVETRF HVGQAGLELLASNNPPAPASQSTGITGV SPCTRPRVYVFLWILANGPS*RAETLV NLATNQEDADSSLPGLSGHCF
8187	22088	A	8247	307	12	MCSFVFSFKQKNPLFLNFFKKEFLFFFP GGRQGGHFGFLAPPLPGLNKLVLPPFG NGDTGKGGPPARGNFFFFFFFGIFSRDFV SPC*PGWSLIPDR
8188	22089	A	8248	392	237	HYGQASLAPLTSGLDLPASAPQSAEVTGV SHRAWPTVLI*SFS*KFNWV
8189	22090	A	8249	153	386	FFPPGWPKEPSLLEPPPPWLKGFPPPTLL GGGD*KRPPPPGPNFCFFKNGVSPLEWE GWF*TSNLGNPLSPPKRVGIT
8190	22091	A	8250	387	166	IETILDAIKNIHDSWEEVKISTLTRVWK N*IPTMDNFEGFKTSLEEVADVMGIA RELEVEPEHVBILLHDIS
8191	22092	A	8251	405	266	LFAIVKR*NHPKCLLIYARINKMWHIST GWNISLISKMGKFSYMLTWMNLEVIM LSEISHSQKVT*YMVPLA*GHLEKLNCL PIKQQTPIPSSSSP
8192	22093	A	8252	379	201	PGANYACNPSTLGRSGWIA*AQELET LSNMTKQPQCSTPQCFLVNQLLQNLV YFP
8193	22094	A	8253	78	311	LTLVFHTRKKKGLK*IFVFI*SILSQKD LKVGTPGAGAAHTYNPRTWGGWKLQAG KRIT*AQEFETSLDNTVKICL
8194	22095	A	8254	303	81	TPCAENFKLRKRFHHIISLQRKMYLIS FLYF**SHSLTILPRLVSNWPQAILLP LPPKVPGLQVSATLPGL
8195	22096	A	8255	2	376	MGYNLVCHLLRPLEKRSSIRVGV*FSG CPPSPPLPARKGYSLTPCASQVRQCLAL LWLTGLGLHPLSCPHCPTSPSVMNPVQ LEMQKSPVFCVSHAGSCRLELFLFGHLG TQSSLDSPFKKVI
8196	22097	A	8256	70	356	LIIAYNLTYDLSWKMFFVYLRKIYTLH WVECSIYTCWV*FVYSMVSWNRIDSPGK KKTNIYDQLIFNKGAKSTKLKNSLFNK WGQDKISTYKK
8197	22098	A	8257	403	85	PFCPWFPFVFIPPPLRKSGTPPGGPEF PGPGFSNGGNPRPLKSPKFSPGWGRGP LFPPSRGV*AGNFLGPGRWGPWAKFVP LPSCLGHKARFFFPKKRRKIK
8198	22099	A	8258	249	2	YCEGDLGSYRPGVSKCMFSPRRDIRIM PWPGAVCYAYNLSTLGGRDGWIA*A*EF GTSLAYIVKPHLYTHTHTHTHTHMY
8199	22100	A	8259	2	189	IQVCVTKSHFCHPGWSAVAQSWLTAAS TS*A*VDFSHLSLLNSWD*RRVTPRLVN LILFPS
8200	22101	A	8260	453	128	FFFFFFLIETVSHDVP*AGLELLSSSH LASAFQSAETGVSHHAQPSVSWLIHS S
8201	22102	A	8261	420	79	KNPTFFFFFFLIETVSHDVP*AGLELL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SSSHPLASAFQSAEITGVSHHAQPSVSWLIHSS
8202	22103	A	8262	1	262	NSRTERLGSWQSHFCHKEMEAHFVVQSGVQWCDLGLSLRPLPPGFK*FSCPILLSGW DYSQCRPCRTC SLIFMHSRSPSQPSEKKWTC
8203	22104	A	8263	321	100	SATKNYLLSRQSF IGK*NNGLGAVAHAY NSGTSRGLGGQIA*A*EFETS*GNMMP HCYRKYNLARHSTYSPR
8204	22105	A	8264	145	275	KPRDYSFFF*WKRDLAMLRLASNSWTHAILPPWPPKVLRLQG
8205	22106	A	8265	73	351	SLCYRSFARCDRPPKGGHFSKSYLQDAQ WARTLLSTIAQNNSAEHHLKTTDW*GAV AHACNPSTPQGRGGRIA*VQEIETSQGN TGRPHLYKK
8206	22107	A	8266	382	232	LVEITGFCHVGQAGLKLTLTSGDPPASASQ SAGITGVSHCAWL*T*YS*DFQ
8207	22108	A	8267	397	130	IGQAGLKLTLTSGDLPTSASQTAGITGMS HRAWPTFSLIAR*NASFQVGHFSPKYQV GTLAKSLKCHQVRSDTLEFILCCRRIYE TLGKF
8208	22109	A	8268	309	97	DTWYTRRRKDHCTITETRIQSVRPLSPR *AITSRVCTYTSR*PEANEPPQKITFR HCDLFLPTLTDQLTL
8209	22110	A	8269	2	224	DSSGIPGSPTRPPTRPKKQKLPDPTVS LLGICIVDQRQ*SVFQORDICHSHMFITA LFTIVNIWQOT*HPLMDE
8210	22111	A	8270	374	2	TSWESARKEPPIHSHTLKGFFFLFMFF FF*NKICKDGS LTM LPRVVLNSWAEGL LPRSPKVVIGIQLATQRRASILCNPTY ACGIFQHVVVNVKLLMKQCPFCPAAPTK TQNEFFPRV
8211	22112	A	8271	1	379	PTSASQVAGTTGTHHHIVLFFFPGIFBK KGVFFFSPPGGF*TPKPKPPPGFGPKRGG KKGSGPPPPARGMGSGVFYPPPKPFFV LIGGQILFKGRTLDFKKRAPPPPFSLF LPKHTPSFWIKWDP
8212	22113	A	8272	80	401	AWGMRFCLLLYSCQYLISDIAHFSKAFF FWKREPPAPQVKGQGNLS*WNPWLQG *RGFSGLTPKGGNGYGPFPPLIFFFL RKNGFFPGWPGWSKTPDLRKPPC
8213	22114	A	8273	405	95	PPKRFWGS SKGFPQREKLGSPFPKKK KDFIYSYLSKSLKE*INRPSAAHTCN PSTLGGQGGRIIT*GQRFKISLSNIGRPH LYEKIKNVKLIKIPNKL
8214	22115	A	8274	167	52	DREQRPGAMAHTCNPSTLGG*GGWITRF LANMVKLRLY
8215	22116	A	8275	276	23	KYVSSRPCTVAHSCKPSPLDGGQGEWIA* VRKFKTILGNMMKPHLLFYKLTFFKNVK CIPFKYCATESRYVTKEKQKDRKKGTK E
8216	22117	A	8276	1	114	FTMLARMVWIS*PRDPPASASQSGAGTTG VSHHARPGLS
8217	22118	A	8277	2	87	TMLRLFLNS*AQAVILPWPAPVGLGQG
8218	22119	A	8278	357	347	SEGLALYQLEAFTVCDLRERGFCRGRSL WPLITWAWRGGVFLLVQFQEVCCRLALG SLSPDFVLLPESGGPTASQSGAGIIGVR DRAQPNCFEIGSYSVTQAGVQ*HNHGS L*P*P

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8219	22120	A	8279	371	125	FFPKINEPPG*PPPK*RKPGKFTLAPS PPFFGGGEFYKLRGVLKQKPGPPGVPK ILKTTPRLGKNKPISPPPGQKKQNF
8220	22121	A	8280	377	63	PPVFPFPWGGQGGGFP*ARGLRTPWPT ENPVFF*NPKN*PGGGGPF*IPPPWPG* ALKFPLPPRGVPLTKNIPPPRFSHKR RVFFPKNLKKKNPCLIESL
8221	22122	A	8281	2	284	LPK*VKNFVHAKICT*MFVAALFVITSS WKQPRYSSIEKWINKLWHISAMEYYSS LKR*ELSSHEKT*KNFKCGLSEKSSQSE KDTWCLIPVI
8222	22123	A	8282	318	40	APRLSLVFMVVFVKRLDSSPGSRITWT NCFENHLCCVCDRELLCQAREQWRVLG SPQSPSPKFKRFSCLSLPSSWDSRCKTP *PANFCGLC
8223	22124	A	8283	30	343	CYQKASHATEKSFMR*RVNPCSKLCCCY KILPOPPQPSAVITLISQNKKKKKKKK KKKKKKKKKKKKKGGGALKKKKIFSPR GGRIFFFFWAKKNLGGGL
8224	22125	A	8284	163	392	FVVLNFSVIYSISDPCWYKEQLCKSVF SFLSS*SLLDEPNPNSPANQAQLYQE NKREYEKRVSAIVEQSWNDS
8225	22126	A	8285	406	63	KKKLILAKPGVNLDSLKRAPPFFFFF RHGVPLCCPGWSKTPEPK*SSCLSLWSS WDYRREPLCLAYSPLNITHLSEFNVL CRDSQESYDPIIMMVIIITEGGMICGV IM
8226	22127	A	8286	1	322	TNTLLALLFIITF*LPQLNGVVEKSTP YECGLDPISPARVFFSIKFFLGATTFLL FDLEIALLLPLP*ALQTNLPLIGMSAL LLIIILALRLAYE*LLKGLD*AE
8227	22128	A	8287	395	181	HGSLHPGTPGLQQFSRLSLPSSWGYRHV PPCLANF*IFCRGGVSLCLGSGVEGLEC QARLPVLVRABGLD
8228	22129	A	8288	3	246	SSTLSFPPSG*DYRHVPPCPANFFFWIL EKTFFCFVPQGGFNLWA*TSPLNPPWA SKGAKITGGTPGMGLINLANGRPP
8229	22130	A	8289	138	421	LLSSVFFFFERDFCFVPQAGGQWGNLG* WNPWFRGLKNFPGLTPPRSNNNGGGPPP PLIFCFFLKKRVSPPRGRANFLDLGT PPPGPPKERE
8230	22131	A	8290	141	375	RTFFFFFKTEGYFVAQAKGQGGDHGSLQ PQSPGLKGSSLLRRWDYGSMPPCPSIFF F*IF*KNGASLCGPNNSKTGG
8231	22132	A	8291	407	209	IGGPPGFSPPFVKNRPNLIFGPPKKK KNFPPPGKNWFF*KGPPPPPPPPPPPP FFFFFYTL
8232	22133	A	8292	86	433	PPXPNKLIEXGGA*KRHFPPPRGRVR FFFFGPKKTPAPGQNPGGGKPGWSPL FSPGEKNXPPTHXGGPVLGAPPPPGI VLI*KKTGLPLFVGRAGTNPNLGGPPAP PPKG
8233	22134	A	8293	147	342	LVKFEYTVLPKNRYRLGVVAHAYNSSSL GGQGGRT*A*EFKTSNGNLRSHLYK KRKEKKLN
8234	22135	A	8294	6	152	CCGHAPHPANFYSL*RRSLAMLPRLVS NSWTQAILLP*PLKVLALQV
8235	22136	A	8295	18	205	IPTRPPTRPFGRLNHFTTATRPGVVY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predict ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GQCSEI*GANHSFMPITVLELIPLKIFEI GPVFLL
8236	22137	A	8296	1	199	VLYIYLSILLSIYLSIYLSIYLASYLAT *LAI*KBIYYEYVLVMTEABIPHILPS PSWRPRKVMV
8237	22138	A	8297	1	318	PTRPPTRLLSRPIKIQTALHKFSLCPEY LQ*ADYLF*SLWIRPDADVPHACNL SIL GG*GGRIA*AQEFEISLGNIVRPCLYCI IKNKIKKKPKPQIIAFFLCFKD
8238	22139	A	8298	416	304	GFLHVQGAGLKLLISGHLP A*ASQNVGI TGMSSHARL
8239	22140	A	8299	352	31	EMILKAAREKK*IIPYNEPLICLTVDFLV ETLQARREWDIFVKVLKKKNKTKNPFYT KIEYLVKLSFYKEKVTKTLDDP*Q*L RD FINTRHANRNNTSNRRKRPIIKHK
8240	22141	A	8300	382	266	RWDFVMLPKLVNS*AAQLHVGLPKCW DYRREPPLA
8241	22142	A	8301	2	273	PLTRGPSASDALSSGGPYHPSECCTTY TTYKIPQRIMDYETNSQCSKPGIV*V VHTHTTGGRGSQQGLEGSREWNNWGD QRTSQV
8242	22143	A	8302	77	430	GMGLSMHRTHFQYLAHIHCPVHVHTHT THTHTHTHTHTHLCM*HTEIHKSRYGTE HAQDPFSIFSPTTPMCACHTHTHTHTH THTHTHSVYVTHKVCBETCLSFFYPESG TISHAQEILKRCLENKTHLGVWCFTSLL SVANIVFFSYKRQVAARGGLFFSLSQA E
8243	22144	A	8303	137	396	SSVKTMNYLKPVVHMVADRC*LFQCLPS KKKKKKKKKKKKKGGLKXKILTRGG GGIFFFFGAPKKISPGRV*KKKKKKKK KKKKGGPLKKKNFNPPGGGNFFFWG KKNLAGARLKKPGGGNPRSP
8244	22145	A	8304	329	144	NGPPFFFFFF*DGVS LCCPGWTAVARS LTFVAVFTLNCSVVGIHSELQHWFQDYL KLKTF
8245	22146	A	8305	404	157	RTYNPSTLRGRSGQIT*GQDFDTSLGDR VGPHLRKRKNYSLVECFYRIKEYPE SHKKAMKMLFQLKPDFLHIPOHIATN
8246	22147	A	8306	394	294	SLCFLTTPRDPNLGALIKNFYSPTPGWV SCVLSKGPPPPPPFFFDGVLSCPH*S QNPFVFALEWSGTPELK*SSHGGLPKAW DYTYEPHQVVELLRY*RSFPVLLLDG ICIFHSFFSPRGSLIP
8247	22148	A	8307	280	2	VVDShVTFFT SVITV MLFSIQYVKOLEN IKSWPGIVARACNPALGGRDG*AEFD SSPGNTAKPCLPQKNKTKQTKNKG GT LET SWRL
8248	22149	A	8308	136	330	MSYQKRSVNKYKSNNACEVTTWARHSG SCLRLYNPSTLVGSGGKIP*TQEFETSL SNIARPPLY
8249	22150	A	8309	3	118	IFVVLVQMFGHHVHGQASLEL*PQVIHP QPCKVLGLPA
8250	22151	A	8310	2	366	TRVDPRVVRSTRHNLC L PGSSHASTSA S*VAGTTSACHHARLIFSFPFFGLGFSE KTGFNFFAQGGFEPLGEREPFPGPPGF WGGGGGGTFRPRRWKFQKDIIPLVSN RGDQPEPFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=-possible nucleotide deletion, \=possible nucleotide insertion)
8251	22152	A	8311	253	446	SKTFQARGGVTEMGFRHVGTGLEILTS GDPPASACQAAGITGVSHHARLRI*YFI RIFILMTC
8252	22153	A	8312	430	88	GVGRIQISWSPWLKPKNSPGSPQ*VG APGGPPPPGPFYFFFPQKGFPLFSGRV *GGGSKNFFVFPKPNWGTSPPPPEGR GFFFFFLLSRDGASPCPPRPPKVLGL QV
8253	22154	A	8313	400	323	HRLMPPHPIDFFLFFVETGSCYVAQGAC ELLGSGNLPGSAS*NARITDVNHHAQP* KSSSGPGTQQC
8254	22155	A	8314	4	421	GGRIARTQBAKVAVSQOCTTALQGRHS KTPSQKTKKKKSPGGPPGPPGKFFFFF KT*KKGPFLLKPPQORGDPGRGKKRGGG LWKKPGGKLGGPPTKKKTRGGGANPPPLW GKGGPKGAPRAFPTKKKPPSGRNQ
8255	22156	A	8315	213	32	RCPGTVGHGCHPSPLGGQGRIP*QGF ETSLANMVKPYFFLNSKKTKNHPTKKN SQAW
8256	22157	A	8316	422	153	AATLYTHKTPHCYFFFLDRNLLCCPGWS QTPGLK*APCLSLPSSWDYRHKPPRPVT SPIFRKSYDVI PPPYLE*NPMMLYLPS YCHHI
8257	22158	A	8317	1	284	ERQDWESRLAMECAFHLEKSVNQSLLE LHQLAMEKGDPLQCDFLSHFLNQQVKA IKKLG DYLSNLCKT*APEAGLA EYLFDK LTLGGSEEDT
8258	22159	A	8318	187	37	TRDFFWPGVVAHA*NCSTLGGQGRRIA* AQKFESNLGNRVSHCLYKKFKN
8259	22160	A	8319	2	250	KYEQSLQEVWDCVKRPNLRIIGVPEEEE KSKSLENI FGGIIEENFPGLARDLDIQI REAQRTPEKSI AKRSSSRHIVIRLSK*E VWDCVKRPNLRIIGVPEEEKSKSLENI FGGIIEENFPGLARDLDIQIREAQRTPE KSI AKRSSSRHIVIRLSK
8260	22161	A	8320	371	196	NNFSILFFFFETRSH*VAQAGLVLLGSS NPPCSASRVAGVTGVHORYQQDDFKNFR HN
8261	22162	A	8321	3	235	FISVSFKYSKHIPNNMHLKFLVLFLNFF FRDGFWLRSG*SVVAILRCGHSSSLQPLT GLKQSSHLSPQGSWDYRRAPH
8262	22163	A	8322	1	395	LEVPLLNTSLLASGVST*AHRLTIES NRNQIIQALLITILLGLYFTLLQASEYF ESPFTISDGIYGSTFFVATGFHGLHGII GSTFLTICFIQQLIFHPTSKHHFGFEAA A*YWHFVDED*LFLYVSIY
8263	22164	A	8323	322	83	MHQSFVLAKVKKGKGRWFYSCLMIKSA PVLSTHTNTLLCWPGAVVHACNPSTLGG QGRWMA*AQEFETSLDNVGKPHP
8264	22165	A	8324	12	249	GFFLPPPPGRGEGRGPPPPPLFFWFFFK KGEFFLGGGNFLTLEPPRLAPPKGGK*G GDPPPPGFFFFLKKKPKPLLK
8265	22166	A	8325	139	335	ENILWAATVVLDCHPSTLGG*GGRIT*G QEFKTNLANIERPHLFFFFLKRNFPA PRVEGRGPV
8266	22167	A	8326	1	246	FRRLAVAPRVLLCYPGWRAMVQS*LTA ASNSWAQAIHLSLPKCWNYPYPTC *NSACWDESSFLLVSAMEVCGQPHS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8267	22168	A	8327	422	107	IYYVRQQRKKRGLFFFFFRPLPPGGGQ WGHFWFLQPPRGV*RRFFLNLPNRNPW DFKGLPPPPAYFAFFLKKGVFPFGQGD *ILAPKGPPSTSTSQKGWFKD
8268	22169	A	8328	1	161	FRGIRWVCHVLFYLSFFLRQGLAVLPR LIILNSWAQATLLPQLPB*LGLQTSS
8269	22170	A	8329	422	103	PPYSPFFGGPGGGVPKVRSGPPGPPQG NPFFFKPKNNPGGGGGLIPPSGGG*A KGMGLSPRPRLPLS*NWPPPPPGGQNK LPFPKKKKKKKKKKFNFEHRG
8270	22171	A	8330	46	422	STPFFLASQSAGITGVSHRARRSSSFQC TQILPFPETLPNLGFGSRHGRGFSQVL PAQSSSFDDLISVLGY*MLSHISLGN RALGFIPPHLSKWENGSTLRSIVLSQIE GLSSTLSFPHPV
8271	22172	A	8331	429	112	FSHLGSSPRQGFTMLARLVNS*PCDPP TSASQSAGITGVSHHAQPHAVFYIRLPD SQVLCHQMPYWPHTAHYPHRWIFSLVLQK NLSVPPPLWPIQSQPKASILLN
8272	22173	A	8332	291	19	KTFPPPKI*KFPNPLKFTPGCGGPPPP FLKKFVSPGNPPPKIFFFFFFPPPPFF FFFFFLRRGSLISIAQDGIQWHYHGSQ PQLPGLR
8273	22174	A	8333	307	123	KYFRGGGGGR*FPPLGGVKQKRGNG GGGSKPKLGSPPTRGKKKNFSPKKK KKKK
8274	22175	A	8334	3	169	HASADMCHQAQLLLLLLVETGLCHDGRA GFGS*SQEIHPPRPKVLGLQHPGLIY
8275	22176	A	8335	1	208	LCVCVCVCVCVCVLC*WRKGLALSP RGECSGTNMAHCSLNFSGSSNPVSPSH VARTGVVRPILG
8276	22177	A	8336	1	352	ILFYFIFYFVSFCFEMGSRVSQAGVQC PDLSSLQPLPPFRFRFFCLTFPSSRDYR CVPPLAKFCIIIRR*AAIGQAGIELLT LSDPPASAS*SAARTGVSHCSGPFINF LNWQI
8277	22178	A	8337	420	272	KAPCQFSGEKTVFPHCWNSWVPFRKKQ QKKNLCPCLVLYTSINSQ*TMGLNIRA RTVNIS*KYKEDP*TGKK*INKSCPWTG KKKKFLARTQKTLAIWDTLINWTSPLK MSTKQRHHLKMN*PKWLLFFVS
8278	22179	A	8338	427	202	LIIFYCHQSVQKKGVLPLLQEREGWAEA SLKISNISLSHTHTHTACAHHTHTHT HTSS*NGIKTVVITIKSFA
8279	22180	A	8339	2	164	TFGHGISLCRPGWSAVAPSRLTATSASW VQTILLPWPE*LGLQESRLLRDHL
8280	22181	A	8340	422	1	PPGPPGGKTRAPPPFFKGPNNLLKKG GPGAKPPKNGVFFPPPKVKGPQKNFG GTQISQPNKRG*AFTFFFL*KPPQKKK GPPPGKIFKGPKE*KFPSPGFFFFFLK QGLTSPRLERSGANTAHCSLKLSSSD
8281	22182	A	8341	1	456	RTRGAVSQGHAIALQPGQSETPSQKKK KKNPAPGGKGIKGTAKKGRNFDANI LGPNRPGGAPFGG*TAPPGKKRSGPGP IFGGGKGGPKKILSF*KAGGAKFFPS PVGTPFFRFG*KGKILLKKKPSKPGGG NPENLSPTNFF
8282	22183	A	8342	407	2	RQFILGAPGVPPPPGF*KPPPKIIFWGP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to-- last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKNFFPPPRGGEKFFSFKGAPPLFFFFF FFFFFSPFFPGALFFFFFTILFKTKPG VFSCCKGIPPKFFKRSRPPNGAGRLPLLG VGPLPGVPQGGAEERKISQGSFQ
8283	22184	A	8343	441	1	PPFYILGGPRVFSPPFFFKTPPQIFFLG PQKKNSPPPPGKKIFFF+RAPPFFFFFF FFFFFFFFPPFFGALFFFFFTILFKTKF VVISWKGIQPKLFKRSRPPNGGRLPLL GGGPPPGVPRGGAEERKFSRGSFORTGG SAPEFRA
8284	22185	A	8344	466	323	FGVAGTONPGRNFRVPSFRGGPPPGVQ GRNPPPPWFFPLNPPKHFLTP+VFPFLE PPIEWVGPP+PSYGFSSPVARK
8285	22186	A	8345	657	347	LPPWFLLRQSFTLVAQAGVQ+CDLGSLLQ PPPPGPK+FSRLNLPSSLDRCPPAPCPA NFVLLVETGFHHVGOAGLELLTSGDPPA SASQSAGITGVSI SAQPAQ
8286	22187	A	8346	3	212	DCSRGPPPHLANFGLLEKTGSNHVDQAG LKPLSLRDPASAS+SPGITGGSHRAQF *FIFKRGMAPKGF
8287	22188	A	8347	9	255	IPGPTHPSDFFLYBIDLFKN*KGFPFP PRGGGKNPPPPPPFFS+PPWKKITF QTPLTGVFGAPKNFNFWGGFKKIGF
8288	22189	A	8348	79	312	NAAGFEVGISKA*ALETLOITREHNSN KPRYAVTFESHMGTVLHLVQEHTVGY ITASCALKC+IESGGFLNDYI
8289	22190	A	8349	1	369	FFFFLKRDRVSLSSRVKWKHYSSLLQ LQTPGLQ+SSCLRFLSSQDYRHPPCPT NF*KCFVEMGSCCVTQGSQTPGAQAVL PPWASQRHWGLQGVRLCSLLLSNCPHS RLVWSWLFSGC
8290	22191	A	8350	434	324	LPILSPVWWHMPVVPVGTREAEA*EQ*SL EPGRRRLQ
8291	22192	A	8351	3	253	YMCSKFFLECSQAISAHCHLELPSSSD PPPT+NF+VIGTTGTCHHEWLLFELFG KMKPHYIAQVGFKLLERNFLKTKKVPF
8292	22193	A	8352	3	1431	SPRGGIPSLKQVYSSLTNSRFSQHLF+ EEALQRAREEBEKRKEITSHFQSTLTDI QQQIEQQSERNMKLCQENTELAEKLSI IDQYELREEHLDKIFKHRELQQLVDK LEQAQEMMKEAERHKREKEYLLNQAE WKLOAKVLKEQETVLOAQLTLYSGRFBE FQSTLTKSNEVFATFKQEMDKTTKMKK LEKDTATWKARFENCNKALLDMIEKAL RAKBYECFVMKIGRLENLCRALQEEERNE LHKKIRDAEISEKDDQSQHNSDEEPSN VSDQEI DAAEVNSVQTAVKNLATAFMI IHHPESTPHQSKETQPEIGSSQESADAA LKEPEQPPLIPSRDSEPLPLTPQAEA EGGSDAEPPSKASNSPAGLGAETQCBGL PVGAQADQASWKPEAASGQAPQAPTEA SLQKMEADVAPACAAEHVAMVPACE PSRQPPRAAABELPVGASAGQPQRNVA
8293	22194	A	8353	376	65	IHCGDHVQEVPKLVKALHMSWACSQI PKAGDKILTFDQLTLTKGCGTILLSG PHKGQEVYWHFSKALGTQHSHTKPCVHS RDQKFKHIRG+WASQGYKN
8294	22195	A	8354	459	85	LEEVSLEERVLEKKMIESEBLKSKQTRF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LEETKNQDKLNKSLKEEAMLQKQSCCEL KSDLNTKNELLKQKTIETLTRACQKQYEL E*ELAFYKIDAKPEPLNYYPSEYAEIDK APDESPYIGKSR
8295	22196	A	8355	231	158	PFFIFLYQSNDIARGLERGLEPEKVG ATDSCGDLMLMKW*ESVAPMTFSGSRP LSKPRAISLLWYK
8296	22197	A	8356	2	164	IHRGVENQMAEQGWKDVSVYVWGAVA HACNPNTLGGQGRWIT*GQEFETNLP
8297	22198	A	8357	23	291	CTHTRAQAHATHHLFFYFLYIFNFFBE TGS*IVQACLELPASSDPPASFSQSAG ITGMSHAWPTSCILKVKMALCSINCSA ACFLY
8298	22199	A	8358	1	307	FFFFETIESCSFAQDGVQWCDLGLSQPPP PGFKQFSCLSLLSSWDYRHVPRIANFC IFSRDGFHHVQAGLQLLTSNDPPT*AS QSAGITGVSPRAQPCPAF
8299	22200	A	8359	75	266	FVKTRNLFLTIVLEAGKSNIKARAG*VSG EEHGLCLQDQALLPLEGRNAVSSHPRGQ NMMRAKC
8300	22201	A	8360	1	295	NTWVFCFVLLFRDRVSLCCSVRSTVASS *LIVNMNLSFPSS*AYRHVSSHLDFFFF FKIQRIILPRLISNFWPQBIILLWLPQG LGLQPRPQVLVGN
8301	22202	A	8361	376	293	MGFPHVSVQAGLKLTLTSGDLPASASQAR ITGAGHHAQPDF*HSGDSWQAPPEPRDQ G
8302	22203	A	8362	375	142	PQEEFLRFATDVGEYRAVTELERPVSES WNTQKDL*QKRGRVSTYCRHTYGVGES FSVQRRGEHVGRGLGPCELEI
8303	22204	A	8363	36	363	QLSFNPLIGKKVLRVTFIGKQFLFLG GGVREAGAHSGAQATVRWHNLSHAKRP SCLSLPSCDHRHLLPHANFCIFWTD*I PPCRSGWQTPPELKQFTHLGLPKR
8304	22205	A	8364	455	235	GAQARAPRGIIFFFW*RGKFCMLPRP VSKFWG*VVPLPWPPKRVGLDSWAPPR DFIFFSFVKKRVCILW
8305	22206	A	8365	432	175	STDQVSVAMGPS*PGAGYNLLVCRWLRP LKKCSIRMGVS*PSRYCLSWLPLDKKGN SLTPCASRVRRCTVMLRLMLRGLHPLSD KP
8306	22207	A	8366	383	83	RRLIVFICYFSKK*GLPLLPRLVSNFWP QVILVPWPPKVLGL*ALKKLWLDVTHA YNPSTLGGQGTIT
8307	22208	A	8367	27	304	PFGFILTLKSSN*CTLRFCPLSIGKVR IHTLGNILSRRGYGERCSLPHCLWESIC LPVQSN*ALHKKVQMHPFDQAIPSRGI LPDTGTHK
8308	22209	A	8368	165	204	QNIPIAVSFFFFLKRVSCPPG*RAGG QSLFIGALTFOV*GILIPYPGNWELRG PPNLTNFF*FLNLRPLLGPINLHYVHD KTSPLLYLFFFF
8309	22210	A	8369	400	201	KERPLPRLIGSPFQGTWPRFSSKGEVK NSNFSKY*PPFINPAPRVCFEGIEVIT KFFQVRFFP
8310	22211	A	8370	21	408	LIPLSTYVCVRVCEVCVCVCVNI*GYA CNTLLIACNILDVPTSPTKDKIFSGD FLTIVGKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8311	22212	A	8371	1	94	NTLGHEN*LNSGFGGCSEPRSCHCTPTWATE
8312	22213	A	8372	546	972	PIHSLYGR*PSFCLGLALFKTLQVMHFLKDSVRNLKSSNLKVLNFRSPQIQATISPPLPQKTKTYEEDPKSKPKKEKNMEVNMKEWILRYAEQQNEEKNENSKSLBEEEEKFDPNERYLHLAAKLLDAKEQAATFKLEKK
8313	22214	A	8373	502	178	QHFWRRLRQKDSFALGG*KQPGQKGENPFFQKKAKNILG*WDQPVVPTTQKGGGGESL*PGRTKSPPTSGWGKKQNPVLKKKKNPQKTNCIPLCIYHIFLINRKTNTV
8314	22215	A	8374	362	112	YRMSVNPQVRAKRVSRQNTNTPPNFFF*D RVLLCRPG*STVVQSQLTVASISWAKAILLPQPROQAKYFLRLVKCSSEKGERIE
8315	22216	A	8375	411	21	VLGIYPTLVSPSPGLKMTKRVKLPSSGSKKVISSSNRPVFGVVAAGG*FDKPIKLAGRASSKYKAKRNCWPRVRGVAMNPVEHPFGGILQRIKPSAIRIYAPAGRKVGLIAVRRSGRLRGANTVQEKEN
8316	22217	A	8376	450	108	AEGGRGPRK**LRSCRVDGSAGQSPGP LRTSLETPGCSQGVVQLEPPRRRPQWWPGPPGHRDRRQHRPGRSRRQQGPESH*QRSGESRPPAVPRPPCLPWNKGVLE
8317	22218	A	8377	25	306	EQQPPPVAVHQSGPPGAPPEASPSHPGSEKQPVPVPPRAPLVPQPKP*LSPPHHPAAGLLAVHALAGGPGTVQRGLPGRAARAVSVRVAARC
8318	22219	A	8378	376	149	PAHCSLLTPGFRGSSCLSLPCNWPYPGRAPPRVGNFFFFF*EMESCVVAMLPSLVLT SWALAILPVLPPKLPGLQA
8319	22220	A	8379	98	374	SVPPFVGTYEGDAAPTGGGGLPALGR*GAAGGHVQQGHGPHRGHAAPKPSAQGGPGHSRECLEPSGGAAGGEREPFRAGGGQSWMRAPSM
8320	22221	A	8380	2	807	RPQCCVRAPRAGAVSGVPKLWSVP*SGRSAPHPTRS*VRSWSRWLRTQSWQTSRTRRSESKVRVSYQAWTASPPPAASASARP A*RTSSRSYSSSTCCSWLWPSWSTGPSQTFVRNSSTLSCLCLTRKWIAMMPQVLPCTFVRPSCSAVSTITRSFLL*QALASRVT*IAPPRGSTTRTPSPIRL*NLP*LSRGP GK*KSGSWSSSSSA*TRVVRTSAPLITSSLLSRSSCKAQTG*ASCRPVRVPIPAGSSLGASAPGSRCHW
8321	22222	A	8381	104	327	CIAPPEMLGIKYEVGKCPSGLSKLSKILKNTHHTHTHTHTHTHTHTHTHTHTLYLIREGRKK*CVCMRKTDSTCVS
8322	22223	A	8382	400	270	KPKLEVRASGQVQWLSPIIPALEEAKAGG*LEPRSLRHFMVCN
8323	22224	A	8383	178	588	ADLLSGAPGPPGSGSDNANSSEHSRACAPAAPGP*WLQPWLC*WQSPLEARGS*NPGVSHSSRIPGIPGAAGTSRPSGALPPQPAHGSGSGELHVARGCAGRPLWSHRPGCGQLLRVTAADSHRCASRGAAPM
8324	22225	A	8384	423	78	QQQELAEITGVTVESPEEPQRLVVS*GGTVPCCLACSLHRTL*TVGHGSASSFLAAG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DMEPLGDRGLQGTEQLH*GGDRASLQDI CFLLPVLSLLCPRSLDLHRHRVGTGFT ED
8325	22226	A	8385	434	176	FADDSRFDPLLLV*CAMLMLIREQLLEG HFTVMRLMQDYPITDVCQILQAKELQ DSK*PGGKRPMFGREASRPCAVAPGTHR NL
8326	22227	A	8386	2	305	RLWEDPPGRNTPPGAR*PGPCGEGGCHII REEQACGWPRGHSGPWRHPQAGPLQLGQ WRGKAGQGARRSPQGSLESRPPTLSAA PPAIHICSVGGVRLHCY
8327	22228	A	8387	331	91	EMRSHSVTQAGVQWRDYGSLQTRPPGLS FNVNWDWVGL*GDPSPPMLLPSS*ARP GGGWGPGGEGHVSKEAAGRLQGPP
8328	22229	A	8388	2	250	IHVRLWSQLFRRLRWEDLLSTGGGSCSE P*SCHCTVTWAFPLESLRCAHVYVYVTL LTALLGSLPCANPRQTAVSLPQAQLV
8329	22230	A	8389	388	176	YWDSQ*CMPSFAVPVESACICAIGHNFS KSVNSVLAVCVDGSSHKYVFTHDGRCHR EAFDVYRDCDDDA
8330	22231	A	8390	445	330	PPRFTPFSCLSLRSSWDYR*PPRPDNF LSLYSVLHET
8331	22232	A	8391	559	142	LRTLPTVTLGKSLALSVPSFPYVGNWIT NREPSAKGRGSGPNRGPCHAASCPARTH SLRHSPAGGVMLTQPRPILIPETOHPHS ESAVARTDISKARRWLHRSRSPWPH*DET SAGAERPGIRCYIGHPAT
8332	22233	A	8392	104	400	YYEIPKKEMYSYVHILHFFFPFFFFFFE TKPNSVNGPEGKGPILG*LKPWLLG*KH FCLTLPSCGNRYRHVLPVPVNGFFFFFFF KKKKVFPFVAPRGV
8333	22234	A	8393	408	169	DQVWIKDWNIGSLRPR*KGPQTILITTP TAVKIEGIPAWIQHSQVKPAAPETWEVR PSLDNPKCKVTLLKMTSPAPVTLRS
8334	22235	A	8394	1	269	YCCPLFSSKALTQENSPYSSFRLVNPPG LSLHPEGEQKWINERGERLGPAGPLL LFLHFAEAGRRQPPDWADSEADLQVVRH KLQGP
8335	22236	A	8395	2	204	KDCKVNKEVERVLREFHQAGKPIGCDAS TSLPAPAPWWSWNAALCCPGLSCVWCWQ GESRTCVEHQ
8336	22237	A	8396	3	285	KVTVKYDRKELRKRNLBEWILEQLTRL YDCQEEIPELEIDVDELDMESDDARA ARVKELLVDCYKPTFAFISGLLDKIRGM QKLSTPQKK
8337	22238	A	8397	1	192	ETGFHHAGQDGLELLTSGDCPSLASQSA RITGVSHCTRAQLLTEQYFKQNHLPS APFYKRAF
8338	22239	A	8398	8	241	LNPFLYAFLDPRFRQACTSMLCCGQSRS SGTSHSIRGEKSASYSSGHSQGGPNNMG KGGEQMLEKSIPIYSQETLVVD
8339	22240	A	8399	2	240	SCLNPFYAFLEPRFRQACTSMLCCGQS RSAGTLHSSRGEKSASYSSGHSQGGPNN MGKGGEQMHKSIPIYSQETLVVD
8340	22241	A	8400	10	272	CNWQNAYLTVVRCAQDCEDYFAERLYRS MKGAGTDEETLIRIIVTRAEDLLGIKP KFHQKYQKSLSDMVRSDTCGDFRKLIVA LLH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8341	22242	A	8401	47	248	TRGIFFFFLNTRSHSVAQAGLGHDS LKPQPPRLKQSFNLSLLSTWNYGGLPH SALWKAEEAAS
8342	22243	A	8403	497	303	TVEASVSYLIVAMVMQLPWGKSPASGA ESHRQCGGSGWPGGMEERGGAERGGC LLPQALLY
8343	22244	A	8404	3	235	LTLAHCRRMAAAHMGPPMPPMMPGNT PGMMPVGPAPGMRPPLGGHMPMPGYPM MRSAPRLMMVPSQPRMTRPDR
8344	22245	A	8405	3	246	LVFSDVDGLLAHTRQGLKRSSGMSLL GKIGAKKQKMSLEKSLDWESFKKEEG IGEELAIHNRGKEGWIQGAQLQ
8345	22246	A	8406	1739	804	WEPDVSGSAAWLASAAGMATFSGPAGP ILSLNPQEDVEFQKEVAQVRKRTQRKK QBQLTPGVVYVRHLPNLLDETQIFSYFS QFGTVTRFLRSRSGTNSKGYAFVEFE SEDVAKIVAE TMNNYLFGRLLLECHFMP PEKVHKELFKDWNIFFKQPSYPSVKRYN RNRILTQKLMEERFKKBRLLRKKLAK KGIDYDFPSLILQKTESISKTRQTSTK GOVLRKKKKKVSGLDTPEKTVDSSQGP PVCTPTFLERRKSQVAELNDDDKDEIV FKQPI SCVKEEIQETQTPTHSRKRRRS SNQ
8346	22247	A	8407	2	241	CLRFPSPPAMGLLRSGTKLIFRRRPKQK EAGLSQSHDDL SNATATPSVRMKAGSFS RRLIKRFYFKSKPKANGNPSQL
8347	22248	A	8408	285	186	KQGLTSLPRLVSNWAQAFLLWPPKVL RLQA
8348	22249	A	8409	1	246	RHENREELQVIADLCIKYDTLCISDEEF MNGVEYIWKGPCFCLTFTLYLKGDIFF RPPSGCLNLWIVLNPMPVVIHLITSC
8349	22250	A	8410	1	102	AGSYTLHIKGGDGTGRVTRFTTLHR IQTSEE
8350	22251	A	8411	877	647	FFFTESHSVTQAGVKWGLGSLQSLAP GPKKFSCLNLPSSRDYRSPPPLANFCT FSKNGVSPCWPGRSSTPDRR
8351	22252	A	8412	1	130	RMLNDKTLRTDIGGNFPKNGWAAIATHS FEFAQDFNLEER
8352	22253	A	8413	97	401	CNPENGLTASALGRMCLATCKAPRTL DSGDTASCRFPVPRPPHSRRSSGSHL PGRPRCPALPGLWSNPPGPPTSGYLF TFSTPAAHSHQKTLGI
8353	22254	A	8414	348	516	VSAYGFI TEGHERFSDHYDTSWKRLIF YINHDFKLEREVWKR LHDEGIIRLYQRL
8354	22255	A	8415	714	410	LGVFRSALHGSLLWLLRSFPQKSPNPLA LLFLQCNATAYQCLLIADQHCRTKYFL CLASGIPCVSHVWVHDSCHANQLQNYRN YLLPAGYSLEEQRILDW
8355	22256	A	8416	2	102	GHDPQDRLLAQDSEHNHSDRNWQRNRPW PKDSY
8356	22257	A	8417	1	309	FYFENALSKSNKPIHTIILNPHVLVGD DAACIAYIRLTQYMDGSGMPKTMQSBET RVWHRRDGKQNVHFRHSGSPPTVPIKPP CIPNGKENFSGGTSLWQNI
8357	22258	A	8418	3	242	ARALTNAASHVDDMPNALSALNDLHAHK LRLDPVNLKLLSHCLLVTLVDHLPDEFT PVEHACLDNVLASVSTVLTFRKYR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid-residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8358	22259	A	8419	711	296	NVANS DGLIASLWKEYGKADARWVYFDP TIVSVEILTVALDGSALFLIYAIVKEK YYRHFLQITLCVCELYGCWMTFLPEWLT RSPNLNTSNWLYCWLYLFFFNQVWVLIP GLLLWQSWLELKKMHQKETSSVKKFQ
8359	22260	A	8420	3	97	FVVSSLCNGLIAAQLLFYWNAPPHKQK KAQ
8360	22261	A	8421	1	279	GCGIADLAMS AIFNFQSLT DILLICT CAYIPSLAPNLLDRNKTGLLGIFWKAT IVERKSPYVAVCCILMAFSILLIQKLVK MPQCICHNI
8361	22262	A	8422	1	228	RHEVFIELNHIKKCNTVRGVFVLEEFVP EIKKVVSHKYKTPMAHEICYSVLCFSY VAAVHSSEEDLRTPRPVSS
8362	22263	A	8423	3	182	SEDTGEEQVVTAEFINRGEYEIDIAGYR FQAKAKLYPVASLFTQKRKDDMELSDL HGK
8363	22264	A	8424	1	70	VQVFVDAVTDV I I KNNLDCGLF
8364	22265	A	8425	2	151	ETTASSCTPASLESRRCCAPCRMPTGF FGSSPLWRPSSGSRSLKPGFQ
8365	22266	A	8426	1	187	RGRVGPGERLVPVPGAEAQPGAGGV RAGPLQARPPAPVGVSQRCQAAGAAG PPREDG
8366	22267	A	8427	520	423	GKYLQSQENFEAFMKAIGECWTERQSC GSHQ
8367	22268	A	8428	1	627	GTSGTRGVGTGYFTTLYLETPKPSISS NLNPREAMETVILTCDPETPDTSYQWWM NGQSLPMTHRFQLSETNRTFLFGVTYK TAGPYECEIRNSGSASRSDPVTNLNLHG PDLEPIHPSYTNYSRGNLYLSCFANSN PPAQYSWTINGKFPQQSQNLFIPIITK HSGLYVCSVRNSATGEESSTSLTVKVA STRIGLLPLINPT
8368	22269	A	8429	3	390	ILGCNLRVEYSLVICSVPGSKKVILD LPLVIGSRSGLSRTSSMASRTSSEMSW VDLNIPTPEAPP CYMDVIPEDHRLSP TPLLDDMDGSQDSPIFMYAPEFKFMPP PTYTEVDPCILNNVQ
8369	22270	A	8430	3	208	NGTHVITLLCLKTCGTVVNVANDMIVAS NLGTGVPNQTPVSSGDLIRSNGLLIPG TCEITRLYTISE
8370	22271	A	8431	3	563	LPTSRVDPVRVLRMKKQEEEDQGGP CPRLSRELPEVVEPEDLQDSLDRWYSTP FSYPPLPDSQCPYGCFSYSLSEEHVGF LDVDEIBKYQEGEEDQPPCPRLNEVLM EAEPEVLQDSLDRCYSTTSTYFQLHAS FQQYRSFYFSEQDVSLALDVDRPFT LTVIRHHLAFQMGVIFPH
8371	22272	A	8432	2	119	DGNILVTTFIYIKSVTELNGDIITNAS WRCSEVAPSA
8372	22273	A	8433	192	1285	AGVLSIIETDSEGLQTKVVENQTYDER LEINDSEEVASYTPTPRHQGLPRSAHL PNKAMADNSDECEENNKEKKTSQLT PQRGFSENEEDDDDDSSSETDSDDDD DEEHGAPLEGAYDPADYEHLPVSAEIKE LFQVNLRCVPTDVLDHKLKPFIPDFIP AVGDIDAFKVPDPDGKPDNLGLLVLE PSTKQSDPTVLSLWLTENSKQHNTQHM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KVKSLEDAEKNPKAIDTWIESISELHRS KPPATVHYTRPMPDIDTLMQEWSPFEE LLGKVS LPTAHIDCSLAEYIDMICAIDL IPVYKSRIQSLHLLFSLYSEFKNSQHF ALAEGKKAFTSSNSTSQAGDMETLTF
8373	22274	A	8434	3	251	TLQADHFNTRLSCGDAQTWARTGYLG FVRRTELTAATGERHDALYVVGALDETL ELRGLRYHPIDIETSVSRIHRSIAEW
8374	22275	A	8435	1	225	QTFNLEGSQIYEDSIVLQSVFKSARQKI AIEEESDESNEEDEDDEEYHEWKRYD RLGENMCLNCIWNNGGYIV
8375	22276	A	8436	95	340	CGCGIAGLAMSATFNQSLTIVILLIC TCAYIRSLAPSLDRNKTGLLGI FWKCA RIGERKSPYVAVCCIVMAFSILFIQ
8376	22277	A	8437	1	317	GPKPLVRTSREPQKDVTTSGYSSVSTAC PTSSVDGGLGALPQPTSVLSLSDSHTQ PCHHQARKSCLOWRPSPPESTVSQQV KRINLCIHSEEDMNLGLVRL
8377	22278	A	8438	80	213	PHLSFNAGITTIKVNIRNANSLGGGFHC WTCDARRRGTLQSYLD
8378	22279	A	8439	3	767	HEDNIKQLEKMKFTYLINIQDEINTIF NDYIPYVFKLLKENLCLNHLKFNFIQ ELQEASQELQOIHQYIMALREYFDPSI VGWTVKYEELEEKIVSLIKNLLVALKDF HSEYIVSASNFTSQLSSQVQFLHRNIQ EYLSILTDPDGKGNKIAELSATAQEI KSQAIATKKIISDYHQPFYKLQDFSDQ LSDYYEKFIAESKRLIDLISIQNYHTFLI YITELLKKLQSTTVMNPYMKLAPGELTI IL
8379	22280	A	8440	103	354	NGCECDLFLFLFFETESRSVAQAGV QWHCLGSPQSSPRFKRFSCLSTLGGRG GWIMMSGVQDQPGQHGETPFLMQAGLKT
8380	22281	A	8441	3	160	KLYPLKIVFGMNGRVVWVGKTVQQTLL ANVLEACELMTLDQRILMFLAES
8381	22282	A	8442	459	3	CGGLHPVRASWLLCLPQAWAMAGAPP AWLPPCSLISDCCASNQDSVGVGPSEP GAGYNLLVRRFLSLSEKRSIRVRVTRFS RCHLSPLSLTRKGNLTPCTSRVRQCLA LLRLAHGALHPLSCAHCLALPSEMTVP QMENAEITRL
8382	22283	A	8443	2	318	RQGNMTAALQATLLNPPINTKSQAVNDR ARGIVLNLISFKANDIEKAVQSLDKNG VDLLMNYMYKGFBSPSDNSAMLLQWHE KALAAEGVTSIVRVSTALIPA
8383	22284	A	8444	2	109	VTPPFMSCDLQGDACRNPQAQEHRSKD LRGYSHG
8384	22285	A	8445	1	69	LVLNSWPQVIRRPWPPKVVGLOV
8385	22286	A	8446	1	163	PSEKHNIWVGVTQFSRCRLSPLSLTRKG NSLIPCASVRQCLTLLRLVHGACTH
8386	22287	A	8447	1	147	GQAGLELLMSGDRPTSASQSAGITGVSH RARPSISIFILELRGSVRKKF
8387	22288	A	8448	914	729	GLTMDTKQDVQPPKQPMIYICGECHE NEIKSRDPIRCRECGYRIMYKRTKRLV VFDAR
8388	22289	A	8449	134	392	TCPPPEPPSPLTCAVLVPQTRRWRLG SLFRRACCVALLQLLLFLLLFLLP IREEDRSCTLANNFARSFTLMLRYNGPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PT
8389	22290	A	8450	37	248	AKITPLLQPGREQDSISNKKILRCCLT MLPRLASDSSGFKRSSHFLPTSWDYRH SPPLASVPFLLMC
8390	22291	A	8451	367	165	NFFVFLVETGFCCHAGQARLQLLASCDLP VLALQSAGITGVSHCARPISTLKDITKT SHFVPLKISGK
8391	22292	A	8452	2	282	GKRMAGGPMMQLRLDGNRLYITTSMF AWDKHLYPDLIREGSAMLVHDVDTALGG LKLNPYFLVDFWKEPLGPSLAHELRYPG GDCSSDIWI
8392	22293	A	8453	4	163	HHDFAQSLLANIERIALVFAACEAAA VLSLLVSISNTYGLDYHLNKLKLLQC
8393	22294	A	8454	374	197	TPEPKQSSHLGLSKCWDYRHEPPHQARN STFDSNHSSLAARDKLLGYFGLSQWQPG YQP
8394	22295	A	8455	343	161	MGMGPSVPGTGYNLLVCRLLRPLEKCSI RVGVSQFSKYHLSRLPLPRKGNSTPCA FWVR
8395	22296	A	8456	1	193	MGFLHVGQAGLKLPTSGDPPTSASQSAG ITGMSHRVQPYVLSICQTLHSVCICLL IILLTTVL
8396	22297	A	8457	342	263	WLRPVVPALWEAEAGGSLELRSSRPA
8397	22298	A	8458	101	303	KAAYLFQRLHFCFLNLKKNMLLFNHR MENFKELFGPGTVAHTCNPTLGGRGGW ITRSADRDHPG
8398	22299	A	8459	3	140	YLKHLCMYCKYLRLQGLMLPRLVLNSW AQRILLPWLEKVLGLQV
8399	22300	A	8460	327	248	FPRLVLNSWPKAILMPWLCKVLGLQA
8400	22301	A	8461	327	79	SIPFILAFFIYLSFFFKETGSQSVTHAG VPGIIIAQCGQLGLGSGDPPDSASLVVG TTGTYPPTILSVFPNMPSPFILLCLP
8401	22302	A	8462	365	273	MGFQHVGVGLRWVQVICLPWPLKVLGL QA
8402	22303	A	8463	375	217	QAGLKLLTSDDLPASASQSAGITGVSHH AQPRHFFFKTRFIYIFFSSPSSVLS
8403	22304	A	8464	238	354	RGKCFVQAFLYKECSGGQARWLTPVIPE LWEAEVGRWIT
8404	22305	A	8465	367	248	FQMRIHKWLIDLHSPSEIKQITISISIEP GVEVEVTIADI
8405	22306	A	8466	341	153	NMILGWAQWVTPVIPAIGEAHWGGLLYP RSSKPAAWATQONLLFTKKKKNIYIYIYI YIYERY
8406	22307	A	8467	368	101	VEMGFRHVQAGLELLTSSDPPASVSQS AGSSTSLPTADLLTPGWVGVGLVDKNP VTLIAMQRLPAVLEKKSARKNSENKIV LKRQ
8407	22308	A	8468	362	248	HVGQAGLALLASGDPPTSASQSARIAGV SHRARPEAPL
8408	22309	A	8469	384	196	SARLGLPKFWDYRREPPCPADDMILMV GILETFSLIPTATMESRNYCVYFKMRNK HIISKTS
8409	22310	A	8470	386	300	LAMLERLVNSWSQVVLSPPLPNMLGLQ V
8410	22311	A	8471	380	178	PKKNKFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFYIYIF AIVYQTLACNNKFLQMERVTRKLRQC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8411	22312	A	8472	3	154	FLVDMGIHVSQAGLKLTSGLDPASASQSPIFFLFFFFFEKQILAQAGG
8412	22313	A	8473	3	162	GLYHVGQAGLKLPLTSGDPLASASQSVRI TGVSHRTRPKIIFKLIFLFFLVA
8413	22314	A	8474	266	107	LCLFLIEMRFPYVVOAGVKLLSSSHLPS SASQSDRITGVSHCFWPEVFKRGIF
8414	22315	A	8475	361	169	RLPGPSNPPTISASLAAGITGARHHAQLY FVFLVEMGLCQAGKHNFKEYSRVLIYSP IVSFTHFI
8415	22316	A	8476	1	154	KKLIPTLMDHGAQFKSSVKEITTAVVEM AREVELEVEPEDGNELLQSRGKT
8416	22317	A	8477	3	193	SHYQSLISSNHGHKHCGRPQGPLPRKTY DLCSLDYQLTFPPLLTHTDPVKSPSVRNT QELSLIP
8417	22318	A	8478	408	103	TGSRLTLSSRVECSGVITAHCNLELPGS SDPLASASQVAETTGMMHHVWLIFLGIF LVKMASHYVAQDDLKLLGSTDPVVSASQ SVGITGISHHAWATICYK
8418	22319	A	8479	59	166	NVNTCLCLHTHTHTHTHTHTHTNYFKE TPIHQYI
8419	22320	A	8480	394	253	FLLLLLESQFCHVAQAGLKLSSCDLPA LASQSAEISGVSHCAQPLA
8420	22321	A	8481	379	184	CPSLPKCWDFRGVPISPGDFWNFIKLG VCPFCQGGFELLAPNDVAASGFQNGIS GINFWAWAL
8421	22322	A	8482	367	170	CGLSSGLGGRSGRESERIKERERERDRE KKKEGEGEKRRERERESVSSYKDTNSMG SGHPYSLI
8422	22323	A	8483	324	136	QRSSCLSLPSSWDYRRMPHLANFCIFC RDGVLPCCPSSWSQMTTSFLSLNFLICLV GIILGRG
8423	22324	A	8484	1	57	GERRYGTCTYQGRWLAFCC
8424	22325	A	8485	35	339	GWLLRFFWQWKNGNNLVSLIDGWLSY DTLGYNGILNCHMYILTEGDSQKKKKKK KKKKKKKKKKIDPAGNSKIYNRKIFKT PRGFFKWALGPLLILFF
8425	22326	A	8486	330	66	RPGVSRFPNPWPLIFFLRRVFLCRPGWNA VVQSLLTKISASQVQAIPLGGGCGCSEPR SCHCTPAWATTAKLCFKKNGKNFTDIM FSK
8426	22327	A	8487	3	209	CLSLLRSWDAQPPHPANFFLMFNPCR VGVLCCPGLASSDPPPLVVSQARITGM SHCTWTIFLSFK
8427	22328	A	8488	3	216	GQSITVSCATATNSDVGSSNLVSWYQSSN LVSWYQQHPGQAPKLIIYEDNKRLSSEK KKKKKKKKKKKKK
8428	22329	A	8489	326	62	PAYFSIGSFFLFLFFFRTECHSVTRLEC SGAISAHCKLRFPSSNSPASGGGGRSE PKSHHFTLAWTTTRAKLHLNKNKIKTVE FLSS
8429	22330	A	8490	2	156	SSAGIGRTGCFIATRIGCOQLKARGEVD ILGIVCQLRLDRWVCCKQGGQR
8430	22331	A	8491	399	254	KNNKRNKTINNKITNKLITKLKNTISFLY FFFFFFFFFFFFFFFFFFFF
8431	22332	A	8492	2	130	FRRVGQAGLELLTSGDLFASASQGAGIT GVSHRAQPTFLKSC
8432	22333	A	8493	3	94	HLPAEFTPAVHASLDKFLASVSTVLTSK YR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8433	22334	A	8494	327	70	KSGFSNVGOAGLKILTSSDLPVSASQSA GITGMSHCTWPLYPYFGLGSRFSIES HCWYQLAPFPSCRNPFFVVPFFVHRFYL TF
8434	22335	A	8495	97	219	PGTVAHACNPGVLGGQGGWMTSGQEFQT SLASAAKPRSTRP
8435	22336	A	8496	3	191	GIRGEILEVIEFTSNEEMLCRDPKGY GYVPRTALLPLETEVYDDVDFCDPLENQ PLPLGR
8436	22337	A	8497	144	304	SYFYEEILFSTVIKKNAIVSFTATWVEL EAILSELTEQEQTKYHMFSLVSGS
8437	22338	A	8498	2	90	LTILVLAMWKVGFFKRNRPLEDDEG E
8438	22339	A	8499	1	156	PSSQDYMHAHPHLANFLNKFVKWCLAM LPRLSNWPQTILLSPKALGLHV
8439	22340	A	8500	67	319	KLMSFGPTLLSARCSTGQICMNEINLN IDAMSVAAATINNEIMSFAITWMKLKAIT LIILTLHKTKYCMCSLISGSLRMTTQG
8440	22341	A	8501	3	299	ETGSHCVDDGGVQWHISAHCSLDLLGSS DPPASASRVVGITSAAHPLLWSISSLPP LLLHPHNLNLNLLLLLLPSLSIVNLHL PPLPLRLRLCSPC
8441	22342	A	8502	56	142	NNSAKKKKKKKKKKKKKKKKKKKKKGG AAF
8442	22343	A	8503	486	348	TGFHRVAQAGLELLSSGNPPALASONGG ITGVSHHAQPAEYNFKK
8443	22344	A	8504	158	403	RIFFFETVGFVAQDGVQGRGAILQPR FELKRFSCLSLPSSWDYKRAQPNPNDFF KROMAFDPKIQIRISLGSKKKKHPIE
8444	22345	A	8505	3	78	DWHIAYVLLYGPRRVEIMEESEQ
8445	22346	A	8506	164	291	TRFCCCWLFVWVFCVLCVCVAVFPWC LFFIVVLFFFFFFF
8446	22347	A	8507	372	69	CAPLEPLKFFPPRGFIIRGGGSPIFPP PKKGVLKPNPPKGFPPPPFLKPAAGGA FNYPPFGKIFFSPPRGKWAPGGFLKG APPPPPPPPPPPFLF
8447	22348	A	8508	282	1	SFOHVAQAGLKLGSRDPTLAAQSAGI TGVSHHARPVLYFSSVLPSMEFLSTMSA VILPCICSFVSLAVPSSCILQQPLPPT CTYIKTETCI
8448	22349	A	8509	400	45	TPPVSSLFFPLPLKEIIFCPCPPRQSLPP PPPPPPPLFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFKYLSLPFTL SKEKNK
8449	22350	A	8510	241	419	TPLGGWEKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKGGGFLKKPLGGANFIGA GNN
8450	22351	A	8511	317	28	QSLSPSPQTVYFIYLIYAVFTTLTII LIFSPSRMELKFLRLCYFPAPFYAFLF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFSOPCAQT TAGRAGV
8451	22352	A	8512	124	292	MCCYIMSLKVICITIIKEFSTKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KGGVPL
8452	22353	A	8513	1247	910	QAQLGDIGTSCYTKSGMILCRNDYIRLF GNSGAAGACGQSIASELVMRAQGNVYH LKCFTCSTCRNLVPGDRFHYINGSLFC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EHDRPTALINGHLNSLSQSNPLLPDQKVC
8453	22354	A	8514	99	262	MNKRFLNKKKKKKKKKKKKKKKKKKKKGG PFKNPGGAQIFPGGEKIFFLKQGL
8454	22355	A	8515	85	2	GWGWAQWLTVPVIVLWEAEAGGSRGQE
8455	22356	A	8516	244	423	VFAVFNFLGWVMDMLINLAVVITLQCAC ISNHVHVHLEYIQFLFANYTTSIKLGKKP SKSV
8456	22357	A	8517	3	114	KINGEDKQKILDKCEIINWLDKNQVCV FFFFFFPI
8457	22358	A	8518	413	91	GGVRGKISFRGGGFLKKKKKKLKKKKK WGGGPKEKKRGGFFFFLLNPFVWGGV KKKKKKKKKKKKKKKKKKKKKKR GRKEGREGRKEGEGRQINMTA
8458	22359	A	8519	1	163	SRLPGRSRRRSRGRRRRRRRRRRRRRR SRVLIFPWNLDNLNIVYIIEDVDA
8459	22360	A	8520	191	21	RFTTHVDATVTVFLIESVFLHVQAC LELLPSDDLPAASENARVTGVSHRAWL
8460	22361	A	8521	2	144	AAATSQANWCMPVVPATWEAEVGASLKP GRQLQLPTMIALVHLSYAI
8461	22362	A	8522	90	8	KPTPFLPTLIARTLLLPISPLILIL
8462	22363	A	8523	305	146	VFRHSCGIRGSVDVKITDGLLVIRRIE NVPPGPNNKNKNPYAIFQSSSIESQ
8463	22364	A	8524	176	2	LAWPFLFLPKCWDYRHEPLQPSLTTFV REWDKIGAWWLTVPVIALWEAEVGRSQ GQ
8464	22365	A	8525	2	200	CLIPSSWDYRHMPPRPANFCIFFFFLGD HVSQVGLKLLTSKDPLAWTSQRAGITGF SHHTKPQGGF
8465	22366	A	8526	2	217	SFSLFPSPSFLSLLPPLASLLPLPSF SLLFPSPSFLSPPSFLSLLPSPSILL HPTFSLYPPSPSFI
8466	22367	A	8527	2	186	IRGLRPLEKRGIRVGVSRFSRYHLSRLS FARKGNSPTPCASRVRRCPSSLHGLHPL SDKPQ
8467	22368	A	8528	3	153	CLGFLSGWDCRCIPPCLANLKKLPVEMG SLFWPQWILPPWPLKVLGLQV
8468	22369	A	8529	2	388	RTAVHTFILVLQVCVCRHLSLAALTPA HLVCSSHRILSYLSIRGSWDHRCMTTTP GLVISIFFVEMKYRYAVHAGHILLGSSY PASAYQSAEITGVSHWAWPTDSLWQKPH MVIWCISCFLNLVIGTM
8469	22370	A	8530	293	64	YRISIKVSKWFKGWVSSFWIFFFVFFF SFFVFVFCFFMFLKQVLKFIINIIIL TQALYICTTSKICYSFLYFR
8470	22371	A	8531	2	250	SCGLPSSWDYRGTLPCLANFCIFNRDG VSLCCQGSQTPGSQVIDEAVYSIYAYY ILALLIVYVAQWEVWLKHFCCLIKYT
8471	22372	A	8532	2	201	FHHVGTGLELLSSGDLFASASQCAGIT GVSHCTWPSILYRMNFKNLSAVPIAWVI EGNYTNKTCI
8472	22373	A	8533	319	200	TFTFFLQRWGLTMLPRLVSNWAQAICL LQPPKVLLEWA
8473	22374	A	8534	160	297	KTETLALVAHACNPSTLGGIGRQVSSAH EFTILGNMTRPILYTKL
8474	22375	A	8535	333	228	PNRGHYIAIVKSHDFWLLFDDDDIVEVSS FLISYF
8475	22376	A	8536	3	325	PPSSLLPCSWILDCCASNERDSVGVGPS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EPGAGYNLLVCCFLSLEKRSIRVGTR FSRCRLSPLSLTRKGNLTPCASQVRR LALLRLAHSALHPLSCSYCLALP
8476	22377	A	8537	216	5	KLGLVNLVBFQVKFFFLFFLEIILIE MRSHYVAQAGLELLGSGDLPASASQAE ITGMSHHALPNYSF
8477	22378	A	8538	136	22	RPRRLVLNPNWPQAILLPWPVKVLSQV WATCGRRPAS
8478	22379	A	8539	136	22	RPRRLVLNPNWPQAILLPWPVKVLSQV WATCGRRPAS
8479	22380	A	8540	8	319	YIYMSMYMLIYVCIYVSIYICVCIYNS ISFNTRYMIYMLIYVYVMCVYICVCVY IYTNISISFNTHITPIKHSVDVHTVSTTRC NLGGRGFCHTWPLPHLAGW
8480	22381	A	8541	331	156	SVNGLLSLPACLFPVCLPACLPSPFLPSFL PSFLSFFLLLLLLLOKPVNSLIFSQSLS IS
8481	22382	A	8542	72	1	KIGQARWLAPVIPALWEAEAGGSP
8482	22383	A	8543	2	83	QAGVQWRDLGSLQALPPGFMPFSSYLGG
8483	22384	A	8544	293	2	KTVWHYLVNAPEVEIQAIYSQETCKSMY QETCTRIFIAILFIAPNWKORQDTMNP GNKENGKVATLSDSGFLVRFQSLMRSNC PLYPFNKFPILLK
8484	22385	A	8545	314	122	LVETGFLHVGRAGLELPTWSDPPTSASQ GAGIAAVSHRGQPVDKFNISTQIQGRP IICNYKTF
8485	22386	A	8546	316	123	LVKTGFLNVGRAGLEIPTWSDPPTWASQ GAGIAVVSHRGQPVDKFNISTQIQGRP IICNYKTF
8486	22387	A	8547	3	247	GIMATERLANYTGGIYAEYQDTTYINHV VSVAGWGISDGTEYWIVRNSWGEPWVRC FHFLKVIIPRKTSWYSSRLNGSVYV
8487	22388	A	8548	289	25	QRREKFFKNGPPIFFRGPFQIFVVSF PFFFPKIGVFFVFFFRFSLVLKGDFFSN FLKINCFFFFFFFFFFFFFFFFFIKN RPCL
8488	22389	A	8549	289	2	KKKIGETLCKLCKKFLDVTPKAQFIK QKKEKLINWQFIKIKNFRSPKALLRRGK GKPGTGRKRANHISDKGPLCRIQKINS RGRAQWLTLLV
8489	22390	A	8550	290	187	ROENPLNLGGGCSEPRWCHCTAAWVTE QDSINK
8490	22391	A	8551	293	183	RDEGRGISYMLPRLVLNSWPQAILLPQP PKVLELQA
8491	22392	A	8552	364	87	MLPLDFFLGPSLDFCPPFCESGSGGIKV PESTTPRASAFPLPPGAANLHHILQLVGA PRVPPGFHHVGQDGLDLVDLVIPLRPP KVLGLQGG
8492	22393	A	8553	57	225	KWQKWPWAGGVAHACNLSTLGGRGKI ACAEEFKTILENIVRPLSKNKWISFS
8493	22394	A	8554	326	2	KSKRGYSEPLVFSICSARAPRSHSVSQA TVYGHAASTQPPPRNLRSSYLSLLSS GDYRHDPPPLAYICISVIGNDVEHLFLC LLSTCISSVNRSHVYSTLVPIFGP
8494	22395	A	8555	372	148	YICFLRSSVRQILFTPDSCDCSMWVPCN IRLPGSTHWCASASQAGTTGARHHARL IFFVVVFFCIFSIFSRENH
8495	22396	A	8556	422	269	AADQERLHTYQLNYHFCRWGLTTFPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						LVSSSWVQAILPTWPHKVLRLQA
8496	22397	A	8557	669	407	AGVKWRNLSTLQPPRRFKRFSHLSLPS SWDYRCPLPCPANYCIPLVEKEFRHV GK AGLELLTSGDPPPAWVSLIAGITGVSHRA HPD
8497	22398	A	8558	195	352	LGLQAGTTASGYSTVILGGMKPRSWAW WPVVPATREAEVGGSLPGRSKLQ
8498	22399	A	8559	345	219	MLARMISTSLPCDPPASASQSAGITGMS HHGWLNLFKSIHL
8499	22400	A	8560	137	2	VKYCLPTRSLIKTVRPLSFSQATASPV CTYTPRWPEVTBESQKN
8500	22401	A	8561	324	193	RSSGNLPASAAQARITGVSHRTRPKCI ISKEYVAENHLKSTS
8501	22402	A	8562	326	121	HNHTHTHTKNHKKHQPPQHTHTYHTQTD IYVLQAASQKSLILISSLA
8502	22403	A	8563	3	85	HEHTHTHTHGHHTHTHRHTHTLTCARM
8503	22404	A	8564	2	153	ARDRHIPPCLTNFSVFWRDGGLAMLPR VSKLWAQAVHPWLLKVLRLQA
8504	22405	A	8565	2	177	ARVGFHYVQGAGLRLTSGDPPASASQS AGITGMSHRARPMSLTLHLQDTWRAY AG
8505	22406	A	8566	353	212	AGFRHVGRAGLELVTDGFPRTSACQSSG ITGMSHCAHPEKSTAFILF
8506	22407	A	8567	76	191	ELIFCRDGGTLTVFPKLISNTWPYAVLPL WPPKVLGLQV
8507	22408	A	8568	1	142	GTRGFLHVQGAGLELPTSGDPPALASQG AQMTGVSHCASQKKEFLEW
8508	22409	A	8569	250	95	SASRAPLPLPPSHLPLRAAGLSPLCPPR LVSSYRPHVILLPLPPKVLGLQV
8509	22410	A	8570	3	226	HEHTHTHTHTHTHTHTHGHHTHTHTTLV LVYSLCEHIWRFIVISRARVCCIVVVVF FECGYADRRVADKWLNIH
8510	22411	A	8571	1	216	GTRGLGVGVSHLVSKNTHHTHTHTHTHT THHTATASQLSVFKIWAQFQRLDKGLT YISNSYCSSKFYLYNH
8511	22412	A	8572	356	268	LTMLARLVNFRPQVTPQWPPKMLGLQ A
8512	22413	A	8573	12	175	RWGFHPVQGAGLELLTSSDLPTLASQKA EITGMSHCARPSFFSFFLSFFFWKHL
8513	22414	A	8574	1	163	GTRTGFFHHVQADLELLTSGDPPVSASQ SVGITGVSHRAWPVGLCIIALISNEY
8514	22415	A	8575	344	176	EFLVETGFRHIGQAGFELLTLGDQSTSA SQNTIEITGVSHAPGLAIFKSGNQAFF
8515	22416	A	8576	2	179	ARGILCHSGTFKLDSPSMVAHTCNPST LGSQGGRIACQGEIDTSLKVARPRLYG QIF
8516	22417	A	8577	1	100	GTRGFTMLPRVVSWSAQVILLPWPPKV LELQM
8517	22418	A	8578	3	114	HERHEILSIYLTIIYLSIYLSIYLSIYLI YLPITRI
8518	22419	A	8579	1	264	GTRPCRIELRVVESLAKAQETSGBEIS KFYLPNCNKGPFYHSRQCETSMDEAGL CWRVYPWNGKRIPGSPEITGDPNCHIYF NVQN
8519	22420	A	8580	1	245	GTSGTSGILGFYLEREDRLQIRTDIT LSHGYSTFSLNRCDSRHMMNRMFQMLYQ SPFLGYIQLSHEVLAFGISYINTE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8520	22421	A	8581	1531	1457	QARNETIARRLWDVSCDLLGLPID
8521	22422	A	8582	191	2	TITSYFSPPTAPGSHYATFCFYKFDYSR YFIKVELWEAETGSGRQEIEITILANTV KPLRSRA
8522	22423	A	8584	2	212	ARAGIYPKEYKSFYKDTCMRMFIAGLF TIPKTIQSKCPSWIDWIKMYRQGPIL SPMLECSGEVSGFK
8523	22424	A	8585	2	192	ARGNSPASSSRVAGITGAHHHARLIFVF FLFVRFFFSFLKTGFKLVAHSNFQPLTL FAPLHFK
8524	22425	A	8586	277	66	PLDFRLGHKRRLPFPKPKKKESKFCVC VCVCVCVCFKQCLVTLPRVLSNSWAQA ILLSWPPKILALQV
8525	22426	A	8587	395	286	PHLGLPKCWDYRREPPCLAEVVLKRYVW VTYFSFR
8526	22427	A	8588	307	177	RYPSTINYSILNRDKIMPKLDRMVYKAR PRVMCLPWPVKVLGL
8527	22428	A	8589	167	349	RNLRELGEFFFFFFFFFFFVGKFS VLLVGNLFLFFGGGIFGLSRVMCFKEF RCFS
8528	22429	A	8590	375	240	LLSRFSWFCFVFRQGLTMLPRLVLCWA RGILLPWSPKVLGLQA
8529	22430	A	8591	347	215	ETGFPVHGQAGLKLASSDPPASASQSA QITGMSRRAQPSAKRF
8530	22431	A	8592	340	114	HRTAHCSLYLSGSSDPATSSSQVTGTTG KDQHTWLLFKYFCRARVSKINKYKSINK PYFLNTQTTPSEYKASPG
8531	22432	A	8593	86	253	LRLCCGLSCSTAKKKKKKKKKPKKKKI KKKNLHPKRGGFEEILFFFPKGGKNLF
8532	22433	A	8594	3	135	GFCHVGQVGLLELLTSGDPPALASQNAEI TGVSHRAWPPVLFFF
8533	22434	A	8595	2	274	PRVRTISLLGILVYRSHLISLLCLEGI ILSLFIIATLITLNTSHLLANIVPIAIL VFAACEAAVGLALLVSISNTYGLDYVHN LNLQC
8534	22435	A	8596	3	316	SIPYSWGEKEGIPCMAPPQIQGTSRLND FTALSLHLNTHTHTHTHTHEIQHLPP QGITALIILNSLLRHYCPSLAFPSLSPKQ NLTVRHCLSRDTWLATASK
8535	22436	A	8597	385	291	KAPPLFFFFFFFFFFFFFFFFFFFFKPV KKILGV
8536	22437	A	8598	275	369	GVQVLKLLTSGDLPALASQSAEITGVSH RAR
8537	22438	A	8599	98	344	VHYEEFMCVCVCVCVCVCVCWPRVRGVD MNPVEHPFGGGTHQHGKPCITIRRNASA GRKVRMLAALWTVRIGGKTIVTLRKT
8538	22439	A	8600	328	195	THVPPSLAKPVFLVKMGFLHIGQAGLDL STSGDPPALASHVFKR
8539	22440	A	8601	2	214	HVDVVMGTFAILSELHWDMLHVDPENLR LLDSVLNCELANHFGTDFTPPVQAAQK VVADVANAALAHMYH
8540	22441	A	8602	89	181	GLRHENRLNSGGGGCSEPKLCHCTPAWA TE
8541	22442	A	8603	340	57	KEGHQEMEQAEDGGHGRKAPGTSPTWTLG ELPKSARGHTGLFVSYRGCRTOFRPKKV LFGGDRNRGLAMLPRLVLNSWPQEIILLP QPSKVQGLQK

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8542	22443	A	8604	330	132	TGFLHVQSGGLKLLTSGDLPTSAPQNA ITGSGHCTRPFSLFHSYLVLFYGCSSQ VLSLILARM
8543	22444	A	8605	546	279	RPGPTVSPRLCICMIMAHCSLDFFGSG VSPTSASRVARTTSTHHHAWLIFYSSVE TGSHVQAQGLELLGSSNPPIASQSAG ITAL
8544	22445	A	8606	3	249	NRFNLGSGGCSEPRSHHCTPSWATQET CITYLEYCFPPVSHTNLVYFKPLNVTIR SDYCILGLHASSIGGSDSLIIDCWD
8545	22446	A	8607	159	324	VIQYRTNHLHLCEVLVFWFLPYFFLK KTYTGIGQMRWLTVPVIALWEAEAGGS
8546	22447	A	8608	334	179	TGFPHVQSGGLKLLTSGDLPTSGSQSAG ITGVSHCTWLEVIYFLNISITYPS
8547	22448	A	8609	278	202	QQPSTLRQDPPAKRLHLSGSDGH
8548	22449	A	8610	236	66	AASTFFLQKIKRHLLSGTVAHACNPSTL GGRGIRISRGREFKTSLGNMVRPRVYKK
8549	22450	A	8611	29	177	GKQVMALHCFIFFHFFFRSLAMLRLV SNSWQEIPLPPWPLKVLRLQA
8550	22451	A	8612	1	215	HTSRTLFLVHLRLKFNKYLIEWGLSMLP RLVLNSWAQAVLPPWPSKVLGITGMSHC TWLYLHLSTDLLKLC
8551	22452	A	8613	3	91	LRHGNCLDPGEGGCSEPRSCHCTPAWVT E
8552	22453	A	8614	2	167	FTISLLGILVDRSLTHHINNPKPSFTRE NTLMFIHLSPILSTRKQLAIQHLRLE
8553	22454	A	8615	2	281	FCILVETGFHCAHAGLQLSSGNPPAS ASQSVGITGMSHCTSPNLSLLTQSKSPC LLIQNHNPYAFINSQLTFSILFLLSYFI FYDSLFLF
8554	22455	A	8616	282	182	GQAWLTPVIPALWEAEVGGLEPRSSR PAWST
8555	22456	A	8617	379	207	SNQTKKYINFFFVEMRSHYVAQAGLKF LGSSNPPTSASQSASITGISHYVWPISP S
8556	22457	A	8618	705	483	DKSFALVARAGVQWHHLGSLQPLPPGFK QFSYLSLPSSWDYRHAPPRPANFCILSR DGVSPCWPGWSRTPDLR
8557	22458	A	8619	359	220	RQSLTMLPRLVSNWAQAILPPNLSRL GLQALAPIPGKSYNEKTP
8558	22459	A	8620	3	186	HEVSWVKRKQDEWIEFDDDTVSTVAPED ILRLSAGGDCHIAVLLYGPVRVQILBE ESEQ
8559	22460	A	8621	1	116	GTSFCRDGGLTVLAQLGSSFWPQRI LPPWPKVVELQA
8560	22461	A	8622	369	188	MYSLEMGFIGNGHAGLELLASGDLSALA SESAGITCMSLRYRTRFSFKRATCGLDL SLQS
8561	22462	A	8623	202	22	YILGFYFMPVICYQERKKDKKNWEVTTI MSFVGICMELGAILSKLMQEQRTKYHI FSQV
8562	22463	A	8624	387	315	SNLGGGGCSELRLCHCTPAWATE
8563	22464	A	8625	2	135	TRDLCSLVLLTFPPLLSDPAKSPSVR NTQELSIKKKKKGRPF
8564	22465	A	8626	3	232	HASAFEEFVYIKSRQKRKESNPPLVSS QPHGLKKKKKKKKKKKKRGRGLKKKKK KHKKKFKKGQKKYNFGRGAF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8565	22466	A	8627	97	373	QHGFLLKKKKKKKKKKGGPILLKKPLG GPNFTGDGKKKFFPKKGGIKKPPGEFLK KNLFLGGKKNGKNPPKKLNPLGKKNFK GKKGKNPP
8566	22467	A	8628	2	188	RYGCPFPYHTFEPEVYIKSRQKRKEWNP PKLVSSQPHGLHDFKKKKKGA AVLKD PSGGPS
8567	22468	A	8629	287	68	GEEGRTOQGERNGGGSERKEGEEHEAR RTGRGEGGGGEAKGRPRSRARRRGSRG SKSQTPSRHLPAHIITN
8568	22469	A	8630	364	136	VSLLLGLEYSGTITAHYSLNLFLLFIVET GSHYVAQTGLKLLGSSNPPTS DSDQTFR TGVSHGAQPKVQFWKNDLT
8569	22470	A	8631	355	70	LFPPRFFPFFSPLSPLKFFFPKGFNFF REFFPIFSPPKKRVLKNSPGGFYKPL RGKIFTFPPPVKFGPPRGLFKGPPPPFF FFLFFFFFLVI
8570	22471	A	8632	2	266	AFTISLLGILVYRSHLYSSLLCLEGIYL SLVLIATVITLNTSHLLANIVPIALLVF AACBAAVGLALLGSISNTYGLDYGHNLN LLQC
8571	22472	A	8633	1	186	LTHHINNIKPSFTRENTLMFIHLSPIILL LKKKKKKKKKKKKKKKKKKGGALKKK PGGGQN
8572	22473	A	8634	2	80	VLEIAVALIQAYVFTLLVSLYLRDNT
8573	22474	A	8635	713	333	EGPPPPRSKKKGTTQGGKDPSPPEPKT PGNPQGRKTGPPPPGRPYTGPRPGSGP TRGGGSRSSSSNTNAPGEKIFFSKNPGR KIFPPRAILVFFSPFLKNFFFSRLILI FLGGCAPFFPPPK
8574	22475	A	8636	389	1	FIFSEFLFLIIFFFLNINFFFIYFSSLSF FFFLNFNLLKHTPPILFFFSLSPIFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFGTKKELY LLRARGCKQYKNQKLIWYLT
8575	22476	A	8637	2	192	VRTGLRDTAIPGRLYQTFTATRPGVY YGQWYEICGANHSFMPIVLELLALTIFE IGPEFTL
8576	22477	A	8638	1	87	PTRPLEIAVALIQAYVFTLLVSVYLHDN T
8577	22478	A	8639	2	132	INLASTLIIFTILILLTILEIAVALIQ YGVTLVSVYLHDNT
8578	22479	A	8640	2	113	LFPIAEYTNIIINTLTITIFLGTTYDA LSPELYTTY
8579	22480	A	8641	375	22	FIFISPLAYLFFLPFPFFFIPLCFFFF IPLPFLFLSFLSFLIFFLSLILIFPPS LFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFCWLPHRVMIAKVGISVVSKEI
8580	22481	A	8642	180	34	WFISDSLWLGMAVHTCNPSTLVGGGWI TCGRSRPSVPKRTPSQTCAPI
8581	22482	A	8643	338	133	NLPLGLFYSLQKKKKKPLRPGTLGAPK GNFQGAFLFGKFAFFFFFFFFFFFFF FFFYGFFFLFK
8582	22483	A	8644	156	287	LTYPFKPPLCSQKKKKKKKKKKKKKK KKKKKGGAFFKKNPWGAQI
8583	22484	A	8645	1	325	LHCHTHNFVNKVVCFIRKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKREKKKKKKKKKKGGGFLKKPPGGPK FSGGKKKKIFPQGGYKKPPGGFLGKTL FLGGEKMGENPPKKIKPLGEKKIF
8584	22485	A	8646	370	3	PVRSRLLCLPQAWAMAGAPPPASLPP CSLISDCCASNQRDSVAGPSEPGAGYN LVMHCFLSPSEKHSIWVGVTFRPSRCCPS PLSLTRKGNLTPCASQVRQCLALLRLV QGAGTHRTRG
8585	22486	A	8647	341	88	KKKKIFSPPIKRGPPSVYFICPPPPFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFRMGCDRWHGELYNKI PIWHKL,CGDL
8586	22487	A	8648	1	108	PTRPRTRGVASVLYFTTILILIPTISLI ENKILKWA
8587	22488	A	8649	3	96	EICGANHSFMPFIVLELIPLXIFETGPVF TL
8588	22489	A	8650	457	297	SPSFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFLEFYFALF FIYLI IKDNYMFQC
8589	22490	A	8651	84	352	YEKTDVKIISILFNIDYMLBYNVLHLIG QIKMLLISKKKKKKKKKKKKKKKKINK FFWGGILITLLGIVLYSPLEALKISPSF GFLBK
8590	22491	A	8652	2	111	NNIKPSFTRENTLMFIHLSPIILLSLNP DIITGFSS
8591	22492	A	8653	1	305	RQQQQQQQLRNLRDPLL VYNRMTELCFQ RCVPSLHHRALDAEEAECLSCAGKLIH SNHRLMAAYVQLMPALVQRIADYEAAS AVPGVAEQPGVSPSGS
8592	22493	A	8654	129	268	LSEVLYLFFPKKKRLIILCLFFRNPGSS NLQKITKEPIIDYFDVQD
8593	22494	A	8655	281	117	CIITLSFINTLQAYI IWL VVFSEVCLYV SLSIYLSIYLSIYVFERYIKISFHL
8594	22495	A	8656	3	177	DLHAHLGVDPGNLNLLSHCLLETLAGH LPGEFTPAGHAFLDKFLDFVSTVLTYYK R
8595	22496	A	8657	3	270	RRRGRAHCSLDLLGSRNPPASASRVAVT TGTRHLAWLIVVGGFLFFVLRDVLVRFH ATDKDIPKTGQFTKERGLMDLQFMAGK ASQS
8596	22497	A	8658	107	11	QFEHTKPTPFLPTLIALTLLLPISPFI LIIL
8597	22498	A	8659	21	136	VPIEHDVVPVNSRAELLKMFGLDRDALA QAVRGLITKA
8598	22499	A	8660	1	395	LVTALYSLYIFTTQWGS LTHHSNLEK KKKGKGGKKRGGALFKGIFGGSHFFGV WELLFFFLKGGIKKTLGLGKTLFFGG GLLGAPLPRIKGLREKNFKGELGVKN RVFFFGNFSSLGVLKKY
8599	22500	A	8661	1	255	RTRGRTRGRTRGLTRGKKKKKIMKKKK KKKKKKKKGGAFKNPNWGGPIFWGLPKP YFLPNKGSFFNLIGDFLKRPFFWGGAYF G
8600	22501	A	8662	136	358	FHIVKGVSIKFKCVILKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKGGGK NKIFWVGFFYKRVWGYF
8601	22502	A	8663	198	368	LINLVQFTCILGTLGLFIYLFLLRAI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino- acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
8602	22503	A	8664	407	82	TMLARLVINSWPQAVLLPQPPKVLGLQA KFLPHLGFPFFKRFIFIKKEPFQWFFFLF GFFFFRRSFFLLPRVQCNGAISGPCNLC LNVKVRLSFKKKKKKCDYTFEPLCPAL HFSFINKTEDCLFVCFTVYWPHEF
8603	22504	A	8665	166	293	KIIAKHNIARTNPYTFICIMKKKKKKKK KKKKKKKKKKKKKKGGAL
8604	22505	A	8666	1	164	RAKAKRRNTTVSCRMHRLKIVYRRFRYR LYVGIIGPGGLNETLVFTCKKITVP
8605	22506	A	8667	295	85	YIYMSHICTLSLSLSIYKRVKCFCKFT WSHVAQAGVQWRDLGSLQPPPPKWLIC ISVFTVLVFMKKK
8606	22507	A	8668	2	131	INLPSTLIIFTILILTLILEIAVALIQ YVFTLLVSLYLDNT
8607	22508	A	8669	423	107	HCALPKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKK
8608	22509	A	8670	432	301	SQILGRFSQKQHLSLGGGCSHPRSCHC TPAWARGRLRLKKFIK
8609	22510	A	8671	1	106	LKLLTSSDLPEASASQVAETIGMSHCARP LSRIYMC
8610	22511	A	8672	383	252	CPANFVFSVEKGFLLHVQAGLELPTSGD PPGCWFCFLQQQLHW
8611	22512	A	8673	560	135	SSWMDSIPTSSNMEETQKSNLELLHI SLLIESRLEPVRFLRSTFNNLVYDTS DSDEYHLLKDLLEGIQMLMGRVEDGSHL TGQTLKQTYSKFDTNSHNDALLKNYGL LPCFRKMDKVVETFLRMVQFRSVEGSCG F
8612	22513	A	8674	2	326	SLLMCVHRCEVCVMRACLCAGVCMCIAS CLGLPMNVVECYTWRLVPHQFQDEELH DTVDLETIPLERQPRDVQHPVSTRILYL HVYFVAVTLTLIRLLQLWTEAFSP
8613	22514	A	8675	171	272	TQCCLLKAEEKKKPKKKPKKKKKKKKK KGGPF
8614	22515	A	8676	60	409	LVWLESHEDVGPLIKDSKQEKKKKKKK KKKKKKKKKKRGGAFFKKPGGQNLRG GEKKNFFFLRGEKINPRGNFGKKTFFWG GENWAKPPPKKKSPEGKKKILKGKGGK YLNFLGE
8615	22516	A	8677	106	286	LPWNKEGNNWKKKKKKKKKKKKKKKK KKKKKKKWGGALLKISGGGPIFPGGGKN FFFFFGGGF
8616	22517	A	8678	1	97	IIGQVASVLYFTTILILIPTISLIENKI LKWA
8617	22518	A	8679	1	141	NEHQPGQHGEPPSLLKIQKISAWWSMP VIPATQEAEMEKEQSISIM
8618	22519	A	8680	499	140	GVFFFSRRKRCGVSPPPPKPVFFPLPG FFFWGGCPSAPPPPGGGPPNPGRGPF YPPPLKGNFFPPPPAGGGPPRGFFWAPP PPFFFFFFFFFFFFFFFFFFFFFF FFFFFS
8619	22520	A	8681	60	224	KQTKYIKEITKHICTWQGRYHDEGGFP RVKLIHCTPDMLTPVISPDVGNSTTV
8620	22521	A	8682	252	383	SQXKKKKKKKKKKKKKKKKKKKKXGGGL LKNFWGGPNLTGGGKI
8621	22522	A	8683	405	145	KFFFSGGCFFFWGPPGKNVPPPKMFPF LIPPPKKKKPPPKIFFPPPGVFFPPP PPFFFAPPPFFFFFFFFFFFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFF
8622	22523	A	8684	1	406	LYYFLTKSTTTYLAVPQPPPTPTSPSR AKKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKRGGGPKKKTRKGGGQKKKKGR GPBKNRGGGETTPGEKKKKKKKGGGKK KKKSGGGKNGGKPGRGGGGGR
8623	22524	A	8685	391	265	GRPFFFLDGVSLLLPRLECSGVILAH NLCLPGPSDSPSSA
8624	22525	A	8686	2	177	DTALYSLYIFTTQWGLTHINNIPKPS FTRENTLMCIHLSPILLLSINPDIITGF SS
8625	22526	A	8687	479	366	GLPKCDYRREPPHPAANFCIFSRDGV PCWPGWSCL
8626	22527	A	8688	35	161	SNPPSSAFQVAGTTGVRHHDQLTFFFF FLGGTGQILCRGGD
8627	22528	A	8689	1	122	THINNIPKPSFTRENTLMFIHLSPILL SLNPDITGFSS
8628	22529	A	8690	2	152	NIILAFITSLGLVYRSHLISLLCLE GIILSLFIATLIYTPSPSCY
8629	22530	A	8691	541	85	IFLRQFLSPRLEYSGVIKAHCSLNLGS SDPPASAFKVAGTTGIRHAWLIFVFFF AETGFHYVAQGGLELLNLRNPATAFQS AGIIGISHDDLGIQITTWLLQKLSYLQ KKICKDQETGLLHAFHLHPYPYMPSSP QLLQGPDLITNG
8630	22531	A	8692	122	38	GRVDHSMFPIVLELIPLKIFEIGPVFTL
8631	22532	A	8693	276	77	GVSPCEPVFFFIILGRGNPPAWGVKGRD FFVLSFFFVVFYILLEFFFFFVFYFLF SFYCFNGSNK
8632	22533	A	8694	3	70	FMPIVLELIPLKIFEIGPVFTL
8633	22534	A	8695	230	3	GSGIPSHPGHPSLPYHLEREWLAKTGIR DTSNSVHLELCLRSQRHGRARWLTPI PALWEAEAGSRRQEIEPI
8634	22535	A	8696	401	240	PPPPPPPCGSEPRPHPSLPPGSRMF VLALSQESQMTFFFQLRKKLHLYL
8635	22536	A	8697	103	313	EKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKGGGPKKKKFEATFGKTP GGVSQGGGPEPLNFFFLNPGPPFF
8636	22537	A	8698	354	110	KKGTLFEVSESFYTTTEGVSAKINRIRSI VSVNKVARCIGEIFTDAVQSAFQKEVGG VSDSMVHKVEYAGCVDVKAVCSHGL
8637	22538	A	8699	2	164	FLVETGFLHDGQAGLKLLISGDPFASAS QSAEITGMSPHACNSSTLGRRGRIT
8638	22539	A	8700	191	371	PPDSRWAIQGGHLELTPTRQDLAQAPR RKLALLEGSFQQAQWLTPVIPALWEAR ASGS
8639	22540	A	8701	2	170	ARAGLYHVQAGLKPLTSGDPLASASQS VRIITGVSHRTRPKIIFKLIFLFFFFF
8640	22541	A	8702	31	229	MEKYNVPHPSGILRSHEKEQAALFTIAK RWRQPSYPSIDWINIMWSSHTVEYYTA MKRNKQLYSQ
8641	22542	A	8703	3	126	LQELRDPTLTFRLLGSPRPVVVETRPVD DPTAPSNLYIQE
8642	22543	A	8704	438	31	SEPCAGYNLLVCRFLSPLKHNIRVGVT RFSRCHLSPLSLTRKGNLTPCTSRVRQ CLALLWLHSAHPLSCMHCLALPSENN PVPQMEMQKSPIFCIAHAGSCTPELFLF GHLGSTPLTHLLSLRINVLRTSE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
8643	22544	A	8705	429	319	PGATLAHRSINLPGSSDPPTSASQVAGN TGVSYCARE
8644	22545	A	8706	426	245	RAATPSPIKLTKKKKKKKKKKKKKKKKK KKKKKKKKKKRGAPLKKTLGGPQINRGK KKIPFFF
8645	22546	A	8707	1	108	KHPRGGSFGYCFALAWVAFPLALVSGII YIHLRKRE
8646	22547	A	8708	3	146	QIEGHTISALGDGAAWPVQGLIRHFRPE LEERMORFAQQHQARQAAS
8647	22548	A	8709	2	83	LVLELAVALTIQAYVFTLLVSLYLHDNT
8648	22549	A	8710	1	81	RPLSKTVRENVLEKTKAAGTKKQFQKF
8649	22550	A	8711	156	4	RPLSFHPGGKKRLFLKKKKKKLCAVAHA CNSTLGGRRGRIMRSGDRDHG
8650	22551	A	8712	440	233	TPSYFVLLVERGFSMLPRLVSLTSGDPP ASAFRSAGITGMSHHAQRTGRSKAYLP FLEBPDCLKHIPP
8651	22552	A	8713	92	302	AMHPTMGPDQGHGTGGLYAHTPLPHSH THANTLIHSHIYAHASHITIPATCPKGP TQPYLCLLSPHIEL
8652	22553	A	8714	2	166	KKINSFFSQGLTQAKVHGGRPSSLGPO PVLKRSSCLSFPPSSWDYRHEPLYPAN
8653	22554	A	8715	1	129	GFRHVGQADLELLTSGDLPASASQIVRI TGVSPCAQHEFFKSN
8654	22555	A	8716	381	105	RRSLHSLVINGAQAGVQWRDLGSLQPPP PSSLPWPKVPRLQPLGRHPVWEVRSV SARPPIVWDVRSPSANLPSLESEERLCL AATPSGK
8655	22556	A	8717	385	125	FFFFLPPAPLLSGXPWFFFFFYIFSSFFF FFFLGSPPEPIFFFFFPLNKIFFFFFF FFFFFNNLFFFFFFFYYYYFFFFF FFF
8656	22557	A	8718	409	264	KTDQRWSTSSSKIMSQSQVSKGVDFES SEDDDDDFPMNPSSLRRNR
8657	22558	A	8719	3	269	KKHVKRVLSHLKASCPEELLHFSSWPQL LELQLMGGGSHTHMDQHTHTMHMHIYT HAHTHTVAVAKLNELPWVEMNLLSLGAFO QRLP
8658	22559	A	8720	430	141	LFFFLSFFEDGVLLCHPGWSVVAQSOLT ATSTSKKKKKKATPPGIPKFLIGKSGK PPRVLLIGHWAPKFFFFNPRLAFF
8659	22560	A	8721	386	290	RWGLTMLPRLVLNWLQAILLLWPPKVS GLQA
8660	22561	A	8722	3	157	HEVFLVETVFLHVGQAGLELPTSGDLPT SALWEAENGGLLEDRSSGPAWET
8661	22562	A	8723	493	186	FSPQGGKRAILGLRNLCPGKDF SAR PPKEVGNEGRVPKTKLFFVFLKKGFPL IGRGGFKSRPWESP RPQKVG VQRLNP PPGPPFFFDLIWPNRNGS
8662	22563	A	8724	3	186	GGGTFFFPVGVGKNGGGTTPAKTLPPF PSPLFFFSPPSPGEGGSREPLSTPLA CICI
8663	22564	A	8725	370	67	FAPPKNFYKGAPPFFIFLFFLFIYFF FFFFIFPKFLVFLLETGFHHVSEQEDDL VIHLPPPKVVGLOAWATTGQFFVFLI ETGLHPVNQDGHNLLTL
8664	22565	A	8726	966	652	LGSLKPPPTGFKRFSCLSLPSSWNYRHA PPCPANFVLEETGFLHVGQVSELLTS GDPPTLASQSAGITGMSHRDNLGQHLIV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						NHCYLFYQGHKTRSLPP
8665	22566	A	8727	85	425	HMHSFAHELHTFLHHTNSHTNSQNQSP TYTSKSHTHSYMRFDSHDSQMQQTHRH SLLHMTQLYCTHTHTHTRTVPLHLHS VKGWLNTKVALGGRTSHGRBSHIAGRLL A
8666	22567	A	8728	393	124	LGSGEPLQFQSPSPGPGPKSHWNSWG NANPPVPPYIIESAPPPHPPFGAQSKY SGGQAARLCPPPFLKKKKKAPGSGT GTFSFQ
8667	22568	A	8729	25	217	AVQPIRVQRRSLQSPQEQTILAPSLAK VDMEMTQLTQENADPATRDYHSSLVN REQLMPHY
8668	22569	A	8730	1	611	PGIFYSALLSLDTSILNQLCFIMHRYRK NLTAACKNELVQKTKSEFNFSKTYQEF NHLYTSMVGLWTSKPFGRGIYIDPEIL EKTGVAEYKNSLVVHHPSFLSYAVSFL LQTSRSSSSSSSSSSSSSSSSSSSSSS SSSSSPSPEERTVNVSSIRGKKWSWYLD YLFSQLQLGLKLFIRSSVHSSIPRAEG INCNNQY
8669	22570	A	8731	120	378	VEKQASILGCKCSTPRAALGFRERTLP LRRCPCCGPPEAQMELEKRALGSQAQWL MPVPFALWEAEVGESLEARSFETSLGNI A
8670	22571	A	8732	2	68	VYVCVCVCVCVCVCVCRAKVM
8671	22572	A	8733	382	258	NYHSSLHLETPGLKQSSCLSLPKSWDYR HESPCPALIFNSL
8672	22573	A	8734	479	326	PPLYGFFFFFWGGGFFFFFYFFFF FFFFFFFFFFFQTTT
8673	22574	A	8735	422	2	GRRPPGLYFFFPKKNFQGRGGFLFF FPPKGGFFFPPIGFFFSSELGKDWP PKKKVFSQRFFFPPLFLFLFFFFF FFFFFFFFFFFFSFFFFFFFFF FFFFFFFFFNKQVFIERLLCARHCFRPPAS
8674	22575	A	8736	7	75	IAVALIQAYVFTLLVSLVLDNT
8675	22576	A	8737	2	176	NFGLLAETGFLYVGHAGLEVRSDDLPA SASQRAGITGVSTAPGFNRYFYKQTIYK YG
8676	22577	A	8738	408	111	GSSFPFRAGGENFLKKNAGGKNFPGGEG GGGFYPLYPKKFFSPKGFIFWGGGGGK WPPPKGGFSKKPKQVFFTPPQKKKKFF WPPGGNWGPKNF
8677	22578	A	8739	5	249	YEGLLKLMQASPFQRGHPVNHKKKKK KKKKKKKKKKKKKKKKKKKKKKKK EGALGGKFLAQTSEKGEKQKVFICY
8678	22579	A	8740	1	226	FFLRQSLSVTQAGVQWCDLSSLQLLAFQ GSSNSPTSASQVAGITGVHHHIQLIFIS LVETGFHVAQAGLELNLQ
8679	22580	A	8741	4	96	DGLMLPRLVSNWPPQGLPFPWPSKMLG LQV
8680	22581	A	8742	19	112	FGRILLVREKKKKKKKKKKKKKKKK GGGFL
8681	22582	A	8743	362	234	KMDQKCLSEVLQRWFPCCCCCCCCCC CCFSLFFIFEPSRS
8682	22583	A	8744	3	419	LTLRRFQLNLTLTKKKKKKKKLNKKK KKKKKKKKKKGGPLFKNSLGGPIFG GGKFIFFFWGGFLKPPGDFLKKTFPLG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GEIFGPPPPKNLTPLGKKKIFKGVGGKN PPLFLRRKKFFSGGFFKKIFSPGLGF
8683	22584	A	8745	444	1	KKPSKEILYPENSRRFFSPLSPLKFFFSF KGFNFWGGGGLCPPPKRFPSKNNPPG FFSPPLKEKIFFFPPVNLGPPRDLFKG APPPFFFFFLLWEMFYWLSLSSGSQR LPQQVPTVEPSELGGMGAYFVSKRSTYL QRGWRPER
8684	22585	A	8746	104	222	NRTFCLLKKKKKKKKKKKKKKKKKK KKKKKNWGGAL
8685	22586	A	8747	403	201	MEKYNVQPHSGILYSHEKEAALFFPIA KRWRQPSCLSIDERNIMWSSLTVEYTT AMKRNKQLYSQ
8686	22587	A	8748	1	90	RTRGAVYAALERMGLDGCVEDLRSLQR GP
8687	22588	A	8749	444	85	SPPPPGLFFFFFFPKKTSPPPTKKGFF SPPPPQKFFFLKPPFFLGGGLGNFPPP KKNFFSKNPPRFFFPPEKKNNFFPPP FFFAPPKFFFLTTPPLFFFFFFF FFFFFFFL
8688	22589	A	8750	2	309	EFFFPYWEFLKINACMFSPKKKKKKK KKKKKKKKRGPPLKKTGPGQIPRGCK KKIPPLKGGQKKPPRGFLKKNPLFGGGP FGPPPPPKINPPEKKKNF
8689	22590	A	8751	3	76	TASVSEGGGLQGITMKDSDEEEG
8690	22591	A	8752	433	145	SFFFFFFFSSFFFGKSSFFTPL
8691	22592	A	8753	2	124	GHLMLHLSATLAISTINLPSTLIIFT ILIKKKKKGRPF
8692	22593	A	8754	80	201	FINANSKKKKKKKKKKKKKKKKKK KKKKGGGLLKKTPGGAQF
8693	22594	A	8755	415	1	IYFPTPEKFGPPKETLKKGAPFFFFFQ KPPFFGPGGKQGGFGSLQTLPPGKKKI SRNPPRKRGFDAAPPFGKFVFLKKG VFPGGQGGFKTPTPRDLAPPAPLNPGAL FFFFLRLQSLSLSLRLCSGTILAHAS
8694	22595	A	8756	3	136	FTATRPGVYVGQCSEICGANHSFMPIVL ELIPLKIPEIGPVFTL
8695	22596	A	8757	80	326	KKFSLGSQGGGAGVFPRLPKLQTTAL NSGAKGTPPFLFPEPRKGGPPAPGWE GIFCPHFFPMGQKGGGLWHTGEGPH
8696	22597	A	8758	1	164	SLISSTQGHKQCRRPQGPLPRKTRDPCS HVYLLTFPPLLSYDPAKSPSLRNTQE
8697	22598	A	8759	431	79	FFFFFIPLKKVSTQSPPPQFYFFFLKT FFLFQPLLKEGGSWGGGDKPPPLAPFK KWGVFFFFFSFCCFVFFFLFFFL FFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFPRCVLTRL
8698	22599	A	8760	60	194	ARPTCPATAVTQKKKKKKKKKKKKKK KKKKKKGGVLKKQGGKRY
8699	22600	A	8761	383	38	CASMTFPKKKKKKKKKKKKKKKKKK KKKK
8700	22601	A	8762	399	164	HTTVKSLVPMDDPPKKKKKKKKKKKK KKKKGGGFKNLWGGQLTGKKKIFFF LKGKKKPLGIF
8701	22602	A	8763	353	48	NFFFKVFFFLKDFSHKGAPPKGGPPKK TPPRKKFFFLKIKPLFFIAFFFWSLFG FFLIFSLSFFFFFFFFFFFFFFFF FFIVFTITLMEFKIYLH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8702	22603	A	8764	2	93	FAMLPGLVSNWPEAICLPWPPLGLGQMM
8703	22604	A	8765	398	63	PPPPVFFFFSGGFFFWGGGGQKSPPRER CFFFKMHPGFFFI PPFGKKVFFVLEGV VCPLGFFFLSGGAFFFFFFFFFFFFFFFFF FFFFFFFFGFFFFFFFFFGFSPVSHL
8704	22605	A	8766	3	83	ILETAGALIQAYVFTLLVSLYLDNT
8705	22606	A	8767	450	306	QKKKKRRNKPEGLSTVAHACNPSTLGG RGRWITQPGQEGNFISKY
8706	22607	A	8768	1	111	WSIALVAQAGAPGFKQFSCGLPKSWDY RHEPPCPGL
8707	22608	A	8769	385	261	FLAEMGFCRVGQAGFKLLNSGDPASAS QSAGITGVIAVL
8708	22609	A	8770	3	293	SLGSKPLGLLSLSPVKWFRIFGKERNKV WGKGGTDRNQSSAFKHLQRGSDSPKQ NKIKACSSKFYLRRCKRSFLLIKKKKK KKKKKKKKKKKKKK
8709	22610	A	8771	2	281	CVCVCVCARVYIYIVVYICYTYMVCY MYICYIHYIHYITCVYVYIRIHYIC ICVCIYTCIYTYIYTHYKHSVYLLNF YINPKLLQS
8710	22611	A	8772	295	161	THHTHTHTHTHTHTHTHTHTTCSLPPS LAQLLGNCCIKAAISILYIL
8711	22612	A	8773	1	318	FFFFVRWSEFTLVAQARVQWRDLGSLQPL PPGFKQFSCLSLLSSWDFRHTPPCLANF VPLVETGFLHVGQAGLELPTSGDLPALA SRGAGITGVSHHPQPPLCFLFL
8712	22613	A	8774	3	70	FMPIVLELIPKIFEIGPVFTL
8713	22614	A	8775	369	191	TYKINKIGWAWWCAPLVPAWKAEEVGL LEPGSLRPASVIQDDPHLKKGTYSRVLT THL
8714	22615	A	8776	2	124	GFRHVGRAGLEPLTSGDPLASAFQSAGI TGMNHHVQPIVE
8715	22616	A	8777	1	162	LKYYTADENGKTSRLLPQRPSDECGAGV FMASHFDRHYCGKCCLTYCFIKPEDQ
8716	22617	A	8778	346	138	YNSPPYKEKTIPLQARVNFGPPRDSLKR PPFFFFFKRQSLTMLPRLVLNSWAHGI LLPWPVKVQLQA
8717	22618	A	8779	2	117	LNLDTTAVQVRNYPRIRESYKVSFLSAL EETKKLNTQ
8718	22619	A	8780	2	97	WDLTMLPRLVSNWAQVILPSWPPKVLG LLA
8719	22620	A	8781	403	276	IISTVFQRGSCPIPSRKEVCSEPRRLQ KDSLTGFPHTVYKH
8720	22621	A	8782	2	119	QAGLELLTSSDLPASATQSAGITGMSQR ARPHFQCKNVP
8721	22622	A	8783	245	101	ELQFKMRSGWRRSQPISWGLTLVPRLIS NSWAQVILLTWPPKVLGQIA
8722	22623	A	8784	2	124	AKLEKKKKKTGRARRMQYNRRFVNVP TFGKKKGPNANS
8723	22624	A	8785	3	355	VGPSEPGAGYNLVCRLLRPLEKHGIRV GVTGFSRCHLSWLPLARKGNSPTPCASW VRHHLALLRLTVCGHLPLSCTHCLTSPS EMNPVPQLEMOKSPVFCVAHAGSCRLEL FLFGH
8724	22625	A	8786	238	9	PVKLGAGPPQAPFWLRKWAPLIKPFFKG PIGSLQIPLFFFLRQSLTLPPRLECSAT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, v = possible nucleotide insertion)
						WLTESSTSWVHAILLPQPE
8725	22626	A	8787	336	10	CLSLPSSWDHRRLLPHPASFCIS
8726	22627	A	8788	1	147	IFYLLETGFHYVGOAGLELLTSGDSPAS ASQSAGITGVNHHAPEIHVF
8727	22628	A	8789	3	130	DLBEGIQTLMGRIEDGSRRTGQILKLDH SSEFSKTRELYPVF
8728	22629	A	8790	206	3	VPPSGPIKKGDKKKNLVLIIFLIKVPNK KLKRGVSLAIPFFFFFVFLLETGFHH VGOAGLELLTS
8729	22630	A	8791	124	390	RAGAQSNLMEPPPSGVKAIFFPNFPKKW GNGTPPPAPLIFGGLKKGVSPCGPGGS EPPAPGGPSPLAPPKGGNNGDRLEPPP DKFLN
8730	22631	A	8793	2	301	HEERERERERERERERERERERERER ERERERDALFAFFPPRGARPPPEIRGV FVGAGSVREIYPTLSIFFPSPPAHRGRE LRSRCVSHSLHLISRA
8731	22632	A	8794	1	285	ARGERERERERERERERERERERERE RERERERERERERERERERERERER PLFFLGRGGALRAHAISPPFLGAPPYI YIFFHMRARPPHRYLCAQRETRPAL
8732	22633	A	8795	1	321	ARGERERERERERERERERERERERVSR RIPRGDLRDQPHPLARSRDSFCGSADH FGRGVFNKVSVDTPPTHRTSSLGGSV ERDLLTSLGGGTYPWKNMCATGEDQ
8733	22634	A	8796	2	140	HEERERERERERERERERERERERER ERERERERERERESLPPAGCAKGAGWG E
8734	22635	A	8797	2	223	SARERERERERERERERERERERERVSR RNLSRGGGVPPPLQNVRIHSGGPARGT LHHIKKKTSLTDVGLAQ
8735	22636	A	8798	1	176	ARGEREREREREREREREREREKISF LGGGRGTQFAIERGVIQCGRRYTTGRV RN
8736	22637	A	8799	335	27	PPTKFFFFFVEMGFCCIAQGGLELLS SSSLPASAYQSAKIIGVSHHAWSVF
8737	22638	A	8800	342	191	STSLSLPKCWDYRPEPPCANLSYFFKD PFSKCNPRLYWGLGLQHRNFG
8738	22639	A	8801	104	332	AVPLTMVKIQPLWKRVWRPHNKSLELP CDPAISLLSMYPKEMKSLCQRDVCTPRL STGPLTIAGMWNPPKRSSMD
8739	22640	A	8802	563	258	FFLNLETRSWYVAQARVQLFTGTVTVH YSLDLLASSHPPISASGVAGITDACCQ LTLPLFLKLLGLGGGGVGYPSYFLEG FHNDCSRVRVLCMWSYQ
8740	22641	A	8803	2	199	ARGLLVRRFLSPSEKRSIRVGVTFRSRC RPSPLSLTRKGNLTPCASQVRQCLALL RLAHGACTH
8741	22642	A	8804	266	108	KLVSCKVALPPSFSSSCSSHIGCACFP FTFHYDCKFPOASQAMLEQAVEP
8742	22643	A	8805	1	140	KVVWFKRPGVYGGQCSICGANHSFMP VLELIPLKIFEIGPVFTL
8743	22644	A	8806	2	90	SSAAAEENDEKKEEAERTEDDMEFGLF D
8744	22645	A	8807	229	34	KKKIFFFFPGFFWPPQKFFFKAPPPFF FFFFFFFFFFFFFFFFLDLFIYLIILSYTK LISIRAAPI
8745	22646	A	8808	43	173	NADSGHAQWLTPGMPALWEARAGGSQDQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EIETILAGAGKPRLY
8746	22647	A	8809	259	134	IYMI FKNKFFNRDRGLEPMLHRLVLNWAQ VILLSWPPKVLGL
8747	22648	A	8810	391	193	VLPKIPGIQFPPPCRFKKRPRPRFKKPP PKRKKISFSNPPKIWPPQGYFKRGPPRL FYFFFFVVIL
8748	22649	A	8811	304	3	TTPTNIFFCFLFFIFIFLWYFIFIFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF QCFIGHDDQKMMVHTHTQTSSHLQGGG NPQGGQSPGWVLWCA
8749	22650	A	8812	395	268	FLVETGFHHVGQAGLELPASSDLPALTS QSAGITGVSHHGWS
8750	22651	A	8813	782	1174	LSRLFYFCVLFCLYMKTTQLPYFRGLVC LFVLROGLTLSSRLCECSGMIAACCSLNV PGSTDSPTSASRVVRTTGVRRHTQLIFV CFVEMWFHYVAQAGLEPLGSSSPALSS QGAGITDVSHHTPLELCF
8751	22652	A	8814	95	236	ATMPGLKNIFYFLKNKDKGLTMLPSLVLK SWARVILLPWPPKVLGLQT
8752	22653	A	8815	381	58	SCLLFPPFWGARGGGPPRAGGSNPPGPP GLTFPPPPKPKNYWARGGPPFIPPPREG WAGGFPLPRGRVPLAPGSNNLELGPLP SPPGYQKTPFSKKKKKKKKRKR
8753	22654	A	8817	441	158	FFFFLRTDGYLTMLPRLVSNWPAIILL PQPPKMLGL
8754	22655	A	8818	415	342	RLVLDSWAQEILLPWPPKVLGLQV
8755	22656	A	8819	400	171	NFFFPFGVKFLGGGGPQFPFPQKRGFFQ KTPGGFFKPPPKKKKKFFPPPKIGPPQ GIFKKAPFFFFFFFFFFFFFFF
8756	22657	A	8820	2	268	INIILAFTISLLGILVYRSHLMSSLLCL EGIILSLPIIATLITLNTSLLANIVPI AILVPAACEKKKKGGAVLKDPPGGQSLR VLAR
8757	22658	A	8821	2	258	LCLFNQAWAMAGSPPPASLLPCLSLSDC CASNQDQSVGVGPSEPGVGYSLVVRFL SPSEKRSIRVGVTFRSSWVRWLRTVIPA T
8758	22659	A	8822	250	456	GGGDKFGLIETFPFGLKPFLLNLISGW ELGFLAPPPFKCFKGRGPPFLPRFVF VANLLLTCKKRD
8759	22660	A	8823	492	376	QENCLNPGGRICSELRSCLCTPAWATER ACLKKQKNTNQ
8760	22661	A	8824	1	116	LTPLPSPAPPSVDNLTTPPEWVCSLFP HPQMIISRN
8761	22662	A	8825	2	191	FLVETGFHHFGRAGLKLNSGGALTSF QRAGITGVITGVSHCFEVRVWVTGTQYF LCYILKS
8762	22663	A	8826	393	75	PRFFPPPPPKIFFFPFPPFFLGGFPPI PPPPKNFFPKPPPGFFFPPLKKIIF PPPPFSPPNFFFPFPPFFFPFFFI FFFFFFFFFFFFFFFFFFFFSI
8763	22664	A	8827	81	380	KIITKHNIARTNPYTFCIMNYLKKKKK KKKKKKKKKKKKKKKKKKKKGGGPK NPGGGQNNPGGKKNFFFGGGKKNPPG FFKKKPPFGGKFGAPPPKN
8764	22665	A	8828	354	13	TKPKTPLTKGPRRGLAPRVPGGGGPI TPPPQNFLGEKGTARKKVFPGRPAK RPPRKKNGFEMRPLKKNPGPWKFLGFF

[illegible]

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucleo- tide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						ERERERERERERERERDFVFRWGEGHI DRQYCSFLCPGWCHCPM
8786	22687	A	8850	2	79	PEERERERERERERERERERERERERER ERERE
8787	22688	A	8851	1	178	ARGERERERERERERERERERERERERE REKERERERERERERERARLFARGEK KKHTGGGPPLFYLYI
8788	22689	A	8852	3	76	TRERERERERERERERERERERERESP A
8789	22690	A	8853	5	227	EERERERERERERERERERERERERE RERDFFFFFLEKKYLFSPIGELKGRGG SLTPLLTGKNP CPPPH
8790	22691	A	8854	1	189	ARGERERERERERERERERERERERERE RERERERERERERERERERERERERE RHSRLFRESVCVARAGGASSPPRG
8791	22692	A	8855	2	271	HEERERERERERERERERERERERERE EREREPPRGEKYCIRVPPQKILSPACD SLLYVTNLCVSHSTPRGERYVALENSE ETRCF
8792	22693	A	8856	2	309	HBOQQQQQLRNLRDLFLVYNRMTELCP QRCVPSLHHRALDAEEACLHSCAGKLI HSNHRLMAAYVOLMPALVORRIANYEA SAVPRVAEQPGVSPSGS
8793	22694	A	8857	44	203	GYSTCVGMHAHTHIHTDTHTAHTYIHQ CLIQIGLCTFATCTSQVNKSMAEL
8794	22695	A	8858	329	182	IIFVCLVERGLHYVGQAGPELKASDDL ALASQSAGTSVSHCVSSMS
8795	22696	A	8859	1	175	GLTLPPRLGCHATITAHYSINLPGSSNP PTSASQVAGTHSRPCPETQTALQRGP HD
8796	22697	A	8860	3	350	HEAIGLSRNIKNGLDHFLPLGTPTPLIP ILAMITILLLVQPIALAVRLTANITAG HLMLRLNGSATLAISTISLPSTLIIFTI LILLTILEIAGALIQAIFYFTLLVGLYLR DNA
8797	22698	A	8861	139	3	TFKEADIKGGSPPHLASFCIFGRDGVSP CWPGWSRTPDCLKRSTRA
8798	22699	A	8862	3	134	SPTPPPSKPSSIPRKSSVDLNQVSMLS PAALSPASSSORHES
8799	22700	A	8863	346	219	RLVPPCLDNFNLCFRYSCLTMLPGLVSN SWAQVIFLPQPKD
8800	22701	A	8864	1	147	GTRFFFERGIHVQGAGIQLLTLGDPPPT PASQRAEITGVSHHTWPNFIF
8801	22702	A	8865	267	132	KKKFWFFFFFLRDGVSLLLRLVSNCA QEILLPWPKLLGLQV
8802	22703	A	8866	343	215	LAQGLKTPIPKRVPHPTQKKKFCSERPT RIQTDRCWSVPLS
8803	22704	A	8867	1	242	GTSKKIDKLDIYIELKCFTAKETISRVK RPVEWEKIFANSSPEKGLISRINKEAKK LNSSAIAHNCPNSTLGQVRRIT
8804	22705	A	8868	1	219	GTRRPTWATWONPASTKKKNSFFFETE SRTVPQAGGQGNLGSLSLPPGLKRFS CLSMGPAPKGQSGSLMG
8805	22706	A	8869	1	181	ATGGIFLLLDDVSLAYESHKLLLEGAKSE SAEELKKRAQELGKLNFLT KIH EMLQP GQDQ
8806	22707	A	8870	1	255	AAAPPNAPGGPPGPQAPSAAAPPPPAH ALGGMDAELIDERALTLELELGLHRRVR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ELFELFLGQSEFDCFDLGSAPPAGSVS C
8807	22708	A	8871	383	233	ATTFPNPGFLFVRLFVLVQWPDHEPFGF QQSSHFSLPSSWDYRHPPPPPG
8808	22709	A	8872	211	294	AXKKKKKKKKKKKKKKKKKKKKNIWGG
8809	22710	A	8873	398	100	QKERPPGFPFPKPGPPQKRGKGAPPKD GEHYFFWVLEKSTGFPPKTKRVYVPSPV YPHPPAPQKEGFPGGSPPPRPIASPFGG KKKKKKSYIEKENLF
8810	22711	A	8874	3	214	DAWVLGILVYRSHLISLLCLEGIILSL FLIATLITLNTHSLLLEKKKKKKKKKK KGGAFKKNPGGAQI
8811	22712	A	8875	2	254	PRVRPEGRNRTPOSWFQANPMACMTFSK KKKKKKKKKKKKKKKKKKKRGGGFIKMG GGGKNFREKEKINFLIRGKIKKTGGDF
8812	22713	A	8876	2	135	TINLPSTLIIFTILILLTILEIAVALIQ AYVFTLLVSLYLDNT
8813	22714	A	8877	2	296	LARGAEVLGYGSHSRGRVPGALVGQAG RLFTEHPGSSPATLAIYPTPEGTSVAVS ISAPPKARSRPYPSPRSCHNLSLAGSSV LVPPGPVHRWVGRP
8814	22715	A	8878	164	29	RKIGPARWLTVPVIPALWETEAGGSRGQE IELILANTVKPGACEVL
8815	22716	A	8879	381	219	GKMTTEEVHMLVAGHEDSNGCINVEGK R
8816	22717	A	8880	2	156	ANGNSFATRLSNIFVIGNGNKPWISLPR GKGIRLTVAERDKRLATKQSSG
8817	22718	A	8881	3	402	SGFNIEYAAGPFALFFIAEYTNIIINT LTTIIFLGTTYDALSPELYTYFFKKKK KGGRPFFFFFLKKKKIPPPKKKNFGKK GETLKGRRGAPIFQPKILSPPKKKKK RCGAFKKSLLGAKFNGGGRN
8818	22719	A	8882	1	406	RYSTPSGEVEERYSTPPGETLERYSTP PGETLERYSTPPGETLERYSTPPGETLE RYSTPPGETLERYSTPPGEALERYSIPT GGFNPTGTFTKTYPSKKKGGGRFKEPLG GPRFTGVGRVKVFSLWGGVLNAR
8819	22720	A	8883	484	307	KKILNRRVRWLTVPVITPLWETEAGSSRG QMETILGNTVKPPASASQSAEIKGMRI IIF
8820	22721	A	8884	1	131	GSLTHHNNIKPSFTRENTLMVIHLSPI VLLSLNPDIIITGFSS
8821	22722	A	8885	406	106	KGGAGPKIAPPKKKAFSPIPPPFFWPPP VFLKGPPPPSPNFFPPPPVFFRGPLPF FFFFFFFCETVVLPRPSNLVFTLPHVF AWLIPIDQYLFISHSC
8822	22723	A	8886	425	325	SSTHTHTHTHTHTHTERSLLAFEPSAG ELWMAM
8823	22724	A	8887	394	278	VCVCVCMCVYICIYPCWLPCHWMCLELY KVFKGIMKGV
8824	22725	A	8888	2	86	YSRTAAALIQAYVFTLLVSLYLDHSAY
8825	22726	A	8889	400	62	FLYLKSFPPPPPERGVFSPLPQKFFFSF KALNFLGGGGPKFPFKKRFFFKYPRV FLYPPHKKKNYIFPPPDDEGPPRVFFKA PPHFFFFFFFPPPPPPPPPPTRLEWVQ
8826	22727	A	8890	3	100	SLEPGTSGLGFSCLTLPSSSEDYRHEPP CPAN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8827	22728	A	8891	32	142	VRPTRPGQVASVLYFTTILLLIPTISLI ENKILKWA
8828	22729	A	8892	3	382	TPHNFLSRPSYEPKPASTPSRAPKKKK KNPKKKKKKKKKKKKKRGGALLKKT LGGPKLPGGKKKNFFFRGGKKKPPGDF LKKTLFLGGGNLAPPPKKKNPWGKKKI FWGEGGKKNFFFFG
8829	22730	A	8893	368	199	KKKRISPPSRKRAPQGDPLRPTPIKNL YYLSFFFLILYIFFFFFFFFFFFIFFF
8830	22731	A	8894	3	136	TINLPSTLIIFTTILILQITILEIAGALIQ AYVFTLLVSLYLHDNT
8831	22732	A	8895	1	144	IATINLPSTLIIFTTILILLYLLEIAGAL IQAYGFTLLVSLYLHDYPYN
8832	22733	A	8896	153	375	PQKKKKKKKKKKKKKKKKKKKKWGGGF LKNSGGAPIFGGGGKFFFLGGGFKTP RGFFGKNPFFWGGKKKKN
8833	22734	A	8897	332	400	WLTPVIPXLWDAEAGGSFEVRSS
8834	22735	A	8898	215	359	TELVNNAVLFPCPLCCSGHLLCAIHA KRVTIMPKDIQLARRIRGERA
8835	22736	A	8899	414	73	PRLLCFHKKAWAMAGALPPALLPPYSLI SDCCASNQSDSVGVGPSEPGVGNLVVR RFLSLSEKRSIRVGVTFRSRRCCPSPLSL TRKGNLTPCTSLRQCLPLLWLAHGAR TH
8836	22737	A	8900	374	88	VSPSPSLKIFFSPKAFNFWGGVGFHFP PQKRVLPQKPPGGFFSPPLKKKFSFP PVKLGPPKGSFKGPPPPPPPPPPFGL DFMYTGSSNVW
8837	22738	A	8901	433	56	PEGPPPPGGFYPGKRGFFPTPLVFGGP KRDPPPRGKKNPSWRSGGKQTPRFRDP LLKAFFPGGPPQRLGKAQGPFWFFGPK KGKTQTGPPFFFKLGDWPGPKKKPPPG GAPRLGPPKKKFL
8838	22739	A	8902	3	73	IAVALIQAYVFTLLVSLYLHDNT
8839	22740	A	8903	3	149	PNLSYIIGKDTWEHWPBEDECDRENQ KQCQDLGAFTESMVVFGCPN
8840	22741	A	8904	351	137	FPPEFFAAPKSGILFFSKTWMEVEVLF LSQLMLGQKTQYCMFSLINGRLIIKAPG SLKGDHHPPLGLLEG
8841	22742	A	8905	142	5	KIFLQKKKKKKGLGTVAHACNPSTLGGQ GGWIMRSRDQDHPGQQW
8842	22743	A	8906	367	244	HVPQARAKFFCIFSRDGVSPYWPWSRT PDLMICLLFIVEL
8843	22744	A	8907	146	248	SQILGRLRQENCLNLGNGGCSEPRWCHF LAWAKE
8844	22745	A	8908	2	197	AAASTHARLFLCVCLFAYLLVEMEFHH VAQAGTELLDSSNPPLASQAGIIGMS HHTQPQYIC
8845	22746	A	8909	1	127	KKTRLERAQWLTPVIPAFWNAEAGTLL EARSRLRPWPPNVL
8846	22747	A	8910	368	280	LTMLRLVLNSWAQAILLTWPPKVLGLQ A
8847	22748	A	8911	355	211	QQQNLHLFWPGTVAHTRNSSTLGGQGM RITGAYEFETTLGNTARPHLY
8848	22749	A	8912	325	190	KKKKKKGGGPPQKKKNPPPPPTSKKKK KKKKKKKKKKKKKKKKKKKK
8849	22750	A	8913	1	411	VNVFAPRGGAYRGRQASFSSGGHLPVFA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YRPLCLPNQTTNSAMAGAPPLASLPCCS LISDCCASNKRDSMGVGPSETGTGYNLL VCHFLSPLKCSIRVGVTFRSRLSPL SLTKGNSLTPTCSRVRCLALLRL
8850	22751	A	8914	258	9	GAIPCLHCETNPISHISTQELQTPPEPQL PGVPLELPPPGSCFKCRKSGHWAKECPQ PGIPPKPCPICAGPHWKLDCTGPERL
8851	22752	A	8915	326	42	EKIHRKYFCYSFVFLVEMGFYFVGQAS LKLASSDLPASPSQSAVRKAMSHCVRP VLVIFKNKILQNTENSTKIYVYPPNNQ ILTFCHFCFK
8852	22753	A	8917	3	106	GLELPTSGDLPASASQAGITGISHHAR PIMTYS
8853	22754	A	8918	320	171	AASTDGSYKCLCLPGYVPSDKPNYCTP LNTALNLEKCPFGLPHLSGSS
8854	22755	A	8919	1	201	VKPSDRYHLMPIFTAAYPHQNSTYNVPV STRMVMAEEFKQGRKRLSLCSDLYRKDLR TIVDPVVS CAT
8855	22756	A	8920	3	182	LLRPLEKRGIRVGVSRSFYHLSRLPFA RKGNSTPCASRVRCPSLLHGLHPLSD KPQ
8856	22757	A	8921	142	1	SCHPGWSAVVRPQLLRLRYENCLSLGG SGCSELGSCHTPAWTTTG
8857	22758	A	8922	1	117	LFFNYANGWSTTLLSRLSLNSWVHVILT PWPPKELGLQA
8858	22759	A	8923	357	121	LGAFSDGLAHLNLTGTFATLSELHCDK LHVDLENFRLLGNVLVCLVAHHPGKEFT PPVQAAYQKVAVAGVANALAHKYH
8859	22760	A	8924	343	133	LFFNFNFLETRLREWLIFFVSVEFGPI KRAGLKLQASSDPPARGSQSAEISGMSH YAWPCKSNRAFKCS
8860	22761	A	8925	321	44	PDSGGSPASASQVAGTTGACHDAWLMP FNMDININIPFSAKRDKLSMDKINEIIF SLLINRISSFQIMYFLCSSRIESRKRWL KQTGRKKE
8861	22762	A	8926	335	106	HFVFLIETGFHRVGHAGLELLTSTDPPA LAYKSSGITGVSYRSFTKLHLCAVCCLC IYTYLGLVLSFTPGSWEKKT
8862	22763	A	8927	2	160	LSRVPPRSANLTSISVFAEKRCFTMLPR PISNSWAQGIILLPSQAPKVLGLQA
8863	22764	A	8928	3	140	RVITEEKNFKAFASLRMARANARLFGI RAKRAKEAAEQDVEKKK
8864	22765	A	8929	126	59	NSGGGGCNELRSCHTPAWATE
8865	22766	A	8930	3	104	KNMACYCRIPACIAGERRYGTCTIYQGRL WAFCC
8866	22767	A	8931	311	112	MENYLSKMQQELEKNITRELKEAAAELE SGSIASPLGSTDESINLQDLVWKASREY VQVLKKNYMI
8867	22768	A	8932	345	134	GGGSSPWFPFPWRPRRADSLRVGLNPP GPGGGAPFFLKNPLIGWGGGARLWFQLI LLRVRPENSFDPR
8868	22769	A	8933	262	39	RPRRPHPGNFFFFNSGSHYVAQAGLEL LDSSDPTLPSQSAGTTGMSYQAWPLDRT FENRDCVLLHCSSPVSNT
8869	22770	A	8934	84	22	TPAWVWVLTVPVLPALWEAKAG
8870	22771	A	8935	277	111	ERIINHAAGSHGVSGIFMKYDLSSLMVT VIEBHMPFWQFVRLCGIVGGIFSSSTG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8871	22772	A	8936	2	106	DSATPRRLECLKEDVQRQQRERKELQHR YAEFVF
8872	22773	A	8937	1	193	LMWDFSPSGLDGAQFQGGYVWYNYINV KKGSI SGFTMVLGAYMLFYCLSYKELK HERLCKYH
8873	22774	A	8938	240	69	DSGNQLKRSFSGRARWLTPVIPALWEAE VGESLEVRNIYIILQNMNIGNIHLIIK
8874	22775	A	8939	329	177	RWNLA MLPRLVLNSWAQATCPSPWLKML GLEAEPSCPARTNFKVTSPLH
8875	22776	A	8940	358	120	HPSNFFVFLVRMGFHHVGGQGLELFPAR YVPTLAFRSGGITGISHCAWPKEWALPR KASPGLSGRGSPHCATCSSKAW
8876	22777	A	8941	333	104	PHVYSNGHICLSILTEDWSPALSVQSV LSIIISMLSSCKEKRPPDMSFYVRTCNK NPKKTKWYHKGQFEFVITF
8877	22778	A	8942	1	241	APLVAFTQVNLEDKGGLSKLVEATRINF NDRYDEICHHWGGNVLGPKSGTRIARKL KAKARELATNWKICTLLSFLYIKR
8878	22779	A	8943	1	240	APLVAFTQVNLEDKGGLSKLVEATRINY NDRYDEICHHWGGNVLGPKSVTRIARKL KAKARELATNWKICTLLSFLYIKR
8879	22780	A	8944	306	150	AASTLCPRLECSGAIMAHCSLNILGSGD PPASASQVGGARGSLPEGRWRLQ
8880	22781	A	8945	284	2	GKSRSPDLCTSGFTGTHFTLLICWV PRYVATCPPIGLNFVFIKTWWSHYIVQA DLKLMVSSNPPVSASQSAGNTGMSHTW LENRLTTKK
8881	22782	A	8946	1	226	WSFALFAQAGLEFLTSGDPPASASLSAG ITGMSHHAQPAVSLNSIFSASTFCATSS YCAKMKELKELKFMILIVDAA
8882	22783	A	8947	363	96	NTAPGYMPLLSIPFLVLKAVFLFLLGM FTAALLIIAQRWEQPKCASTDEWINKMW HMHTMEHYSTCCGVHAAVNISIQISEWN CWEW
8883	22784	A	8948	1	208	GRVGQPGRLRLTSGDLPASASQSAGVAG VSHRAQPTPALNCVLTWCWLQHYIKHNH GKRSEYFTIFNDM
8884	22785	A	8949	69	298	SRGHQRVADAALLSFDPVICLGLMLWGS SSIVCILHRHKRRVQHIHRTSVSPTSSP ESGATKTILLEQERTSPRS
8885	22786	A	8951	2	201	LYDLNMRISLPLPSLVCIHSHTREHT YTHIHTAHTYTHTHSHWVLSLKQKRMV KHPRLSVNI
8886	22787	A	8952	1	285	GASPPASLPCCSLISDCCASNQDSVGV GPSEPGAGYNLVRVLSFSEKRSIRVG VTRFSRCRPSPLSLTRKGNSLTPCASRV RQCLTLLWLH
8887	22788	A	8953	341	256	LGLGGGGCSEPRWHRTPAWVTERDFIS L
8888	22789	A	8954	227	43	ILFFIGKHTHTHTHTHTHTHTRAKCLFP PARFPTSPNSTTCTFPTEPAANPRGLV RAGLG
8889	22790	A	8955	310	79	RPRRPGLMERNVFIIFSILRESFYKIRI TNQAQCCMPIVPVTQETAGRSLEPKSL RLAWAIQQNSISKNNNNNFF
8890	22791	A	8956	374	198	FFFFLPNRHGLAMLPRLVHLHWQAVLPQ PPKVLGLQG
8891	22792	A	8957	138	10	RPRRPRLCQAQWLMPITIPALWESVAGGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LEARSLRPWWFFNT
8892	22793	A	8958	354	216	AGPRVFPGGEGGFRPPPPGGSPQGP GGESGGKPPPPAHWVFF
8893	22794	A	8959	364	223	LQAARSKKKKKKKKKKKKKRGGGK
8894	22795	A	8960	259	11	FEALKDPSNNLQSLFSFVTVLVAHV EKLSTLTSLAARRGLAMLPRLASNSRTQ TILLWPWSKVLRLQARATEPGLGLL
8895	22796	A	8961	334	213	AASTKNFERMEWGLTTPLMLVLSWVQV ILLWPPEMRL
8896	22797	A	8962	260	3	KGGFFPIFFIGIKPGFFSPALIFPKVF IFSQNFFVPLKKIFFFFVBTVSSHVVK AGLELLASSNPPAFTSQSAGMTGMSHHA W
8897	22798	A	8963	425	248	ADEWIHKMRHIHMIYYLAIKRNEMLIH ATAGMHLENILSEKDHMYDSIYMKCLAW ANL
8898	22799	A	8964	1	118	GKLMELHGESSSGKATGDETGAVERA DGYEPPVQESV
8899	22800	A	8965	2	130	GRVGPRMALNSWAQVIHLWPVKVLGLQ VAMKRRKIMILTSY
8900	22801	A	8966	119	364	LGWYLIETQICCSPLGADPFQQMISP LRDGLTLPKLVLSWVQVFLPPQTRK VLGLQAEVTAPGHIIFMIIMINTFK
8901	22802	A	8967	238	333	TRCLRLPLRLVLSWVQVALLPSPPKVL GLQV
8902	22803	A	8968	297	169	NPPPHIYKFFFIFFNIFFFFFFFFFFF FFFFFFFFMSKILIF
8903	22804	A	8969	2	212	RVRPRDRPLVRVRGRNKDGAETTPSPG LLPAHLTPPLDYHLNQPFIFGLRDTDTG ALLFIGKNMDPRGP
8904	22805	A	8970	242	357	TLDTIKSFKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKII
8905	22806	A	8971	191	265	ILMPXKKKKKKKKKKKKKKKKKKKK
8906	22807	A	8972	398	97	MFLYNRLWFFSPHPPLRFFFSPRATIF LGGGAPHFPPPKGFFSKKPPGVFLSPP QKEKIFSFPPLFLAPPKOFFKSPPPFF FFFFFFFFVSTGSSVS
8907	22808	A	8973	370	265	YNSSLPSWDYREVPPCPDNFCIFSRGW SQTPDLR
8908	22809	A	8974	3	119	GLKLLTSSDPPASASKTAGITGVSHHTQ TIFVFSSHKS
8909	22810	A	8975	1	110	VAQAGFKLVSSANLPTLASQSARVTGVS HRARSMQ
8910	22811	A	8976	3	152	WNQEKYPSTGEWMEKMWIYITLVQPM HGPHVAQDGFEGSPTQIHKL
8911	22812	A	8977	375	193	FQDLPLGTSNISFFKRWSPAMVRLIS NSWPQEIILPQTPKVLGITGMSHCTWPG GHISI
8912	22813	A	8978	2	395	RAALPTQASAMAGAPPASLPCLSSD CCASNBRESVGVGPSEPGAGVNLVLYL LRLLKRSIRVGVTRFSCRHLSPLSLTR KGNSLTPCASRVQCLALLWLTLSALYP LSCTHCQTLPEMNLVPQL
8913	22814	A	8979	120	19	ARVQWHDHGSTATLNSWVQVILLWPFPK VLGLQA
8914	22815	A	8980	204	48	LNRDKGLTMLARFVRNSWVQVILLWPFP KVLGLQALATAPQMSFLRAPLS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8915	22816	A	8981	335	221	FFFLFLFFCMITSHCSVNVLGASDSPTS VSHIACITGT
8916	22817	A	8982	360	150	LSHMPILLFVSLYPDHRAFMQVIFFFBET ESPSVTRLECSGAILAHCNVCLPGSSDS PASASYAGYSFYL
8917	22818	A	8983	346	116	GQGRGVETESCSVTQAGVQWCDHHSLLS LELLGSSDPSTSASVPTGTTGGHYHTSS HFLFSVSSSYPTTPVCLAYR
8918	22819	A	8984	350	263	LEMLPRLVSNAPQAIFFLLWPPKVLBLQ A
8919	22820	A	8985	3	159	BEYNLLVCRLLSPLKCSIGVRVTQPSR CHVSPLSLTRKGNLSLTPCASWVR
8920	22821	A	8986	2	253	KHVVGELKNDLSICGTLHSDRYLNLKL TNISVIDSEKYPHMLSVMKNCFIQGSVVR YMQLPADEVHKQLLQDAARKEPLQKQ
8921	22822	A	8987	2	115	GARIVGHLTHALKQGEYGLASICNGGGG ASAMLIQKL
8922	22823	A	8988	3	159	GFYHIGQAGLKLMSGDLPASASQAGI TGLSHCAQAGIFFFLPYDIFTVF
8923	22824	A	8989	1	123	SHYVAQAGPKLLGSSNPPASASRSAGIT GVSHHAWPPSLFL
8924	22825	A	8990	462	303	LARTPSRPTREPTRPPTRPPTRSPTRP FMLSVDCLLLY
8925	22826	A	8991	382	178	PPFFFFYFFFSFFFFFQKGFKGF PQKFFFFFGGKPKVKNFQKFLRAGKKG GEKKPPQNKRVF
8926	22827	A	8992	532	432	RDAGLTMLPRLVSNSWAQVLLLPFPKV LTLQV
8927	22828	A	8993	418	172	KKGKKKKKNIFLIFFNYFFFLIFFFIF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFGGAWSLFRGDSGEVKGTDMS RQCQGF
8928	22829	A	8994	2	722	AVRLNISYPPQNLTMTVFCQDGTASTTL RNGSALSVLGGSLHLVCAVDSNPPARL SWTWGSLTSPSQSSNLGVLELPRVHV DEGEFTCRAQNPLGSQHISLSLQNEY TGKMRPISGVMLGAPGGAGATALVFLSF CIIFFVVRSCRKKSARPAVGVDGTGMD ANAVRGASQGPLIESPADDSPPHHAPP ALATPSPEEGEIQYASLSFHKARPQYPQ EQEAIGYEYSEINIPK
8929	22830	A	8995	498	323	EPKAELNEGDIAVVHIKREGEWFKGTLQ RNAKTGLLPGSFVENI
8930	22831	A	8996	21	511	LIIDGVEAYALNASGVVNIIVFDPKGWA LFRSFKAVKEKLDTRRGSNSELETAVKD LGKAVSYKMGYGDVAIVVYSGQYVENG KKNFLPDNTMVLGNTQARGLRITYGCIQD ADAQREGINASARYPKNWVTGDPAREF TMIQSAPLMLLADPDEFVSQLA
8931	22832	A	8997	178	306	GAINAINWPPFNVMGKTLGFPNLMAL KQIPFSPVGEKTKRR
8932	22833	A	8998	351	211	SIQSLRMQVPFCYISGRHHYHSHHHIH HHHYSSYFLKYPQBYLRPL
8933	22834	A	8999	1	381	FRLFKFALMELCSIEGISDQPLFFVFGF FFFGKEASFGPQGGREGGKFLMEPLAK GVKGISCPKPPHPCLNPPKPKRGESSP PEGPKKTGAPGPAKKGLFLLTKGKNPWP GPGKTRKKAVFPKNF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
8934	22835	A	9000	173	399	IKSEWAAKKKKKKKKKKKKKKKKKKKKKK KKIFFFGGGRRFFFWGGDYFWGGGGVKK KGGGKKNPGPQKNGGGKK
8935	22836	A	9001	2	81	EFTPAVHASLDKFLASVSTVLTSRYR
8936	22837	A	9002	3	835	DAVRANDDLKENIAIVERRNNLLQAELE ELRAVVEQTERSRLAEQELIETSERVQ LLHSQNTSLINQKKMDADLSQLQTEVE EAVQECRNABEKAKKAITDAAMAEELK KEQDTSALHERMKKNMEQTIKDLQHRLD EAEQIALKGGKKQLQKLEARVRELENE EAEQKRNKSVKGMRSERRIKELTYQT EEDRKNLLRLQDLVDKLQKVKAYKROA EEAEQANTNLSKFRKVQHELDEAERA DIAESQVNKLRAKSRDIGTKGLNEE
8937	22838	A	9003	429	280	RGFRGHKFLBPPGFPFPIMGPPSPFP GSPQKNFPLQPKPLGFKPPP
8938	22839	A	9004	2	108	LSAYQGTPLPANILDWQALNVEIRGYVI IKPLVWV
8939	22840	A	9005	3	158	SSTQGHKHCGRPGGPLPRKTRDLCSVPY LLTFSPLLSYDPVTSPPRNTQE
8940	22841	A	9006	3	370	LLLTGLNRLTDLVSLYIFTTOWGSLT HHINNIRPSPTRENTLMFIHLCPIILLS LSPDIITGIFSYTRHYVNSSTYLETNER GGSYKNRLGCPESKGLRIKDDSLCWGPL HDTSAYYENK
8941	22842	A	9007	363	76	KLPNVGGGGLDKPPPPKFFFKKNGLF FFYPPLKKKNFFPRELLWGPFFFIKT PPPYFFFFFFFFFFFPPFFFFVMS FFFFFFFFFFFVMS
8942	22843	A	9008	1	87	KMLKKPKFELGKLMELHGGSSSGKATG D
8943	22844	A	9009	420	3	RFYFPKPRKGGGVFFPPPKKFFFL NPPPPPPPPPKKKNIFPPPRKGGGS KVQTMGPPLFFPPPPPPFLFFFFF FFFFFFFFFFFFFFFFFLRETSSNNV LAYQIENSLKLDLQRFCLPLGRV
8944	22845	A	9010	2	74	LHRLGGPEAGLGEYLFERLTCLKD
8945	22846	A	9011	33	132	IDPRCRNSARAPLSLAGPHPGMGDASNH MGQM
8946	22847	A	9012	83	607	RRSGTPCGYNVTSQNGTIYSPGFPDEYP ILKDCIWLITVPPGHGVYINFTLLQTEA VNDYIAVWDGPDQNSPQLGVFSGNTALE TAYSSTNQVLLKFHSDFSNGGFFVLNFH AFQLKKCQPPPAVPQAEMLTEDDDFEIA ITGEGKPTRMPQSRKKSCHIIISVLISAK LNRAFL
8947	22848	A	9013	483	364	PPPPPPFLNPAPGIFPPPLGGIGARFP PPSFFFFFFFFF
8948	22849	A	9014	74	180	LLSTYVGRLSARPKLKAFLASPEYVNL INGNGKQ
8949	22850	A	9015	488	317	HVGQAGLVLLTSGDPPTSASQSTGITGV SHRAQPLRSFSFVLSLLQKRIVLC
8950	22851	A	9016	149	13	DERGGLOAVAHTCNFSTLGGRGWITRL GDGDHPSCRILAGDASQ
8951	22852	A	9017	20	107	FDSTADSDQVNFIQGLASKWDYKNEWK K
8952	22853	A	9018	448	239	VDHQQVIWNRERISNSQNGIVKEIKGAD TFIFGHTPAVKPLKFNQMYIDTGAFC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GNLTLIQVQGEA
8953	22854	A	9019	3	209	CPPLSPGCTNSARAEPVHALPDALNNL RTHGSGDGPSSSVDDWNRFPEDVYPQGIY VISAPSIYAREA
8954	22855	A	9020	504	20	NYAQMSYSTARASANESWAYFMGRRKPV ASRQASQMFLCWLEEIVRRVVTLP SKA RFSFQEARSAWGNCDWIGSGRMAIDGLK EVQBAVMLIEAGLSTYEKECAKRGDDYQ EIFAQVRETMBERRAAGLKPPAWAAAAF ESGLRQSTEEKSDSRPAAGS
8955	22856	A	9021	3	168	LPRLAAARIRHEERERERERERERE RERERERERERERERAPPPTLCET
8956	22857	A	9022	2	89	LCSLVYLLTFPPLSLCDEPAKSPSARNTQ E
8957	22858	A	9023	508	371	FFCRDKVLATLPRLLANAWPQVIFLPQP PKVLRQLQPCITPSLKDL
8958	22859	A	9024	2	170	RTHSAGRPYQCNCCEKAFRHSLSLTVHK RTHVGRETIRNGSLPLSMHPYCGPLAN
8959	22860	A	9025	3	185	PPAATPQGPSPINSPPTKKAKNKNRTK KTKKKKKPPPSKKKGPKQTPKKTMGGPL KTT
8960	22861	A	9026	104	319	LVFLSKYTPPLLVSILWIGLSLSLFLPS LPSFLPSLLTYLLPSFLPSFLTSTVINPL PSLFFLVFKLSQFWT
8961	22862	A	9027	476	364	SLKRLTSGDLPASASQSAVITGVSHRAR PIIYFKYVQ
8962	22863	A	9028	36	154	FLVGQAGLKLLTSGDLPASGSQSARITA VSHRTWRTHYF
8963	22864	A	9029	2043	1237	WLRTRVAPALPERLGACTQLGVPVLPSCQ PYVVCRCQCEYRRQAAQPPHCPAPEGEP GAPQALGDAPSTSVSLTTAVQDYVCP LQ GSHALCTCCFQPMFDRRAERQDPRVAP QQCAVCLQFPFCHLYWGCTRTGCGCLAP FCELNLGDKCLDGVLNNSYESDILKNY LATRGLTWKMLTESLMALQRGVFLLSLSD YRVTDGTVLCYCCGLRSFRELTYQYRON IPASELPVAVTSRPDCYWGRCRTQVKA HHAMKFNHICEQTRFKN
8964	22865	A	9030	15	389	IVDHYPCGGIPTSGSVTQAGA QWHNLGP LQPRPLGLEGSCLSLICSWGHRHAPPH LARGHFSSEVEQLRSRLQHGAVFVKQRK GTPEDPRQGLRTLISSCILHLVALALWF SLPFHGPRIMQ
8965	22866	A	9031	3	243	RHSLAFNRFSCLSLPSNWDCHRPSPCPA KFCTFVMEFHVGOAGLELLTSGDLPT LASQSAGITGVSHHAWTRCCCCF
8966	22867	A	9032	1	245	PTRFAGIAICMCMKNHRATRVGILRT THINTVSSYPGPPPYGHDHMEYCADLP PPYSPTPQGPQRSPPPPYPGNARK
8967	22868	A	9033	46	124	QELMTHGAKSPDGT RVHNAFLPVTTV
8968	22869	A	9034	235	435	KKKKKKKKKKKKKKRRRPFKLKGFKFP LKPGGGLFEAPPFGGPPPPGFFFAGGGA PPRGFFKICKGK
8969	22870	A	9035	333	70	CPIYQIPILKDQVNLSSISSPFSHLYKD LWKTLFISYITELIFVCFVEMMFHHVAQ AGLELLGSSNPPTSTFQ SARITGISHA CLNI
8970	22871	A	9036	297	411	NKTM SFAATWMQLEVILSKLMQEQKTKY

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						CMSSLISGS
8971	22872	A	9037	461	167	NKNYPLLGGFPFGSPSPENINGGFPLTP GGGGPINPNSPPPPPPGRRPPLKKKK KKKKEKETNTYILQDTCRCSAVLPIMQ VKIVMICLIMHRLF
8972	22873	A	9038	466	292	NGCLLEPASWNSLANIFIFCREEGLTML PRPQVILPPLPPKVLRLLEPPPLSS
8973	22874	A	9039	34	124	GIRNIKFSLSLTFIAHKKYCYCSHAABH VK
8974	22875	A	9040	54	239	RRRRKLRRWGLAMLPRLVNSNWHQAILW PPKVLRLQACATTPLTRRWLHGQIWSF GAGSV
8975	22876	A	9041	469	223	PWARVVCVCVSVVCVCACVRVCARASES QTCAAVPSLGPAGAGRPALGCCAVCEDE VGSCPHARPLPRAAVDKAAGRRLCF
8976	22877	A	9042	491	380	SPGVVAHSYNPSTLDGRGSHITRVRKFM TCLATEGAV
8977	22878	A	9043	144	360	IHSWGWYLDVSLIAAHLAINPDCFMVY YIFSQCTDKLTEKEFIEGTLANKETLRL IQFEPQKVKEKMKNA
8978	22879	A	9044	23	263	RWNSDGKGSRLPAAWATWDPVSIKNTON THITHPTPHSPHTPHGQQPFLSPTFFFW PVSSSPSPFPFSHTCLSCLLPPGA
8979	22880	A	9045	461	287	PPSLANIYLFYLYFGRDGVSLPRLVS NCWAQAILLPWLPKVLGLQGEPPNLALK SL
8980	22881	A	9046	485	6	NNKNSWAWWRVPVLPATREAGAGESLES GRRRLR
8981	22882	A	9047	475	307	LFLRDGSLTVLPRLVSNWFOAILLPWL LKGLGLQARATLHMACSSCINSTONILQ
8982	22883	A	9048	483	338	LREGERQREQERERERERERDRERAH TTAFTQLLFQYVAIILLPCY
8983	22884	A	9049	680	303	NDLLFGSLYVKQFAASGTGRVTLPEPSE EQVCLRCFQDLFGDDHNKNGFKMFDSS NYHGQDLLFKDATVRAVPVGEKTTYRGW LGLDYVAALEGMSSQCSGAGRTGPPCR LPWCYSDPFTPEP
8984	22885	A	9050	26	165	AFGYHRVGQAGLELLTSGDPPASASQSA GITGVSHHARSQYFFVYV
8985	22886	A	9051	461	83	HKINLP SHKKKKKKKKKKKKKKKKKKK K
8986	22887	A	9052	475	209	MAAPPKKKKKKKKKKKKKKKKKKKI
8987	22888	A	9053	531	404	SVTQAAWQWQHNSLQGSTLEFKQSSLL SLPTIWDYKHADLS
8988	22889	A	9054	66	416	KKKTNKIKMGGGLPFFKISPPFLKKTLS WKKGAPKTPPLEMAFFFPQGGKNSPF KGGKIFFFFPKKTFIKGPPGGEHTPPL GGGPQIFSLPPPQGVQKPNPPPLRGGL FFTI
8989	22890	A	9055	1	104	ILAVNGETLEGVTHEQAVAILKHQRGT TLTVLS
8990	22891	A	9056	3	106	LKRWGIAMLTGLVLNSWAQVILESWPPE VLGLQV
8991	22892	A	9057	1	299	PTRPINIIAFTISLLGILVYRSHLISS LLCLEGIILSLFIATRIYPIAPPLPPL EPEKKKKKKKKKKKKKKKKKKKNTKK RKIKAKRKNLGGGGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
8992	22893	A	9058	482	146	LTSSKKKKKKKKKKKKKKKKKK
8993	22894	A	9059	2	290	YFLFAYTILRSVPNKLGGVLALLLSILK KKKRGPPFKRTLGGPKFNRRGGQGNIFFL MGGGLKPNLGLILGRNLSLGGGKNWPNLP PKIKGFRENKNF
8994	22895	A	9060	413	48	PQKKGFFQKNPKGFLKPPPKKKKKKPP PGKIWPPQKIFKKPPPPPPPPPPPPPP PKPPPPPPPPPPPPPPPPPPPPPPPPPP LRSLDVCHLLPITPQVPGPTPVLLFST LPDCNHSLL
8995	22896	A	9061	2	274	FTISLGLILVYRSHLISLLCLEGIIIS LEIIATLITLNTSHLLANIVPIAILVFA ACEAAVGLALLVKKKKKKGRPFKRILGG PQINPG
8996	22897	A	9062	42	255	QEFRTRRRERERERERERERESSGVVR AKFRSNFSAGAIHTIRVMLPPSGIYSN EKSINKCGFALLFF
8997	22898	A	9063	20	413	YALRNSARAGDPHGQLGRRDGA VGGRGW LMPREALHPWWANVQAWAGSPGLEFGAP WPQGGVWLPWL CVSMSASSSSINGLPPQ KKKKKKKKKKKKKKKKKFWGGGPGQSPF WGGLKKFGGRFLKRGGEN
8998	22899	A	9064	6	306	ECEHSTTYSHFAGGGGPMVGGDADARS KALLGVCVSGSTEAYVLVLDPHYWGTPK SPSELQAAGWVGWQEVSAAFDPNSFYNL CLTSLSSQQQRTLD
8999	22900	A	9065	463	126	AHYQLVYTCKVCGTRSSKRISKLAYHQG VVIVTCPGCQNHIIADNLGWFSDLNGK RNIEILTARGEQVHRVAGEGALELVLE AAGAPTSTAAPAGEDEGPPSPGKTEPS
9000	22901	A	9066	23	244	SCHAGIRHEERERERERERERERERE REREREIYFLALFSQKGRVHGFFKTPRG GQKRELLSNRVNTLCTE
9001	22902	A	9068	396	143	KDIONFGQAWWLTVPVIALWEAEAGGSR GQEITILVMVPHLSVLLAKNSSSHC PMCWLAEQWYDLCSEFQKIFFGIILIPG
9002	22903	A	9069	828	99	VDREPVDREPVVCHPDLEERLQAWPAEL PDEFFELTVDDVRRRLAQLKSERKRLLE APLVTKAFREAQIKEKLERYPKVALRVL FPDRYVLQGFRRPSETVGDLDLDFVRSHL GNPELSFYLFITPPKTVLDDHTQTLEFG EPLPGRSGCNLGAEPAGVYLEPGLLEH AISPSAADVLVARYMSRAAGSPSPLPAP DPAPKSEPAAEAGALVPPEPIPGTAQPV KRSLGKVPKWLKLPASKR
9003	22904	A	9070	20	427	DGTRRRERERERERERERERERERLVTEDT LHSLSLEGARSGASVCVQSVYPTGASAP HSIINGHKKRVLVLVETETHTFPLAEKDR AFLGDTSVFVGAAPVGGANTGASAGGAP PSRGEPEESGESHEDEMGFLFV
9004	22905	A	9071	297	126	CSIYDKRIPTFGLGEGVSEQRLLTLLP CLPPALTETPTSSDWQSTDTATPTLINS
9005	22906	A	9072	117	286	VVLRGSEKMFQVQEQINEQVLCILIKGI FLVKKKKKKKKKKKKKKKKKKPRPEYIK
9006	22907	A	9073	3	302	PPMETLRQWTTIVHSQEEEEHFEVTKD EVKVVARKHGQPGTPVAIATQLPPTSA APPAQQQLQPLAPTTVLSVSADWNALL QRPNKYIWGLQYLEM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9007	22908	A	9074	437	79	NQKREEEERKRRRRRRRRRRRRKKK KILRQKKKKRRKAGSREKKKILRLPEK NKRSKKHYELINALSRLQDTRLIYQKM FYILAKNNWKIKLKIQVHLQALENKVPR HKWETYA
9008	22909	A	9075	51	185	CRADFMFFHDKIIVYLCSLVYLLTFPPL LSYDPAKSPSARNTQE
9009	22910	A	9076	452	310	QFSRCHLSLSLDRKGNLTPCTSWVRR CLALLRLTLGALHLLSDNPQ
9010	22911	A	9077	438	326	LIHCWWDCKLVQPLWKSVMRFLRDLELE IPFDPTLHF
9011	22912	A	9078	37	169	GIPGFRHAGQRRQLLLITGDLPTSASHS AGITGTSRARPPSTF
9012	22913	A	9079	1	408	RKGRLSKEETERMVQEAKEYKADEVQR ERVSANNALESYAFNMKSAVEDEGLK ISEADKKKVLDKCQEVISWLDANTLAEK DEFEHKRKELEQVCNPIISGLYQAGGP GPGGFGAOGFKGSGSGPTIEVD
9013	22914	A	9080	31	168	VRRNPRLEHTVTTTAYCSLELLGSSNLP ASASQVARTTGLQLNLQ
9014	22915	A	9081	460	319	YFFVEMGSHYIAWAVLELLGSSNPPASA SQSAEFTDAHKPTDCRPLR
9015	22916	A	9082	465	326	PCVAEFTCTHTHTHTHTHTFKCVGSHL HTNND
9016	22917	A	9083	33	269	PGNSRPISSVRGIHPPCLANFCFLNVFV EMGSHYVVLGAILGSSDLSALAVQSGR VTGMSHCANPEIFFLENNIIL
9017	22918	A	9084	47	300	DLITSLFLKQSSSLATMNIQTFFKNITYF DLIIKTLFLRFFIFCFIYFFFSYGG FFSFFFFFLKGSSFLPRLNGGAKIWN
9018	22919	A	9085	437	220	NIAKSLSLSLSLSLCVMCVCVSACVC MCLSLSLSPSSLSHSLFPFSTPNMDIS HLPILSTQENMLLLQ
9019	22920	A	9086	227	23	DCPKANILGLTPRLVSNWPQVILTPWP PKGQSLLCRQGEGRDIWTWHPWLLHPP PQAREPPRTHFH
9020	22921	A	9087	206	326	PHWAQWPTPVIPALWEAEAGKSQGEFE TSLANTVKPRLY
9021	22922	A	9088	364	123	SRVVLPLKAPGEDTSLPLPASGGSRCSL AWGSIPPIASIPWPSVLCPCBIFFLL FLLYGDCNLGPTLIPDDLIMRSLP
9022	22923	A	9089	373	205	MPPRLANFCYPSRDWVSPYWSGWSQTPC WDYRREPPFPFCVTSYSVQYCACIAGL
9023	22924	A	9090	283	2	REFSFSAVVLAFKIFWKLFSPFPWRVRP EDWFI PGCGPNBNFPFPCPGVGKKE PRFKKKKKNFISSQAQWLMFVPAFWE AKAGGSLEP
9024	22925	A	9091	16	261	CPEDLLVGQNVKVEDSDMGDPDRRPMCM FACFYLLVYRRLAMLPRLYLNSAQVI LLPQPPASLELLQAHATTHPALCLSF
9025	22926	A	9092	17	109	RQGLAMLPRLISNSWTQANLLPWPKEL GL
9026	22927	A	9093	282	114	KKGKGLLVFLKTRKPFFFFLRQGLA MLLRVLNSWAQAILLPWPVKVLGLOA
9027	22928	A	9094	205	337	NANLHGRMQRLTPCLPEIWEAETGGSGG QEIETILANMVKPCLY
9028	22929	A	9095	62	287	EHSKALFCFAFESGFPYSAQAGVQWHD HSLQSQTPGLKQSSCLSPASAGFYKE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SPSFYKDKSCHHLGKHSGA
9029	22930	A	9096	170	9	AASTGYCIGRFCTKLKIQSGGQVRWLSP VVPKREAEVGGLLLEARSSRP I WATW
9030	22931	A	9097	2	104	RRPGGRAEPRARVRGDRDPVLLRHYPH IFEECG
9031	22932	A	9098	350	142	LCLSCPKGGGYRAMAPWRNFCSEFGKNG GFPMLGRVVLKWPQMGPPLPQPPKRVGFQ GLSPPPGPPFFLV
9032	22933	A	9099	494	342	YFFYFVEMVSHHVQTQAGLELLASSNPP ALISQHAVITSGSHHTQPKLYF
9033	22934	A	9100	30	232	GGIMLCHGRACFPFAFCHDCKFPKVFO PCFLYSLQNCSEFLYKIPSLRSCRLQLAE LLSIYLENPL
9034	22935	A	9101	26	171	RNSRRLRHKNRLSLGGGGCSEPRSCQCT PAWQTARLSLKNKKQKKK
9035	22936	A	9102	486	239	HHTCPHQVCVCVCVCVYRVCVCVCVCVY IYMYMCIYIYIYIYIYICIRERERERE REMFHVAQAGLELLGSRDLAPAS
9036	22937	A	9103	487	344	TGFHHVQAGIELLTSSDLPASASQSAR ITGVSHHAQPLFMIFCAK
9037	22938	A	9104	470	221	TPGLKRYTCLSLPKCWDYRCEPHARQGA FLCAFSPLSQQPWPGRPHFHSYETNK VERGKRLPLRSPSTEQGFDFRCVLFQT
9038	22939	A	9105	468	259	YVFFCRDGGTLTISRRLVNLSCPQQSPCL SLPKCWDYRHEPPCPSCCSNLLMFHFT NVFLIDSECSHFT
9039	22940	A	9106	466	329	RVAGTTGTHHAWLINIPSVETGFHHVG PQVIQPPRPKALGLOA
9040	22941	A	9107	409	306	AGFELLASSDLPASASQSAEITGVSHHA RPSLIF
9041	22942	A	9108	417	269	MVVAQADMESSEKPEGLFNVIINDSLVQ AYPELKEALYEEIKKAQRGA
9042	22943	A	9109	533	399	RGSLRHETRLNAEARRCSELNSRQCTPA WATERDAVSKKTKQA
9043	22944	A	9110	16	239	LVHFEVRWNSHEVSLTADSRKSHLIFPQ PNYADTLINQESYEKSEPLITQDLLET KGEPRQLQVSFFPPKREE
9044	22945	A	9111	68	219	EPPLHLANFLQRLVFTMLLTILNSWPGV ILPPGPPTVLGLQDKLPVLLPS
9045	22946	A	9112	192	57	DRVPLCPPDWSAVARSWLTAAVSQVKG ILSPQTECAPPGNST
9046	22947	A	9113	21	201	TIVSVVEFMNLGGGTCGEPRWCHCTPDW GTERDSVSGEKKEDKDVARRHWVGSFYN GPQ
9047	22948	A	9114	2	144	TFTIDRCADLFVAKQVGTKLSVNEPLS FSVESILKRPSSAITRVSQ
9048	22949	A	9115	156	316	MILNKKKKKKKKKKKKKKKKKKKKKKKK KGGGPFKKTLGGAKITPGWKNYFFFFMG GV
9049	22950	A	9116	1	84	TKPTPFLPTLITLTLLLPISPFILYIL
9050	22951	A	9117	1	176	HLNLGGGVCSEPRSCHCTPVWATEILSQ KKKKNGFKFWEPRPQKEGGGGRKKPPG VP
9051	22952	A	9118	1	184	AAAGYPGQQNFHSVREMFESQRIGLNN SPVNGNSSCQMAFPSSQSLYRTSGAFVY DCSKF
9052	22953	A	9119	69	374	IIFSXXXXXXXXXXXXXXXXXKGGPPKRP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WGGPKIFVLRRVLSFFPIRGEKNTFGDP LKKTFWGGGKLGKPPPKKKTTPWGKKI FKGBRGKKPPFLGGKKK
9053	22954	A	9120	405	93	EFSPLLLTTNQKRGFFPPSPPKIFFFPK RIYFLGGGGPHPPPQKRGFPQKNQKGF FFSPPKKKYNLPPPGKFCPPQGFFPPP PPLFFFSFFPPFFFRCCQIK
9054	22955	A	9121	2	380	WDYRCPPPHPTNFCIFSGDGVSPHWPGW SWPQVICLPQPPKVLTPWVRDRTRDLE GGDLWYGACLGACLHLGQAASFHGHIL GPASLLCCIPKHVMDTILSPGVKLQSCD TGVALRVGEKREGS
9055	22956	A	9122	2	534	DMIREQKIYHKYLAQRREERKAQKEFPD RILEBDKAKKLAEKDKELRLEKARRQL VDEVMTCKRLQVQEKLOREAKEQEERAM EQKHINESLKELNCEEKENFARRORLAQ EYRKQLQMQLAYQQSQEABKEEKRRFP EAGVAANKMCLDKVQEVLSHQLVLAQNI HPMPQGMQ
9056	22957	A	9123	389	46	GPNFLPPPIFGFFSPFSLKFFSPKTL IFLGGFFPIFPPPKKSFFPKNSPGVFFC PPFKKKNFLPSPLNFAFPRVFFKPPPP FFFFFFFFFFFNFYRLYFIWVNLAKV VW
9057	22958	A	9124	422	59	AQKKKKKKKKKKKKKKKKKKKKKKKKK K
9058	22959	A	9125	333	168	KGPPCIVCMVEFHKLEAGSHSVAQAGA QWCDGNLLQTLTLGLKRSFHSLSR
9059	22960	A	9126	175	89	KPPPHFFFFFFFYYYYFFFFFIFC
9060	22961	A	9127	368	250	CFNYLSRDRGLPLLPGVLKSWPQAILL PQPPKMVGVOG
9061	22962	A	9128	392	157	FFSEKRLNFGGGGPKMPPPKKVSPQK PHPGFFSPQKKKKKFFPPVKMGPPKS FLKSPPPFFFLISSIRGLFL
9062	22963	A	9129	396	13	PPPPPPPIFFSPRRFFRGGGSVALSP PKVFFLLNPPPVFFFSPPFKETSFP PPFFCPPPQILFLAPPYFFFFFLLF VFFFLFFFLPLLFLGKTSFLLLLFLF IYLETGSCSVAWARVQ
9063	22964	A	9130	55	180	LLYNKLIPTLKKKKKKKKKKKKKKKKK KKKKKEKYEKTRAY
9064	22965	A	9131	2	95	SFVHMEHEKAVLLLSFQNTVDLGIQR LTV
9065	22966	A	9132	172	404	KKKKKKKKKKKKKKKKKKKKKKWGGGF FKNSWGGPKKRGKKIFFFSLGGKKKT LGVFLEKPLFLGGRKMAPPFP
9066	22967	A	9133	1	125	QPVSYPTTIIGQVAYELYFTTILILIPT MSLIENKILKWAY
9067	22968	A	9134	1	120	QPVSYPTTIIGQVASVLYFTTILILIPT ISLIENKILKWA
9068	22969	A	9135	7	269	IATGQPRQLKLTLDPTLLKRLTLTKK KKKKKKKKKKKKKKKKKKKKWGGGHK KKPPGGPKTPVKKKIFFFRGKIKKPP WGI
9069	22970	A	9136	1	64	LVSISNTYGLDYVHNLNLQ
9070	22971	A	9137	400	259	SQPLRLRLRHKNILNPGGGHYSELGSC HCTPAWDTEQDSIHWSLLSSV
9071	22972	A	9138	3	310	ECFFNSPNMNGHCNLLVQSTSPSISTMP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CPKYVALEKVFLLNVLWFFYLKYRDNRP GSVAHTCNPSTLGGRGGWITGAQEFETS LGNIARPSLIKRRKKYKLF
9072	22973	A	9139	34	142	NCKKLNTHTHTLTHSHTHMLTHSDTFTHTHTTKYK
9073	22974	A	9140	146	2	PPPPPPPEGVSLCGPGWSAVARFRLTASS ASRVHAILPPQPPQQLPTRP
9074	22975	A	9141	3	102	PPASASQSAGVTGMSHHAQPIEPLRCSS HRTT
9075	22976	A	9142	245	51	NREGDLLCCPRWSQTFGLKQSCLGPPKC WEYRRGPPHLYAIMSMRKNLIQIMFYF NNPCLLYS
9076	22977	A	9143	2	108	GAKCVSDRIKHAFLIKBQKIIVKVLKAQ AGSQKAK
9077	22978	A	9144	3	200	MGFLHVGQAGLKLPTSGDLPASASQSAG ITGVSHRAWPVSGFFCSEAKECFWEEQL INLDKNSQK
9078	22979	A	9145	405	227	WFFLGFPPLKGLGPPKMFFRAPRVYSPF FPPFFFWPPPPRIIFPPGFKFVFLAG PIW
9079	22980	A	9146	387	220	PLFFVGCFFFFFFFFFYFFFFFFFFF FFFFFFFFFLLGGCERNFIIRKNINN
9080	22981	A	9147	539	220	VINFKHILIKTVIQSLFFFERGSCLEPPR LECNMIMAHCSLNLGSSHPASASQV AGTTGAYQHTQLIFIPFAETGSCYVAQA GLQLLGSSNPPWPPEVLGLQV
9081	22982	A	9148	3	141	GGGGCCPRWSHYTPAWATSAKLCLKKK KKRFLKESCLTPLLKA
9082	22983	A	9149	413	240	FIFCRDGLTMLPGLTNTWSQVILPPQ PPKVLGLQAYHADELPHLATWGVLYGLT V
9083	22984	A	9150	395	193	LLFGPCLLNLITQFVLSCHLLDIKLQMTL SEGYPFLNIQESPFYRAPLDDPSVRHAR GEILPISLPGG
9084	22985	A	9151	1	77	LVAATVLGGTGWGFKNIRRGSSGA
9085	22986	A	9152	365	181	IVDRPDPDRDADAQREVFTLSARYFKIW VPPGDPAREPFFIQSAPVMLLAAPDELV SAQLA
9086	22987	A	9153	373	251	FKKIFFCRDRALNMSPLVNSRTOAIL PPQPLKVLRLQA
9087	22988	A	9154	204	95	DYHWSQPGMVAHACNPSTLRGRGRWITR SGDRDEPG
9088	22989	A	9155	44	280	AELFGTLMREDGLSLGGGCKEPKSCHC NPAWATEPDCLRKKRKESPYLLVVTTPD SSYSPPFFLLLPAPDNNDYFLS
9089	22990	A	9156	2	117	ERLRHENCNLKGRGCSEPGWCHCTPAW ETKQDSISK
9090	22991	A	9157	3	207	HASAHASADAWDYRRVPCEANFCILYV SHVGKAGLNLTTSSDLPTSASQSAGITG VSHHARTPTTV
9091	22992	A	9158	117	267	NRVLLCCPDWPTPGLKGSSLSLSSWD YRHIPRLAARSSYLGPGFYH
9092	22993	A	9159	415	167	LLLLPIKNXFFFSPPLEFFFFFPFPPX XXFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFLELKQNF
9093	22994	A	9160	217	41	SSQIHRDRNRMVRQGAHAACNPSTFGG KGEQITRAQEFKTSLANMVKPRLYKPC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LY
9094	22995	A	9161	341	164	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFVCF VSVELKKWQYNSFDVRIILRVEP
9095	22996	A	9162	190	402	IHTGKHPKCYRNSYSVLFLASKKKKKKK KKKKKKKGGGPKKKKNLNRGGGEIIFFF WGPKKI FGGGGLKKG
9096	22997	A	9163	108	209	LSVKRCAPKPKKGVAPGIKEIRTRSHQ DSEDI
9097	22998	A	9164	2	145	KHCGRPRPQGPLPRKTRDLCSLVYLLTF PELLSYDPAKSPSARNTQE
9098	22999	A	9165	170	402	ISRCHFPSSLISYVKITKTIKAPKRSKK KKKKKKKKKKKKKKKKWGGGPFKKKNF LGGGGGEIIFFLGAPKKKRGQ
9099	23000	A	9166	399	113	WRLRWEDCLSLGGRGCSEPGSCYCTPMW VTEQDQSSGYEGFQRPSSLSKARIPSWA AERSMCQPACVCNLSVEHLSLYSCLLAQ QGKALYKLLNK
9100	23001	A	9167	3	138	SWITGVCHYAWLIFAFLVETGFHRVGOA DLELVTSGDATTILSH
9101	23002	A	9168	134	301	EKLTQSHSVTQAGVQRLNVHSLRPFPPR FKRFSCSLPSSWDYRNLETVLQETH
9102	23003	A	9169	201	1	GATILRFKTKKKNVFFKKKKKKKKKKK GKGWGSTESRWNLSEGGSSGLRRRRLQA PAGPQEFKLA
9103	23004	A	9170	2	191	FVPQPLPLGFKRFSCSLLSQWDYRCTP PHLANFCGFFFLKFFFFFKKKNFFSPR GRGGALI
9104	23005	A	9171	2	191	GGTESCFVAQAQVQCDLGSLSQSPPTGF SETASQTVDPDKVDPGKLRTMFVAELP KTIVTDS
9105	23006	A	9172	3	143	SWFLYVQAGLELLTSGDPPALASHSAG ITGVSHRRLQTGIFRAV
9106	23007	A	9173	361	174	VLGIILSMSETEIFNTKCLDQSGTVAHT YNPSTLGGQGRVIRAEFETSLGNTGR PHLFKI
9107	23008	A	9174	493	351	LVETGFNVHVGQAGLELLTSSDPPASASQ SAGITGVSHLALVLSRKSC
9108	23009	A	9175	1	115	FRKIWIYITMEYCIKAVKKKEMLSFTITW MNLEDFMLVR
9109	23010	A	9176	286	96	PLFFFNWGLAICLGSVAIHRRDHSA LQSQTPLKRSSCLSLSSWDYRRVPPC LANESHY
9110	23011	A	9177	399	237	RNTKWLFFLRRSLTSTGLECSGAISAH CNLRLEPGSSDSLNGIFKDLALLDM
9111	23012	A	9178	427	101	GRTGRQGRGAPHISHDGRPRGRDAPRFPD VMAAGKRRSSLPRWDGGRAETLLTFQTG QPGRGAPHIPDDGRPGGDAFHPDGVVA GQRLQSQHFGRPRQAAGRRL
9112	23013	A	9179	193	41	IVFLFIYLCFFVGTGPCYVAQAGLKL VSSGPLASAPQHVGITGMSHHT
9113	23014	A	9180	292	119	KITKINKQILNLSYTLDDQMDLTIDICRIF HPTATEYRFFSRAHGTFFRSCTKNSAWH I
9114	23015	A	9181	3	279	ALSPFYSSECKLGSFNRELSSPSPGGQ KSEIKVSAGPRPLPRVQGDPSPLPASG GPRCSWACGQITAVSASGVTHSPPLH VCCVCLI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9115	23016	A	9182	402	238	QMQRHNLWPLQSLPPEVTPFLCFLNLPNN WGYRWPPPPPTNFFFLKGVSLGRPGSV
9116	23017	A	9183	3	207	EFHHVGDQGLELLTSGDPPASASESAGI TGVSHRAQQACRFLHFFEGTCFLSQELS YLKLGRDTIIC
9117	23018	A	9184	3	106	YPHYVKSIVASTFTIISLFPTTIFMCLDQ EVIISN
9118	23019	A	9185	110	248	GVLVGSPLRTRFHSQQAEGABEIGVVT VVMGDGVLPVCVLEVDV
9119	23020	A	9186	925	1132	KCPSAWAAHPTSEIRISQGGSOAAVVLV LFFLLKNPGDVI PALWEARAGGSQQQF ETS LANMAKPRLY
9120	23021	A	9187	399	292	ASQVAGTTGAHHHARLIFFVFLVETGFH HVSQDENF
9121	23022	A	9188	7	82	PCDPPASVQSAGITGVSHHAWQIF
9122	23023	A	9189	1	117	LPISLPSFLPSFLPSLLPSFLPSFLPF FFPSSVTPYLK
9123	23024	A	9190	238	46	NKAFRIKAFVSPSNKKFSSFFFLNEMK SHYVDQAGLELLSSGNPSILASQNAKIT GVSHHVRP
9124	23025	A	9191	2	282	LIFYFVDNMLVRAGLELLSSSDLPALAP KVLRFVTGVSHHTRPETYQRLLAGPTLL INSQAAGTNFP IGLSRIKPTQSGHGMLQ EVWGTSGLR
9125	23026	A	9192	44	136	CLCVCVCVCVCVCVCKQTL MCCFLENF DV
9126	23027	A	9193	469	347	PCPANFVFLVETGFLHVGHAGLKLISG DLPNSDQKFYVN
9127	23028	A	9194	427	238	PPARPTAPPYIEFFVEMVFRYPGKAGLK VLISGDL CASASPGVITGVSHHAQPK
9128	23029	A	9195	34	178	SLVHVVEFERGRAEWLTPVIPALWEAEA GGSRGQEMETILANTDFWTG
9129	23030	A	9196	22	338	CGPYSMWWSIKRERKEGKKRKKRRRK EQKERERKERKEREGGREGKERGRREG KKRKKNRKKVGLIGSPCIVFTWQAAYC EESGGVWPGETBHTQEGLVQ
9130	23031	A	9197	3	91	OGLSLGGGGCSEPGSCHCTPAWATERDS I
9131	23032	A	9198	1	203	RTRGNKSIDTTSNFDFFPESDILQPVFN TTEPDYKSKDWVFLNYTYKRFEGLTQRG SIPTYMKAGKL
9132	23033	A	9199	2	144	PTRTMPCCCCCCCCCCCCRCFLMTGVL FTCCHNQFENHSGCLPRQI
9133	23034	A	9200	1	99	YAAKELVHVDYRPTIEMERRRGLNWLVP RLSLE
9134	23035	A	9201	3	149	LNAVORMEWQLKVQELDPAGHKS LCVNE VPSFYVPMVDVNDDFVLLPA
9135	23036	A	9202	284	21	KGPPLFFFFFLRQGLVLRHLEYSGMT TAHCNLELLVSSDPPTLSSQNAETTGVS HCAQPASLILSKPYIGFLHQIQSCLPV TFL
9136	23037	A	9203	1	77	LRLVLNSWRQATILLWPPKVLGLQA
9137	23038	A	9204	529	340	GVLLWRQAEAGELSLGGGGCSELKVRHC TPAWATRAETPSQKINELIKSMAVELTD DFIT
9138	23039	A	9205	413	241	HPPPPELKLFPSCISLISRWCHRRPPCP YVFVLLAETGFHVQAGHKHTYCCVSLP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						T
9139	23040	A	9206	33	152	QLQGLESWMERCALPGYPVVFTNLCKY RSWIBETMRDK
9140	23041	A	9207	70	402	HVDWEALGNDPRLVNLGICKLKASGIHE WVHTRTCAHTHMTHTTCTHCRSPRVV VNLGCTFELPGALKNARAYPHPNATKP MTSESVGIRPTRQVFKAPRAEQHCSTA
9141	23042	A	9208	46	262	GGIPFAAVRGGRSWLRDVLRLAAAGRR RRGTRRRGRGAGGAGGRDRVGSRRREPA AARTAAEGERAVRGKC
9142	23043	A	9209	15	206	PIEPLSERTNSAGAPPPASLPSCSLISD CCASNQRDSVGVGPSEPGSDMQTSLWA KVPVSKD
9143	23044	A	9210	475	110	NLLAPHLVLSLEKXSI RMGVAQFSRCHL SQLPLARKENSLTPCAGVRRCLALLRL MLGGLHPLSCTHCPTGPSEMNLVSQLEM QKSPVFCVAHAGSCRLELFLFGHLPL
9144	23045	A	9211	420	132	PPPPNYFGGAGFPFPPPPFLRPPPPFF LPPKKKKI FPPRGPKKIFFLKAPPPSFF FFFFFFFFFFFFFFFFFFFFFFFFFF LVRSHFILTIM
9145	23046	A	9212	353	87	FFFYKQXFFPSLFFSPPXFSFYDF* YLKYPLPPSFFLFFFTPPPXFFFFF FFFLPPPPPPPPPPPPPPPPPPPP FFFFD
9146	23047	A	9213	2	276	FIQLLKRRLCELGYEVLPHPSYSHDLLP TNYHFFKHLDNFLQKFFHNQQDAESAF QEFASQSMEFYATGINTLISPQKQVD CSVSYFD
9147	23048	A	9214	402	276	LSCLSLPSSWDYRCPPPKPGYFFYFFLF LVKTGFPHLAQAG
9148	23049	A	9215	386	37	GFKKRVCSPPPPPPPPPPPPPPPPPPPP FFLQKKKVTNNPSSNKLTLGLQKKKE IQPALMKKNSISQS
9149	23050	A	9216	1	142	KDFRVQVYNHSSLQPPQPGFKQSSRLS LPKYWDYRHEYLHCQLAP
9150	23051	A	9217	402	181	FFFRXFFFXFFXFFXFFXFFXFFXFFX KKKKXKXKXFFFXFFXFFXFFXFFX FQEKLLFIFYVNIIVTF
9151	23052	A	9218	2	87	SGSLIFGLIYICMVCVCVCVCVCVPC
9152	23053	A	9219	420	271	YYCIPRETGFHHVQAGLELLTSGEPPA SASQSAGITATAPSPFLTLLV
9153	23054	A	9220	139	413	SGYHSKTLFQKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKRGGGAFKKK IFFRGGGNFFFLGPQKNIGGGGLKKR GGGKKPPPPQIFFVVG
9154	23055	A	9221	134	236	LHRWGPAMLPRITLNTWQVILLRPPPK VLELQA
9155	23056	A	9222	364	280	STHLSLPKYWDYRHEPPCLAKKDAQSFS
9156	23057	A	9223	1	147	TLLPMLESSGTIMAHCSLNYLGSSDPST SASQSARITSVSHCTQPPLPF
9157	23058	A	9224	1	208	AGAPPPASLPSCSLISDCCASNQRDSVG VGPSEPGAGYHLVVRRLSQSEKRSIRVG VTRFSSLLSSHA
9158	23059	A	9225	1	145	FQHVQAGPKLLTSGDLPASASQSAGIT VSNRVRPKTKNFYTGNTNPN
9159	23060	A	9226	396	210	KCWDYRHEPPYPALTNLLFIEMGSYGVA RAGLKLGGSSNPPISASQSAGVPLSHH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AQPIF
9160	23061	A	9227	2	154	FHHFGQAGLELLTSSDLPTSASQSABIT GMSHHTQPRMVFFSNFSSTAQC
9161	23062	A	9228	1	238	FFLLALGIFILHATYLSIYLSIHPPSMH PSLSIYLSIYLSIYLSIYLSISLSLSLS IYLSIYLSIYLSIYLSIDFLSSAR
9162	23063	A	9229	3	65	RGDLITEPFLPKLLTKVKGS
9163	23064	A	9230	25	188	YFRTAWNQAWWYVPIVSATWEAEAGGLL EPTSSRLRCAVIAPVNSYCTSTWAVS
9164	23065	A	9231	44	232	YDLKFNNHVVYFLEFETEFHSLSKVECN GAISAHNNLCLCDGARLHRRGGKKTCK QKTLPS
9165	23066	A	9232	3	195	FFVGLGSPYVVTGLELLCSGNPPASAS LNARITGMSHQVQPNTRLSFYLGSSIIY GSIHAMI
9166	23067	A	9233	380	244	SVPLAEMGFHHVGGQASPELLPPVIHSSQ PPKAIGLQARATAPSLH
9167	23068	A	9234	11	101	LLLINTLMFIHLSPIILLSLNPDIIITGF EG
9168	23069	A	9235	411	226	FFFFFATNSQGGPTSFWGPRNNAQVAGP LRNKIFTPVGSPKKIFPSWETPVF
9169	23070	A	9236	404	262	QGLAMLPRVLSNSWTQAILLPWPPNQSA GGSGVSHHTQPIFISENIH
9170	23071	A	9237	369	152	HAFVSVIWRSPHVSNSYMTVTVMYHNL SIPLDPHPFFFRGGGLAMLPRVSNPWP QAILPPQPPKVLGLQA
9171	23072	A	9238	389	190	RPKKKKKFFPPPGGKGVFFKGAPPFYFL NFIFPPPPPPPPPPFFLIYTHNFLIL FLNCDKLYIT
9172	23073	A	9239	330	3	GGMEPPPPPTGAQWGYFGSLQNSPPEF KQFLCLRLPNVLEYKSIPPCPTNFCSFY KNGIFPCWPGWPFKFQKKKISWVWCA LAEAGGSLEPRWRWRLOSAKMAPL
9173	23074	A	9240	122	248	KKKKKRGGLTPVIPPLWEAKGGGRGQK IQTILAGGKAPLY
9174	23075	A	9241	2	286	FFVQTEFHVAQAALQLVSSRDPTTSAS QVSDITGVSHCAQPVIVSCDDQVTLVQR RQVTVTSLIAFCQVAYPKGAKSQWPSF FFSSPFLFSL
9175	23076	A	9242	2	95	HMKKCSSSLAIREMLIKTMRFFFKLI TCY
9176	23077	A	9243	377	293	PLSPRLVLSSWAQMILLPLPPKVLGSQA
9177	23078	A	9244	422	147	KKGGTQGFSPPRVFKRGRNFFFGPPKK KKNPPPPRGKIFFFLKGPSPFFFFF YFFFFFPPFFTHKYFLLDLLLIYHLS KKNYSFF
9178	23079	A	9245	402	208	TIGRCHHTQLNLKFFVEMGSHYVVOAGL KLLDSTNPSSAFQSAGISGVNPPYAWTE IMFLYSIPI
9179	23080	A	9246	314	168	EPYHLHFLPPHHYYYCRWGLIVLPMVLS NSWAQVILLPWPPKVQGLQV
9180	23081	A	9247	3	320	VVOAGLKLSSCDQPASASQSAVITGVN HHARPLIFLYEMDYGSRTVLIIRKWDND EQSNRTIFLKKDBLTGNRSACLKYTPMD INVNSGLGWRYRFGMHQCRW
9181	23082	A	9248	22	303	KGSYFSFTYEAQTESCSARLECRGAIS AHCNLRLLDSSNSPASASRVAEITDHRK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LVPERSCTPKERNVIQKQEESEMSNHLFTWLPILH
9182	23083	A	9249	13	174	LGLKVRHRLWLI FVLSVTEFHHLQAGLELLTSGNPSAGITGVSHCARPTSHS
9183	23084	A	9250	3	141	HVGQTVLRLLTSGDEPTTSASESAGITGVSHRPRQIFISLFTICIR
9184	23085	A	9251	56	262	LRIPLTFGGVVKGEEEDRAVMHLRLCGD DSPMSESLHF I KLPRTVLVDEDAPEKK KKKKKKKKKKKK
9185	23086	A	9252	401	275	PADLFIFIWEDGGLTMSPRLVMSWSQATLQPWTPKVLGLQV
9186	23087	A	9253	411	258	PKVFKYRCDDPRLAWFLFFVQSLPRLGLNSWAQAFLEPPWPRLVGLQA
9187	23088	A	9255	391	167	GLKILTSGDLPASASQSAGNTGMSHCARPLMSFKIRYFLFTIKMKLLLVFPVWSAGVHPHFSCPIVITNKPRI
9188	23089	A	9256	9	255	FFCRYGGLAVLPRLVSNSTQAILSPWPLKVLGLQACTHHFFLMVNSNAARIKTIEMLLEDVNFFVALLCPSFTISHFHL
9189	23090	A	9257	487	42	RYFIFLFYFIFKTETGSYYVAQARLLLGSSNPALAFQ SARITAVSHRAQLTICKYTFLFTHIP
9190	23091	A	9258	1	243	ILSSGGSFISLTAVILITFMIGEAFASKRKVLIVEEPSINLEWLYGCPPTPYHTFEEPQPKKSEIYSKCFFSVFVHFGWG
9191	23092	A	9259	411	2	FFFFSPPVSLSLCVLESSPPPPFFFSPPPKKGGFSPPPFFFSRVPFPVFFFPFPFFFFFPPLKKNFSPPPGKIFFFFFRPPFFFFFLEFFFRPFFFSFFFLRWEVLYFIMCHHISDAYPPNVDNMKE
9192	23093	A	9260	417	219	SVEMGFLHVQASIKLPTSGDPSAGSQSAGITGLSHCARPHSQLSIVCCYSVPVQCLHSLAARY
9193	23094	A	9261	408	172	CPNHFRKWGHRGCPPRVFFVGRDGVYVAQAGLELLDLSNPASASQSNGTGMSHLGQPLLFI LNDVIAVIPLQGSF
9194	23095	A	9262	401	132	HQDNKPAPPGFFFFSPPPKGFFSKPFYFVSRRFPFPFPLNPAPLPYFWGPKKKIFFFPPPAIKFFFFKRAPPLFFFFFFFFFF
9195	23096	A	9263	393	220	LFFLNKIPFFPPGSGKGGDFGPHNTNPPGVKPIFRPHPPPEGGPKGPPRPREFFLGF
9196	23097	A	9264	206	438	FPILKTHFRGLTVAHTYNPTTLGGPGGRNTCSKFKTSLGTWGDPPFHKSENCLGWGVNCGPCFWGAQQKSAWSEGL
9197	23098	A	9265	333	48	ALLAGPTPFFFLGKKKTRFGNRALEFFFFFFLNEVLLCNPGWIMVVAIHRCDHGTLOPPTPGLKRSSCLSLSSSNWYKLPKPLHAGVRFLEFVS
9198	23099	A	9266	3	275	TGFHHIGQAGLKLTLGDPPLSASHSAGITGVSHHAWPMHLESYWRVQYPMPQVLYFWAPSGAQHCAQI IENAIPTLLSRPQEPASEA
9199	23100	A	9267	49	226	HGPEPCMDADAQREGINVSARYPKNWESTVDPAREFTMIYSAPLMLLADPDFASVQLA
9200	23101	A	9268	159	236	PRLVLISWQAILPPWPIKVVGLQA
9201	23102	A	9269	1	208	IFNYCVFSSGVALAYGIYKQDLPALKEK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PRGVVFDVMGHSAYQVSACAFNRGQLKV SIYFFSRRLLVVV
9202	23103	A	9270	1	209	IFNFVCVFSSVALAYGIYKQDLGALEEK PRNVVFDVMGHSAYQVSACAFNRGKLKV SIYFFSRRLLVVV
9203	23104	A	9271	379	263	ESCSVRGLECSGAVPAHCNLCLCLPDS GSFASSSRLC
9204	23105	A	9272	312	3	FRREGLAALQPWWPNKVSSKKRKRKERE RKKERKKERKKEDGATADGISEAE VIRVHPYPVGFGVLSEGDWITEDMRAGR RPHAGESGDTVMLPOAQE
9205	23106	A	9273	405	246	PTKKNKYLHAPPLFHFFFIIPNPFFFF FFFFFFFFCKTGCEPLYFSY
9206	23107	A	9274	2	227	LVTETGRHIAQAGLQLSSSYPPTSASQ SVGITGVSHQPGPSFHFERSLGLKTL LCVKVGVRACFALFQGSS
9207	23108	A	9275	70	304	NLFKASTYPEHLVHLPPPTIVYIRKR LDAMAHACNPGTLDGRGGWIARTPDLC SAYRGLSKCWDRHEPPRFVLV
9208	23109	A	9276	2	260	TVPYHVQAALLELTSGGPPALASESAG ITGVSHAQPLLILVISLPNCQSFI SPYRFSFTQLNHGFNTVLYPLVINISEI FF
9209	23110	A	9277	406	330	PRVLNSWTQTILLPWPPKVLGLDV
9210	23111	A	9278	2	160	ELLTSSDPPASASQSARITGMSHTRLK YIVYRVSRKSKNIPLKHIGIQSFP
9211	23112	A	9279	1	91	GLTVFPRVLVMSWAQMILFPWPKMLGL QV
9212	23113	A	9280	3	107	LGETGFHHVGRAGLELLNKVMHPPWAPR VLGLQA
9213	23114	A	9281	336	234	AHYKLLLIKILKEGQAQWLTPVPIPTLWEA EAGRS
9214	23115	A	9282	3	241	DREPCCWDADAQREGINASARYPKNWVT TGDPAAREFTMIHTAPLMMLADPEIESV QLAQSWFFGAIASLRSPCRKR
9215	23116	A	9283	404	277	IPFVETRSHHIAQAGLELLGSSDPFYFF QVFTMSLSQRALF
9216	23117	A	9284	399	231	HYVAQASLKLLYSGDPPASAFQSAEITAG VSHCTWPTGSLNKIQNNIHRISSM
9217	23118	A	9286	394	231	APFFFFFGGERGFHHVARTVLKLDSSN PPAVVSQSGITDVSHDFLISLYRIY
9218	23119	A	9287	420	311	LNFCRDGLAMLPRVLVNSWAQAVLSPQP PKVMGLHA
9219	23120	A	9288	398	173	LLSFFYLFFYPFFFLFFLFFFFFFF LMFKALLFSCHYFPAMVTFFKFSLSISGV VRTSGYIMLFSYLCCLKTM
9220	23121	A	9289	270	23	TPEQCRCIKLFIYSLILYVRDGVLCCS GWPVVAIHKCDHSTLQHQPISLKAQASCL SLSSWEYRYAPLHLASANFLKVTVV
9221	23122	A	9290	273	46	HLLNMPLFTEIWTERLFLFYILCFVPLV ETGFFYITQAGLKLTTSSDPPAYASQSA EIIGTSECTRICYVNVTNI
9222	23123	A	9291	424	230	CLPFTSHLSLSLSLSLSTHTHTHTHT HTIYNK
9223	23124	A	9292	2	146	NLFLVETRSSHVARASFLLSSSNPPTS ASQSSBITGASHRTWPEVFF
9224	23125	A	9293	393	202	GRERERKRERERERKKERKKERKP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PSGSLTYCVREGITAANLGKRRHKASKT LISHKNKN
9225	23126	A	9294	252	193	GFCCCCCCCCCYCCSDKRHEFG
9226	23127	A	9295	409	269	SQYFGRLLRRVDCLSGGVQDPGQQGETP SLLKYKIYIHISWAGWHV
9227	23128	A	9296	2	213	FCCGLLIHLIYCKTEYSGGSTVAIHRCN HSVLQPTLGFQKQFSLLSWYRYS PLCPAYIFNLSIGY
9228	23129	A	9297	169	408	RFAHRMNSPHEERLPPAPGIRVRPPQP AASLGPPRMAPSISRFRQMTPLYKHND F AGQAQWLMPPVVPALWEAAGGSSE
9229	23130	A	9298	199	51	LHPPPPSLSLSLSTHTHTSHTHTHTH TLWLRPGPAQDVVLVWGNLT
9230	23131	A	9299	1	176	MGSHSLAQARMQWCNQSSLQPPGLKQ PSPPSLPSSWDYRHVPPCLASIFPLKLN YH
9231	23132	A	9300	412	209	MGFHHVGQSGLELLTSGDPPTSASQSAG ITGVSHRNWPHCGFNLVFLMPDDVKHLF MCILAICVSSL
9232	23133	A	9301	195	347	KIKGFRPGATAHAGNPSALGHQGGRTAI AWEFTISMSNMGRCLYRKYKN
9233	23134	A	9302	386	190	GFLFFFFPPPKKEVFPHPFILGFFGFFPP PPFKRAPEFFFWGPKKKNSPPRALN FFFFKGAPP
9234	23135	A	9303	27	173	SFQLWGHKLVPRIRPKRADHLRSGVQDQ PDQHGKTLSSLKKYKISRAN
9235	23136	A	9304	374	121	QWCDHGSQLPQTPGLKQSSCFSLPKRWD YRREPPHPTSLSPYIVAWPCTLCPPPLS ALWKHLIHQKCDGVMVLQVPGRTHNVIL T
9236	23137	A	9305	70	196	PQVIHPGQAGLELLTSGDLPASASKSAG ITGVSHHAQPISHF
9237	23138	A	9306	378	256	QKWVSICCPGWSQTFGLQESSCLGLPKS WDYRRQPQPCLT
9238	23139	A	9307	206	3	PCHLGWSAVVQSWLTAASNSWPHAILPP QPPKVLGLQASLKFLKAGITQVTFSDYN KIINKKEIKRGR
9239	23140	A	9308	338	161	HFKKKIYIYIYVYIHTYIYIYTHIYIT HTYTYIYRYIHIYIHTYIYMYVIYIIPS LPF
9240	23141	A	9309	503	288	FFLNLDKSQEWLMPVIPTLREAEAGGS LEVRSSRPASSDPPTSASQSAGIIGMRH HARPVVLRNGRIQN
9241	23142	A	9310	418	309	FFCKNGISICCLPKLVSNWSPQAILQPQ PPKVQGT
9242	23143	A	9311	442	275	VSPPIGLGGFLSPFPKPPPPFNLKGGP PFPTIPFLIKGKKFCPPPPFFPGLF
9243	23144	A	9312	2	95	HENRLSLGGGCGSELRLCHCTPAWATER DFI
9244	23145	A	9313	318	154	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFF I FILFIYSLLYVVCVGLGS
9245	23146	A	9314	388	199	EQPKCVHRIKQIWHICALEYYAFAKKKK VLPYAVIQIKLEDTMLSEINQSWGKYCM IPLIGGI
9246	23147	A	9315	2	97	STPGLKRSSHISLPKYWDYRRGPPGPAS ILF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9247	23148	A	9316	3	235	TMVNAEGIPIRTLDNSTTVQYACLLH HLTMKAKSTVRDIDPQNDLTFLRIRSKK HEIMVAPDKEYLLIVIQNPCE
9248	23149	A	9317	253	71	LFFFFLFFVDTKFHHLAQDGFQLSSSN SPTSASQSGGITGRSHQAWPYVHLLTLQ KLNY
9249	23150	A	9318	425	95	CLLFCPKKKKKKKKKKKKKKKKKKKK KKKGPIKKKKKQP
9250	23151	A	9319	25	214	VRIDDRPEPCMDADAQREGINSSARYPK NWVTGDPARECGMIHSAPLMLLADPDE FVSVQLA
9251	23152	A	9320	50	231	GHRPEPGRDADAQREGIIASARYPKNWV TTGDPARECTRIQSAPLMLLADPDEFVS VQLA
9252	23153	A	9321	401	226	QWLFNTMIIGHCSLELLGSPNPPIASR LAATTGTRHHAQPSKFRNLKGWLCAKRA RT
9253	23154	A	9322	410	159	LGSLQLPPPGSKRFSRLSLPSSWDYRGC SELRLRHCTPAWVTEQDSVPPKKKKQIF RPFPSYGESLGVLRLHLCFSKPSRRF
9254	23155	A	9323	310	25	KWGLLFFFSPKKRGFFKQVFFCVPVVF FFPPFFKTGPGDIFLGPLKKKIIFPPPG GKKFFFKRGPPPPFFFFFFFFFFF FSEVECCLCR
9255	23156	A	9324	406	289	PGFYHAGQAGLKLTLTSGNPSASASQSAR ITSISQTRPH
9256	23157	A	9325	1	116	LHSVLLPFFYFCVCVCVCVCVCVKHK YVRAGGAPGR
9257	23158	A	9326	2	158	FIFLFTVGLTGTIVLANSSLDIVLHDTY YVVAHFHYVLSIGAVFAIIGGFH
9258	23159	A	9327	3	107	RGCSEPLRHCTPAWVTEGDCVSKKKK VPEAWG
9259	23160	A	9328	257	2	GFFSNISASVIIIPPISRNLFPPFRVY FGPPPKTFKGPPPPFFFFFLSPRLECSG VIMAQCSLTLPGSSDLPLSASCVMATVS I
9260	23161	A	9329	66	384	GNLCGWMKSMAWNPNVVRKADWQIRES LECQPNMGMLKKKKKKKKKKKKKKK KRGGPFLKISWGGPILGGRGKIFFFFPG GGILTPRGVFWKSPFFWGKKK
9261	23162	A	9330	1	98	IIGQVASVLYFTTILILIPTISLIENKI LKWA
9262	23163	A	9331	33	412	NLFVMAETLHTHTQLCCQVKLHLSVPR PSLPLLCCWNFSLVLHEHSQPAEKKKK KKKNKKKKKKKKKRGVFKKKPGAP FCGGGENFFFFFGGLKKPRGVFGKNT FFWGGEKPPPPPY
9263	23164	A	9332	401	311	PTRPVDLLVDDSVKESLIGYGPTEDSKE FS
9264	23165	A	9333	5730	452	TRSAPRAASWLEDPREVRSVCLSATFFT LSLQKPRLLFPSVVLHGVPLSVGVQL QDVPRGQVVKGSVFLRNPSSNNVPCSPK VDFTLSSERDFALLSLQVPLKDAKSCGL HQLLRGPEVQLVAHSPWLKDSLSRTNI QGINLLFSSRRGHLFLQTDQPIYNPGQR VRYRVFALDQKMRPSTDTITVMVENSIG LRVRKKEVMPSSI FODDFVPIPISEPG TWKISARFSDGLBSNSSTQFEVKKYVLP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon- ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						<p>NFEVKITPGKPYILTVPCHLDEMQLDIO ARYIYGKPVQGVAYVRFGLLDEDEGKKT FRGLESQTKLVNGQSHISLSKAEPQDAL EKLNMGITDLQGLRLYVAAAIIEYPGGE MEEAELTSWYFVSSPFSLDLSKTKRHLV PGAPFLQLQALVREMSGSPASGIPVKVSA TVSSPGSVPEVQDIQONTDGGSGQVSIPI IIPQTISELQLSVSAGSPHPAIARLTVA APPSGGPGFLSIERPDSRPRVGDITLNL NLRAVGSGATFSHYYYMILSRGQIVFMN REPRTLTLSVSVFVDHHLAPSIFYFAFY YHGDHPVANSRLVDVQAGACEGKLELSV DGAKQYRNGESVKLHLETDSLALVALGA LDTALYAAGSKSHKPLNMGKVFEAMNSY DLGCGPGGDSALQVFOAGLAFSDGDQ WTLRKRRLSCPKEKTRKRVNVEPKAI NEKLGQYASPTAKRCCQDGVTRLFPMRS CEQRAARVQQLDCREPFSLCCQFAESLR KKSRLDKGQAGLQRALEILQEEDLIDEDD IPVRSFFPENLWRVETVDRFQILTLWL PDSLTTWEIHGLSLSKTKGLCVATPVOL RVFREFHLHLRLPMSVRRFEQLELRPVL YNYLDKNLTVSVHVSPEGLCLAGGGGL AQQVLVPAGSARPVAFSVVPTAAAVSL KVVARGSFEPVGVDAVSKVLQIEKEGAI HREELVYELNPLDHRGRTLEIPGNSDPN MIPDGD FNSYVRVTASDPLDTLGSEGL SPGGVASLLRLPRGCGEQTMIYLAPTLA ASRYLDKTEQWSTLPPETKDHAVDLIQK GYMRIQQFRKADGSYAANLSDSSTWLT AFVLKVLSLAQEQVGGSPKQLQETSNWL LSQQQADGSFQDPCPVLD RSMQGGVLGN DETVALTAFVTIALHHLAVFQDEGARP LKQVREASISKANSFLGEKASAGLLGAH AAAITAYALTTLKAPVDLLGVAHNNLMA MAQETGDNLYWGSVTGSQSNVSPPTPAP RNFSDPMPQAPALWIETAYALLHLLH EGKAEMADQAAAWLTRQGSFQGGFRSTQ DTVIALDALSAWIASHTTEERGLNVT SSTGRNGFKSHALQLNNRQIRGLEEELQ FSLGSKINVKVGGNSKGTCLKVLRITYNL DMKNITTCQDLQIEVTVKGHVEYTMANE DYEDYEYDELPAKDDPDAPLQPVTPQLQ FEGRRNRRRREAPKVVEEQESRVHYTVC IWRNGKVLGSGMAIADVTLTSGFHALRA DLEKLTSLSDRYVSHFETEGPHVLLYFD SVPTSRECVGFPAVQEVFVGLVQPASAT LYDYNNPERRCSVFYGA PSKSRLLATLC SAEVCQCAEGKCPQRRLALERGLQDEDEG YRMKFACYPRVEYGFQVKVLRSDSRAA FRLFETKITQVLHFTKDVKAANQMRNF LVRASCRLRLPEPGKEYLIMGMLDGATY DLEGHPQYLLDSNSWIEEMPSERLCRST RQRAACAQLNDFLQEYGTQGCQV</p>
9265	23166	A	9334	46	324	<p>SKYLPVPVITFQHEI WVGTNIQTISDWVL ICCPGWSAVTQSRLLAAASTSWAQAMSSS SCLGLSSSCYYRHPTPPCLANFVAFVETK LYTMLPGLS</p>

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9266	23167	A	9335	338	178	EVDIAVSHRRKQAFNLCLLKCKPHNNCLNLEGGSSSELKLCYCIPAWATDQSL
9267	23168	A	9336	396	254	KLSTDCTSKEIINRHPTWEKIFANYAPNKGPTSTIHSSCLMFPLYF
9268	23169	A	9337	454	359	SSWDYRHAPPCCPANFVFLVETIFIQGEIGLL
9269	23170	A	9338	540	328	IKKRGAAPRGVLFFFTRKKKFFSYKKSTKERVSLFVAPGCIQGGKKKKPPTKKKKKKKKKKKKKKKK
9270	23171	A	9339	21	209	AEFFPDFKLYYKANQNTYRGQWNRRTETSEITPDIIYLGIQLVSNWPQVILLPWPVKVLGLQA
9271	23172	A	9340	345	2	KIFFFLIYILPFFNFFFFFFFFFFFFFFFFFFFFFLENRWFLMENFIKGRGHVKGPLGQARDHDISGRRWWRREQCRASQLPGVRRSLLQVQAGGFVHIRISGLQDARQGPVAG
9272	23173	A	9341	15	252	LERVIRQSAALTDSEFFNFILLILFIYLF FETGSPCVSQAGLKLGSRDPPVSASQSAARIIGVSHRAQPALTDFFPSISF
9273	23174	A	9342	484	276	RHAPPCQANFFVQTRFCHVAQSGKLIRSRYLFAAFQSVRITCMSHCARPLYFLMFKRLQYLKSPTKS
9274	23175	A	9343	464	326	LVEFGPHHVQAGPELLAPCDPPAPASQSAETTGMSHRARPPANFV
9275	23176	A	9344	486	280	SFSSHSHSCSLPSSWDYRCTSSHLANFPFKRWGFTILPRLIILNSWPQVILLPQSHRH EPLCLETTLKTLNV
9276	23177	A	9345	276	179	DRDFTMLPRLVLNSWPKTILLPLPPKILRLQS
9277	23178	A	9346	45	143	RWNSRQENCLNLGGDCSEPSLCHCPPAWATE
9278	23179	A	9347	229	73	PPPHMIFFFFFFFFLFFYYFFFFFFFFFFFFFFFFFFFSSRLQSVYCSSVLNKNVD
9279	23180	A	9348	391	139	IPSLKRSSHLSLAKCWDYRHKPPCQVTF SFLNVRIYATKFFLSTPLAAWSKYWYLV FLLSFSSKYLTPIISFLTHNVSSSIF
9280	23181	A	9349	53	191	IYVYIYSEVSHAYNSSTLGGQGGRTGAQEFKTSLVNIAKPLLY
9281	23182	A	9350	373	235	EEGELLEPGVQGCSELSWCHCTPAWGTEQDHCVSYNNSNTHNNVNY
9282	23183	A	9351	476	82	YLATYLPYLSIYLPYLPYLPYLYL GSHYIAQAGLKLFGWVGHNGSCL
9283	23184	A	9352	286	142	ELQFKMRFGWRHSQTISWGLSLLPRLISNSWAQVILLTWPPKVLGQIA
9284	23185	A	9353	3	102	FFETESHVARLEYSGAISAHCTPVIKLYLYT
9285	23186	A	9354	3	270	TAGAPPRPANFCIFSRDGVSPCWPGWSRTPGLRCDPPASASQLLGLRLRHENCLNLG GEGCTGAILAHCTSLRAQAILQPPSC PAPQ
9286	23187	A	9355	1	112	GECSAHCNLCPLGSSNSPASTSQVAGIKGVSHRAPN
9287	23188	A	9356	1	63	VALIQAYVFTLLVSLYLDNP
9288	23189	A	9357	244	140	QRRHTHTSHSTYTHTHTHIPNKKIPILTILKCIA
9289	23190	A	9358	464	181	LGAGGMTGILFSLGASVVLGGVQMLAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KARTRRIQTDTNGKQNTYFSSLDNMVAQ GNVLPVLYGEMRVGSRVVSQEISTADEG DGGQVVVIGR
9290	23191	A	9359	11	469	IDLCRFHEERERERERERERERERERER ERERERERERERERERGRAPPPPLFFGGG GPPARAHALSPPHLGRPPPLYTYFFSYVR APPTERSARTQREARRALKSVCVVRERE THSLPRARCVCSHPTGCGGAPGARVLS QSAHCFLVCVGAG
9291	23192	A	9360	22	172	GLSHERERERERERERERERERERDTV CPLFCPTGGFILREARVKSGCLCF
9292	23193	A	9361	15	345	PENRPPAEFRTRHLISLLCLEGITLTL FIATLTLTNTHSLLANIVPIAILVFAA CBAAVGLALLVISINTYGLDYVHNQKKK KKTWGGGRAPNSPYGGRNNNPRPAV
9293	23194	A	9362	61	298	SCDSPFQECCLHTHTHTHTHTHTHTHT LFSDIKHTHTREWALSFLLTTEEZGGGT LFQGTLLFGHTLFWDKPLWQKEF
9294	23195	A	9363	430	2	GGAGPPPPCWTQGPVPPPTLSPRVNGP SLCSDFPSPKFYKEKRKKGNKTPKRKG KTLTPTETIVLHVSPGCEKPGAGSADR RAPGVDRGGSDASSSGTRASELGDGPVR VNFVLGDPGEAGRGFSMLGHPPGTSGPR TS
9295	23196	A	9364	432	291	GITGLRHHSQLIFLFLVETGFHHVQGAG LELLIHQHRSPKSVLRQLV
9296	23197	A	9365	343	507	GQGLTLVPQVGQWGNLSSLQLLPGLK QSTCLSLPKCWDYKCGLPFPASFVFL
9297	23198	A	9366	417	128	MGWNPGRGAPFFLDEMAAGQRRSSLSRV GSQAEGLLTSHTMGGPAETLLTSQTGWR LGRGCNLGSLLEGQRRLLGGGCGNEPSSR HCTPAWAPLSTE
9298	23199	A	9367	500	285	SLPRSWDYRRAPPRPANFLFLVEMGFHH VGKAVLELLTSGVLELLTSGDLPASASQS AGITGVSHRAWQIRE
9299	23200	A	9368	1	229	IVDLTTWGIPTHTIHKYTHIHKYIHTH AYTHHTHRHKHIYTYIHTDMVWLSPPHN LILNFSHNPHVSWEGPNGR
9300	23201	A	9369	451	88	KQNTNIYTCIYMYVYIYTCIYTYVYIYTR TYTCIYVCVYTCIYVCVYTCIYVCVYTC IYVCVYTCIYVCVYIRVYTCVCIYVYIR VCVYTCIYVYVYIRVYTYICIYTCISTY IQCIYTHIYKVTKCSG
9301	23202	A	9370	1	208	ADETIEQRGGIPKPFVHDNYVIRRTAVDR GIPLLTNFQETKLAFAEAVQKSRKVDSKS LFHYRQYSAGKAA
9302	23203	A	9371	354	202	PAAQREGITASARYSKNWTGPDGPAREF TMIQSAPLMLLADPDEFVSQOLA
9303	23204	A	9372	1	336	KSLLIKYKGQVAPAELESILLQHPNIFD AGVAGLPDDDAGELPAAVVVLHGKMT EKEIVDYVASQVTTAKKLGGVVFVDEV PKGLTGKLDARKIREILIKAKKGKSKL
9304	23205	A	9373	2	187	NILVTALYSLYIFTTQWGSLLTHINNI KPSFTRENTLMFIHLSPILLSLNPDII TGFSS
9305	23206	A	9374	96	240	ACWLMFVIPALSEAEAGRLVQPRRLRAA WATWQDLISTKKKKGGPF
9306	23207	A	9375	3	293	STISAFITSTSTATTSTSTATTSTIS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						APTSTTSLSPPTTSTTTTSTTSAPIS SNKLHKKKKKKKKQKKKKRKNDDTKQD TITKIHSGGGS
9307	23208	A	9376	69	160	EHTHTHTHTSHHTHTSHLPERFFCVLNSL
9308	23209	A	9377	336	199	EGITASARYSKNWVTGDFAREFPMIQS APLMLLADPDEFVSVQLA
9309	23210	A	9378	321	128	EPGFTMWASLAPTSLSQVIHRLGLPKCW DHRREPPHPAYHSLYESGSPVQNGEEKG INPIIKMG
9310	23211	A	9379	440	286	SSDPSASAKSAGFTGMSHHTQLLTSYS EGECLSYLVFLVLV
9311	23212	A	9380	392	154	KGSSPLSPPLSLAGGKPPPPRKFLLNFF FFFNRDRVSPCLPRLVSNWPOAILLPQ PHKALGLQAYATTASFIFLIVTV
9312	23213	A	9381	403	178	GRREPCRDADAHLEGIIFSAFYPKNWE TTGDGAREWTMSNSAPLMLLADPDEFVS VQLA
9313	23214	A	9382	303	206	DPVSTKICSLQPPPPGFKRFSCLSLPSS WDHR
9314	23215	A	9383	215	116	SNNFVVCCCCCCCCCLRWSLTSLSPRLH SCGTM
9315	23216	A	9384	2	285	ARHLLMQLSGGATLAISTIDLPLSTLIIF TLILLLTILEIAVALIQAYDITLLGSLY LGDNTYKKKKRGAAFEETKFTSAGMQSK NFFLGLTLNWR
9316	23217	A	9385	12	123	GYENFLPLTLHTQTHAHTHTHTHTHTHI HSKDPMEY
9317	23218	A	9386	3	230	KCWGYRCEPLRLAPLRCFFTPGGISLTS GPALLSNASALAEVRGQQLCPPTPFLPT LIAITLLLPISPFIIL
9318	23219	A	9387	590	396	ARVQWPDLSLQPPPPGFKRFSCLSLN SWDYKCAPPCRADFCIFSRDGVLCWPG WSQTPYLK
9319	23220	A	9388	224	79	GLGPVGHACPTLWEGEAGGSRGQIEAL PANTVVKPRFLKRRKKGKKG
9320	23221	A	9389	249	72	LVYLITVKKILFPVHIRTFNKIDHMIGH KTCLNKLQMTIELQSVFSDYNRIKLEAS NN
9321	23222	A	9390	400	254	LRQPGSTNSPVSASRVAGITGTHHTQI IFVFLVEMVHACNPSYSGG
9322	23223	A	9391	3	64	PPQKSDPPYKLVPHLDSIL
9323	23224	A	9392	266	106	LTANFLFLVETGFPVTRVGLLELLASSD LPTLASQRAGITGVNHLQNFWPGNF
9324	23225	A	9393	430	348	FGKPQPPPKGKSPFPRGNFPQKAPKG
9325	23226	A	9394	481	311	LSLSEKRSIRVGVTFRSRRCCPSPLSLTG KGNLTPGVSGEIHSPWFGLIAYSVCTH
9326	23227	A	9395	3	136	VFPRLVLNSWAQMILLCWPPKVLGLQAC TTRPSHFLPLLNSKYK
9327	23228	A	9396	143	347	NFVFLVETRFHHVGOAGLTLTSSDPAS QSAGITVRPEILTLKRYHFPSSGILGTE GMVEMAYLLKV
9328	23229	A	9397	2	231	LELLTSSDLPASASQSAGITRGSHHARP SFTFRCVIHLEFNFMRGAREERLHFYCR WVIRRLTFGRGYPSAASD
9329	23230	A	9398	383	200	QHYLNRRRLSLAQWMPVVPATQEAEGG LLEPRSSSLQCAMMLPVNSHCTLAATH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						REPHL
9330	23231	A	9399	3	416	GFLHVGQAGLKLTLTSGDLPTSASQSAGI IGVSHRAGCLKSIYLTFTPTKPFVQMSI CDFKVEIEGKIGFISVPIISLQSLHIVN NFFFFLETGSFPPGWRABKFGLIAPLA SGVKGIFLPLPRENLGWRPSPIPPA
9331	23232	A	9400	400	151	FGYPQVFPPLPFLKPGPGIFLGLPKKN FPPPPPGLKIFSPKRAPPFFVFVRKGLI MLLRVSNWSAQVIIPPPPEVLGLQA
9332	23233	A	9401	324	154	FFFFFFFFXXXXLLFFFFFFFFFYIFFF FFFXFXFFFFFFFFFFFFFFFFFFFFF F
9333	23234	A	9402	413	312	PKLVLSNLQALLPRPPKVLGLQARAT ITQPK
9334	23235	A	9403	363	3	FKKKNFCLGGAGVVFVFFDPPPKKNIF YFPSKKIYFLSPASSSFFFLCFPPFIF FFFFFFFFFLENRWFLMENFIKGRGHV KGPLGQARDHDISGRRWRRQCRASQL PGVRPRV
9335	23236	A	9404	401	82	SELPHDPINPTTGYIYPKMKSCFTDI CTPMFTTALFSIAKIWNQPKCLSKRITI FMFLVTYSQLFCTHYPIFYPPFPAPLS SSHNYHYTLVLYENILLDSTYE
9336	23237	A	9405	382	219	WARWHGFLVFTSPGGEAGGSLEPGKRRV QLTQISPLPSSLGGKVGLPLKKKQNN
9337	23238	A	9406	3	195	YLYSLVETGFHHVGQAGLELLISRDPSA LASESAEITGMSHSIQPKSAFYIPIPET FWQPAFK
9338	23239	A	9407	371	1	FRRLRLKNRLNLGNGGCCSEPRLCHCIPA WETRAKLGRRKKERKREKGTMYNKNMY KMYLELNLTCPPEPASPQMTROLEVLS NPSPGTQFQICKKQFKSCCFALRVSIY LLMSVFEYCSC
9339	23240	A	9408	326	229	RQGLTMLPRLVSNWSAQVILPPWPPKVL GLQA
9340	23241	A	9409	81	231	LESASFPPGKVAHTCNPNLTRGCAGWIA WAQKFKTSIGNMAKPCLYKIK
9341	23242	A	9410	367	256	HPGWEWWLVSVIPTLREAKVGRSLEPRS LRLAWDTWG
9342	23243	A	9411	2	192	VFLVEMGFLHVGQAGLELPISGDPPASQ SAGITGVSHHAQALTFLNIPINPSHPPK ACCSKQL
9343	23244	A	9412	3	83	KNCLNLGGGGCSRLRLCHCTLTWATE
9344	23245	A	9413	371	301	EDHPRMVILRLRLRYIVRLVWRMH
9345	23246	A	9414	486	337	AGLELLGSSNLPALTSHIAEITGMCHHT WLAYIFVCAFGWVLLLDLCIAF
9346	23247	A	9415	378	254	IVAHCSLDLLGSSDPLTSASRVAGPTGM CHVWLVVFFVC
9347	23248	A	9416	160	309	VVRYSSNEFLFLFLFYLFKSNFTVFCCL YCCCCCWQSLTLPPKLECGV
9348	23249	A	9417	162	339	RPSSFCEFLHDSVPELALPMKARFEKSR RSQVSWLMPVIPTFWKAVGRYQARSLI PA
9349	23250	A	9418	1	147	GGGGCSEPRSCHCTPAWATRVKLGFLPKK KKINFLFVPPFIFLKSRTGV
9350	23251	A	9419	283	126	KMMYKGAQWLIPPIPAFWEAKERGLLE VRSRLPAWATEQDSTATKNKNKNF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9351	23252	A	9420	133	3	ELMFSWAWWIMPVIPALWEAEAGSSRGQ EFKTSLPNNMVKPRLN
9352	23253	A	9421	3	133	LRGLYSAGIIRFEAKKNALALMAWDI AGDNCAICRNHIMDL
9353	23254	A	9422	409	291	ILILGGGSCSELRSCHCTPAWATRAKHR LKNKSPINVY
9354	23255	A	9423	1	210	RFPHLGLSKHWDYRCESPHAGTRNEVLI YATIWMNSENIVPNEIIQTQRTNIVSFY LYQVGRIGKFIDRR
9355	23256	A	9424	479	306	GVPTNQPSNRVKTSPSTKNIKISWPWW CMPNPSCEGQGRRIALNPGRWRLQ
9356	23257	A	9425	1	209	GFFLFQGGGHHAGQAGLELLTSGDLPAS ASQSAGITGAGPNQGI FVALES PMESAA LLHLAVVLSSPCS
9357	23258	A	9426	628	433	RQGV AHLPGMECSGTITTHCSLELLGSS DPPASASQSSRLAVVSHCAQPSLLFSVL CLKPIFCCA
9358	23259	A	9427	417	125	FLRQSLTSSPRLEYNGAIPAHCNLCPLG SSDSSILASQSIRITGVNHCTWPDAAVL RQNFFFSKPKQFYSEGFQQTHI KSNLL YLKSTKCTCYPYL
9359	23260	A	9428	366	256	SFFYDRSLATLPRLGSNAWSQAILPPG PPKVLRLLA
9360	23261	A	9429	3	140	GFCHVGQAALKLLISSDLPTSPSQSAGI TGVSHCARLTRLFSHE
9361	23262	A	9430	368	3	VRASQLLCLPTQASAMAGTPPPASLPFC SSISDCCASSEQSGMGVGPSEPGAGYNL VVCSSLRLEKCSIRVGVPPQFSRCHLSQ LPLARKGNSPTPCASWVRRCLTLQLML RGLYPLSCT
9362	23263	A	9431	3	131	LITMLPRLVSNWSAQGSSHLSPPKCWDYR CEPLHSGLKDIFLE
9363	23264	A	9432	384	274	LSFAMLPRLVLNSWAQESAHLGLPKCWD YRHEPLGLA
9364	23265	A	9433	431	273	PPFLGYFFIVKMEFPPVVDGFKLLNSS DCSTSASPSGRISGVNHSTRPRIF
9365	23266	A	9434	211	473	CVCTFFSFLSMHIFFLVLVGEAESHCVT EAGVQWHDLGSWQPPPPRLKRFSCSLP SSWDNRRVPPYPANFCIFSRTRVWSCWP GWS
9366	23267	A	9435	391	188	LPGSSDSPASASRVAGTTGGCRHTVLLG FEFKDNIRWIKLVEKAHTQYGNIIYICVI KVMPLFYYPHH
9367	23268	A	9436	331	115	SRDRGFAMLPRLVLNSWTQAICSLDSQ SAHLSLPKCWNRYRREPLCPASGEILSFI KPSSSKSFHNSTKKRQ
9368	23269	A	9437	3	109	IYGSYSLPACFFPSFLPSFLPSFLPSFP PPFLSFF
9369	23270	A	9438	2	167	ECNGAISGHCNLCLSGSSDSPAPAWATR VKLRLIKKKKKKNQILFFYPPrKTLF
9370	23271	A	9439	648	310	VCPCILRHFAFLFAKSGNPBESSLLDHS SPTFKLTDRNLRHVKCTSHSQSLPTSG FQGPLDSTLCAWYPTSPKLS PAGWVG GYRAPVGRRGPGSRNSRWLHWPITSVG D
9371	23272	A	9440	1	170	YEIWFLDVGQAGLELLTSGDLSASGSQS AGTIGMSHHARPLKLTISVSSNKKVKC
9372	23273	A	9441	133	244	LFQYQTRGLAMLLKLDNSNWFQAVLPQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						PPKVLGLLA
9373	23274	A	9442	365	176	RGSMVMVPSSECTGYNLLMCPLLRPLEK RSIRVGVTRFSRCHLSQLPLARKGNSLT PCASQVR
9374	23275	A	9443	368	231	VEAGFCHIAQAGLTFLSSTDPASALASRS ARITGVSHHARPIFLKE
9375	23276	A	9444	88	194	KMLEAKKKIEQQGGFTFENKGVLSAFNF GTVPSNN
9376	23277	A	9445	3	349	IRSGSYACYFCYPRECIALFHCYSMIVS YGPYIFMNIQDQHESSLSTIYIFKFBIG SKHVAQAGLELLCSSSPPAFTSQSAGIT SVSHHTRPQKIFNVIYSCDLHFHPGIEG PQR
9377	23278	A	9446	3	141	HAECSSMMIAHCELELLGSTDPASASQ SAETTGISYHAQPYSTF
9378	23279	A	9447	2	282	ICPTRSRFPFRVLKNGRKKORLECSGAI SANCSLCLPGSSDSPASASRVAGSTVAE EDSTRRAVRHQSSRSAPSGRGSWAGKQ ERADRAQQS
9379	23280	A	9448	307	430	GLAWLTPGIPILWEAEVGGSLVEFET SLASMEKPSLYYK
9380	23281	A	9449	2	253	IQCVCVCVCVCVCVCLSVCLHFIATLGC SPWGSRLPCSVSSPSGRGPGGEDLSPLP PTMSVSPDADFPLAAAAPGNIMTAIT
9381	23282	A	9450	1	166	NTGGGGEEIRVFSSCFABDRLOKQKDRP GAVAHACNRSTLGGRGGWITRSQIFFC
9382	23283	A	9451	1	123	NTRGLVMLPRLVSNWAQVILQPLPPKV LGLQASVTVHINN
9383	23284	A	9452	396	291	SLCIKRVACACVCVCVSGAKLRKLV LDFMRS
9384	23285	A	9453	1	147	FAIRARFSNTYTKIGTIHTYIYIYTYIY TYIYTHTHIYILSQVLMYEF
9385	23286	A	9454	394	235	TRSCYIAQSVVQWLFQTGLIIHYNLQLL SSRDTPVSASQYLGQAHTTTPDSC
9386	23287	A	9455	1	85	TNPVATLLEWQDALCFIPVGSAAPOGSE
9387	23288	A	9456	339	165	KTHWWGKKSFLKNPFFFFFETKRSRV TRLECSGVILAPKQKTKQNDKTTINKT I
9388	23289	A	9457	3	209	LLILFSIKMRNRDPSPALLSTQLPPIFI YIHTHIYLYIYTHIYIPIYIYLYLFA YIHYVSLFPLK
9389	23290	A	9458	374	156	QAGLELLTSGDPPISASQSARITGLSOR AQLSELTITVFTTRHCTCLCAHFLYYTV FLEGRNDEFISIPST
9390	23291	A	9459	287	3	EAGLLWRKATHKYAHTHTHTHTHTHTHI RGLQNMINKYITYQEIIMTQAQKNKGV IPDSFPFTSSPPLTYPPALSFFHQKHIP NKITTYHGHC
9391	23292	A	9460	3	72	KTELKMKFTNILESSFLMNNKS
9392	23293	A	9461	327	92	ISLFLVWGALFFPKKIYPPKKKSPLFF PPPPQENFNPPSFLAPPVFPPOENPKF AGGRKIFCPPPVPVFFVFFVFFVFF
9393	23294	A	9462	3	173	ACRGDSGGPLVTRDLKDTWYLGIVSWG DNCGQKDKPGVYTQVTYYRNWIASKTGI
9394	23295	A	9463	258	39	LKVLPSDPSSIFVCLPLENESRSVTQA GVQWHDLGFKRFSCLSLSSWDYRRVFP PPAKFCIFRKHGVSPC

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9395	23296	A	9464	104	336	NHVSQCEEI FLFDEYYIFSRVAVSMFVW DAELGSDIYLDGKLKNSFLLSFLGFFFF FFLGKKVFFFSQNGGLGRPGQ
9396	23297	A	9465	410	0	LNLGGGGCSEPRLCPTPANATE
9397	23298	A	9466	254	61	KKKKDAFFTIPLYPSSQNLFQTMDDP TNISQQLTWTVLPQGRHSPTFLDKPF KQTSINFA
9398	23299	A	9467	403	255	PAPQLGGPPMPMMAPPSSWMMPMGCAP AMRLPIGGDI IWL CVPTQISP
9399	23300	A	9468	1	1428	PARFKDLNLAGTAEVGLAGYFMDHTVAF RDL PVRMVCSSSTCYRAETNTGQEPRLY RVHHFTKVMFVGVTGPGLQSSQLLEEF LSLQMEILTGLHFRVLDMPQTQRLGLP AYRKFDIEAWMPGRGRFGEVTSASNCTD FQSRRLHIMFQTEAGELQFAHTVNATAC AVPRLLIALLESNQKDGSLVLPALQS YLGTDRTITAPTHVPLQYIGPNQPRKPL PGQPAGPRVGYKALQPWPAQRLGPVGRP PCRPEGQPLSCCCGCSWGRLTRCLAE VVTEVLTVGQVQRPCTALLHKELCGTE PHGCASTEEKGLLLGDFFKQEQAGKMRSS QEV RDEEEEEVAERTHKSEVQEQAIRMQ GHRQLHQEEDDEEEKEERKRGPMETFED LWQRHLENGGDLQKRVASKASDKETAQF QAEKGVRLVGGDRSLWQGAERGGGERR EDLPHHHHHHHQPEAEPRQKEEASERE
9400	23301	A	9469	265	170	GTESHSVTQAGGQWNLNLSLQPLFPFGK QFS
9401	23302	A	9470	289	110	RDLELASFLSFFPSFLPSFFPSFLPSFL PSFLSFSFLISFFPLPSFFSFISFLSL FFB
9402	23303	A	9471	67	210	TVTTGQALTHAYNPSTLGGRGQITRGQ DFETTLVPGDLNFSRVLASS
9403	23304	A	9472	2	186	TSLWRQAKNVEKTKDYTEVLKTHGLL VCTQKSCSFLKNKNKAWLGKQANAPARK VEIRC
9404	23305	A	9473	417	265	FLSSFLFFFFFFFFFFFFFFFFFTV
9405	23306	A	9474	430	120	ASQKKKKKKKKKKKKKKKKKKGGAL
9406	23307	A	9475	1	150	PTRPVVQAGFKVLSSGNPPALVSQCRI TGVSHRARPHLLNLRAPNLPVL
9407	23308	A	9476	404	109	PPPLFFNFGFFFLVEARLHHVQAGLKL PTTSDQPSASQSAGFTGVSTRAQPTLI TLY
9408	23309	A	9477	391	235	PPFFFFCRDRGLTMLPRLISNSWAQVIL LPWSPKMLGLQARATVSGLNKRY
9409	23310	A	9478	438	277	KRAPFFFFCRDRGLTMLPRLISNSWAQV IILLPWSPKMLGLQARATVSGLNNRYS
9410	23311	A	9479	399	279	PPPFVFKNPPPKNKGAPKKKNISPPPG RKKYFFFKGPP
9411	23312	A	9480	247	26	LKAGDDSRITVLGKVHQSPCFSLLLFFIQ VSCRDEGLTVLPRLVLNSRPQAILLPQL PKLLDHRCEPPLANHG
9412	23313	A	9481	2	176	HAPHPANFLFFFEKESCVTVQVSIRLL DSSNPALTSQSAGITGENQHGHPMNCL SG
9413	23314	A	9482	2	178	HAPHPANFLFFFEKESCVTVQVSIRLL DSSNPALTSQSAGITGVSHHGQPMNCL SG

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9414	23315	A	9483	2	151	GRVGBGPVLVSLLDQHPVGTSDHRDA TQLGPOPLMSDLGSTGSTEGA
9415	23316	A	9484	420	325	FFVFLLETGFHHVSDQGLDLVICPPRPP NTFV
9416	23317	A	9485	400	104	LEFFLFFFFFFFFFFFNNBPKTFFKKV FGLNFPTLLKLKFNPPPPGPPKKKKEL
9417	23318	A	9486	117	280	SSTNQANNCFFFFKKRGLAILPRGALNP WAKGILLPWPPKGLKLRGGAIGPGQK
9418	23319	A	9487	76	353	VLWNTLEFCLLYLDLLFLFFNKALIR KKKKKKKKKKRGGNKKKKKKTPWQEK AGLPLGDTIIYSRGAVLKNSGGETPRHT PSGGLWPR
9419	23320	A	9488	3	122	HASEDNVFLHCSHSDLGIVLLAGTASLQ DFSFFQKSPPP
9420	23321	A	9489	1	155	PTRPVCSGAMLAHCNLCLEPGSSSLAS ASQVAGTTACTSTPDFFFFFSL
9421	23322	A	9490	3	212	ETGPHHVGLSGFKLLTSGDLPTSASQSA GITGMCHCVWPQFAYFCLLLVYLDHLKF TIIMLVLCLEFYD
9422	23323	A	9491	2	163	ETLFRHVGVQSFEPLTSGDLPASASQSA GITGVSAMPSWMIKFIFAFYSCINC
9423	23324	A	9492	474	296	SQPAGTADCLLPLPPGSCFPTIPCPAAL VPLPSFPSARLWPPQSLHQLLPLPGTCS SCT
9424	23325	A	9493	7	151	LCAVEFVYMKPPAHEEAKAPSRGFVVRY APWTASSSEKGRDDGMGPRA
9425	23326	A	9494	52	363	TTAPSLSVFLFTFTGELFVYVWVGTLE TSFISFFLFFSFLEKDFSFSPAGRFPWP NGLIQPLASGVGGISRPNPPSRWELRA LPPPPGGLGFFFWKKGGPPG
9426	23327	A	9495	383	118	WKPRPWVPPGAGVQTPPGPQGETPLFLK KKKKRGRGGLFGPPSFGGGGGEIPLTP APKGQEIYFPPPPPPGKKKSLPQKKK KRIR
9427	23328	A	9496	554	419	FFFETKPCSVSQAGVLWRDFGSLQPPPS QVQRDSPCPQASQVAND
9428	23329	A	9497	428	281	GSYVQLTFKYFSIYIVVHTLHVLYTH IYVYVHCYKGYITGSVLA
9429	23330	A	9498	144	16	KVKKKVSQCPGIVAHNCNPSTLGGRGGR IAWGQEFETLSLQKN
9430	23331	A	9499	2	155	NLALGSSDPPVSASPVSIGRVHHHAQ LIFFFFFGKRAWFNPPGGRKGEE
9431	23332	A	9500	2	184	FIYGRDSLTMPLRLVLSNPQAILPPRP PKVLGFRCEPPHLASLILFYRDILFTLG LKSV
9432	23333	A	9501	465	153	PHKVFLNKGPFETPQGEISRGWKTTRPP PPRERSRPFHRKGGFGSPPKLRQGGPFV FFSWPPWCPPPKKGARPPQKGFYFPPP FFNPPFFFFCLFFIFEIV
9433	23334	A	9502	429	11	CRTLGLADCVCCVCVCVCVKAFFPI SYSCHLVPSDLPLLGVPFKCWVHGLSF LTCPPSPPPWGGAGPGSCYWGCLCL FACKLGARLTEQTLGIPASGPGTWATPL GSCASVLRRLPGGSEDTDLKSVLSG
9434	23335	A	9503	436	202	LPGGYIFQGEVETKFSPLLRENNFFS NFFPPKNNGGGPRIPPPPPPLFKKGV FFIPKFPAPPRPKKFKKKKKK
9435	23336	A	9504	3	112	SFDLLSSSDPPALASQSAGITGVSHSHG

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						QKVYICNM
9436	23337	A	9505	426	208	VGHNLLVPRFLSPSEKRSTQVGVTSSR CRLSPLSLTRKGNLTFFASRVRCCLTL LRLARAPTDLRPLSGTP
9437	23338	A	9506	441	189	CPANFFVFLREMGFHHVGQAGLLTSSDP PASASQSAGITGLSHCARPTVGSVDVLSL PSGQCTSALTGFMLGSTTVHSNAAARA
9438	23339	A	9507	117	278	NKALLCHPGWNHKKVNGRLGMETHTCN PTTLGGQGEFENSLGNIGRPHLYK
9439	23340	A	9508	3	126	FFVEMGFRCVGRAGLRLLTSGGLPVLAS QGAGITGVSHCI
9440	23341	A	9509	421	134	FLVERRSHHAAQASLEILSSDSPTSAS QCAGITGMSHCARPKYTSFFRLHRHMPM ATPTKLPPTLASASPQVKVCLYPLLPST SKGEIFTQLY
9441	23342	A	9510	2	200	PQPPTFFPSFLPSTPEPPAFYPRLPST PASRLLPQPPAFYPSACHLLPQPPTFFP SLGNRARLHL
9442	23343	A	9511	414	204	ERDRKKERKKKEGRKERERERKKKKKK KKRRKEGRKEGRKEASKGQRVVIMVD T
9443	23344	A	9512	1	211	FHHVGWAGLGLLTSGDLPASASQSARIT GMSHHARHRHGFNDLSLALAPSPPTLW RRHRRRGHFTVPEK
9444	23345	A	9513	390	265	VFLVEMGFHHVGQAGLELLTSGDLPPLE SQSAGITGVSSQFSS
9445	23346	A	9514	438	180	IGFRHVGHAGLDLFLGLDPLSLASQAR ITGVSHRAWPAMAFVNCHGAGGSVAMRT TRGHSCRHLGIGGFWPASLLQPVLSAGS L
9446	23347	A	9515	126	11	RNLDFFLSLGLAMLRLVNSWPQVIFQA WPPKALRFQV
9447	23348	A	9516	2	249	FLHVGQAGFVLPTSDDFRPTHTPQSSGI TGVSHRTRPLRCYFLRLNNIPLYVYAY ILFIHSVISGYVGGCTAHYCHPKVV
9448	23349	A	9517	403	57	PEGALVPQKKKKKKKKKKKKKKKKKK NIKI
9449	23350	A	9518	406	140	PHYNHTFVYNGVRLLEDLQHMCLTLTVWD REPLASNDFLVGVRVGVTGEIPSPILT CLKASCLFYSYHSRPPTQSSSVMTVVF FPFS
9450	23351	A	9519	3	75	GIEWMVNCVVRNVHRPPRQRDIT
9451	23352	A	9520	183	6	LLTHLILTSALIGEIMVAPILQKNSGSE RECRLPRLVLNSWPQGILLPWPVKVLGS QV
9452	23353	A	9521	89	339	LQCLQKSGKLEPGMTYTKLIDADVNVGN ITSVQFIWKHLFEDSQNKLGAEMVINT SGKYGYKSTFCSQDIMGPNILQNLKPC
9453	23354	A	9522	3	329	PSLMFPWLKLSFPGRPRGRQTSRYQTL ELKKRFLFNPYWRKRRMEVFHALGLTE RQKIIWFQNRMRMGKKENTRDNLPEAQN EEKVVEKGIEEKEKEEKEENRD
9454	23355	A	9523	1	156	AKTSMNVNEIFMAIAKLPKNEPQNPGA NSARGRGVDLTPTQPTRNQCCSN
9455	23356	A	9524	1	272	AKNSARALLGILGYRSHLISSLLCLEGI ILSLVIAITLITLNTSHLANIGPIAIL VFAACEAAVGLALLVSIISNTYGLDYVHN LNLQ

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9456	23357	A	9525	1	62	GNDAWVCTNDMFRALAHNFG
9457	23358	A	9526	1	111	GDI IHNNENMRQGRDKYKTLRQIRQGNTR QRIDEFEAL
9458	23359	A	9527	427	340	IPIGNIMSCDSHSHHELVMSAQLNAIFH D
9459	23360	A	9528	439	27	PRRTDKWLTVEMIQDGHQVSLLSGELTV DQRASIIQRFRDQGEKVLIPTNVCARGI DVKQVTIVVTFDLVPKQGEPPDYETYL RIGRTGRFGKKGLAFNMIEVDELPSPMK IQALFDGRNKQLNAEVPCIQAAEMED
9460	23361	A	9529	1	236	REVLITTNVCARGIDVKQVTIVVNFDDL VKQGEPPDYETYLHSIGRTGRFGKKGLA FNMIEVDELPSLMKIQDHFRRKS
9461	23362	A	9530	437	240	QQVSSARPEPEAGEVSPVPVAGVNSNSW AFKYGPGNPKQSGPEPKQTQVSFLLRR KGEASQPRQ
9462	23363	A	9531	413	260	LFDQVVKVASPSGLRTSTVRYGDPEKLK LEESLRQQAEGSALSVRISNV
9463	23364	A	9532	431	260	ASSGQMFSVKQAPPVRLPPFGISLFG GQIYDNISPRPPQIVAPPGGRNIPNL G
9464	23365	A	9533	2	134	IHGVCVHMCVCACVCVYACVCVGGYDGR IFLALSSTVPSMVNIM
9465	23366	A	9534	419	53	LLLLTNGDRQTQREKIEACACQSYFDAV VVGGEQREEKPAPSIFFYYCCNLLGVQPG DCVMVGDLTETDIQGGNLNAGLKATVWIN KNGIVPLKSSPVPHYMVSSVLELPALLQ SIDCKVRMST
9466	23367	A	9535	439	109	NCIVITDSTPYRQWYESHYALPLGRKKKG AKVTPEEEEILYKNRSKRIQKKYDERKK NAKISSLVVEEQFQGGKVLACIASRPGQC APADAYVIEGKELEFSLRKIKARKGK
9467	23368	A	9536	1	185	NTTSSHHFTIPCLVLYSCTSTHTHTHTH THTHTHTHVRVFSYIPSDVKEGCIPAP SVFSW
9468	23369	A	9537	168	280	NPNSIRLTSCCCCCCCCWKSYPNVYNR LLRTGFTFP
9469	23370	A	9538	142	324	KIVKMGFPFHAGQAGLELLTSGDTPGSTS QSAGITGVSHRSRARSIFLYPYLPSVYL PWRRV
9470	23371	A	9539	3	139	YIGGMGQAWWLMPGKPRQNDYLSPGVQD QPGQHSETPSLQKGFKN
9471	23372	A	9540	383	318	MSTQNNIQSYPIGEDEESES
9472	23373	A	9541	372	207	YGLNMCRCQFRQYAKDIGFIKVGVCRR PCCLGREGCGGYFFRERQTDSSLEW
9473	23374	A	9542	2	360	ARGDDHRRSSDRKDGVLBBQIERLQEKV ESAHSEQKNLFLVIFQRVIMILTEHLVR CETDGTSLVTPWYKNCIERLQIIFLQHH QIIQQYMTLENLLFTABLDPHILAVPQ QFCALQA
9474	23375	A	9543	379	75	TNLQQFAMSHGSAQVKGHGKKVADALTN AVAHVDDMPNTLSALSDLHAHLRVPDV NFKLISHCLLVTLAAHLPAEFTPAVHAS LDEFLASVSTVLTSKYR
9475	23376	A	9544	380	56	RDLMSVRMKSMAIGFCFTALMGMFNSI FDGRVVAKLFFTPLSYIQGLSHRNLLGD DTTDCSFIPLYILCTMSIRONIKILGL APSRATKQAGGFLGPPPPSGKFS

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9476	23377	A	9545	304	92	SKSRVTNNTLRSTRKDTMITLNTHSLLA NIVP IAIIVPTACEAAVGLALLVSNP YGLDYVHNLLQC
9477	23378	A	9546	394	108	KEIDFSLVDVTADDAGNYS CMYYQTKSP FWASEPSDQLEILVTVPPTSSNYSLG NFVRLGLAAVIVVIMGAFLVEAWYSRV SPGESEAFKPE
9478	23379	A	9547	1	335	GNAVGLNLHRINFDKYHPGYFEKDG MKH YHLHRNQSFCTVNLDKLRTLFSEQTRL NAAKNKTGTAPIIDAARSVYKVLGK GK LPKQPVIVKAKFFGSLIFCFRIWILID
9479	23380	A	9548	326	188	NFLRMGTVAHASNPSTLGGGGRITAGAQ EFETSLGNITRCPCLYFKK
9480	23381	A	9549	381	152	VTLISLSLLQVVIQVLLVVIARLNINE VEKQWRLNQLNNAATILVFFTIVINVFI TAFGAHKGTGFLAARASRNPL
9481	23382	A	9550	170	65	IHRSKNKWKPHLKDGINMLNGRDYIFSK AIGDAEW
9482	23383	A	9551	544	361	RRLRQENRLNPEGGCSKPRSCHCTPAW ATEQDSSSKEKKERKNLGNTVKSVP LP LTSHA
9483	23384	A	9552	369	181	GVLGATSGDMQIHTFGSMITGSTITGMVS ELGYKFLTSTADVMIQTLNLHLPSHMS HQKKSY
9484	23385	A	9553	1	516	SLVHVVEFGQAIARRLKPFQVQRFYTG RQPRPEEAAEFQAEFVSTPELAAQSDFI VVACSLTPATEGLCNKDFQKMKETAVF INISRGDVVNQDDLYQALASGKIAAAGL DVTSPEPLPTNHPLLT LKNCVILPHIGS ATHRTNTMSLLAANNLLAGLRGEPMP S ELKL
9485	23386	A	9554	386	56	LFPA CVLRWQFASDGGDIGFVFLKTKM GEQQSAREMTEVLPSQRYNAHMPEDGS LTCLOAGVYVLRFDNTYSRMHAKLSYT VEVLLPDKASEETLQSLKAMRPSPTQ
9486	23387	A	9555	375	150	IVVGKTSFHVSIPLSLFFPGDVLVDLLQ HILKQSKPRILFSPFFHFGNSIHTQPEV ILHQTHEEGTGRGFSFLA
9487	23388	A	9556	3	354	CLPTQASAMVDTPPPALLPPCSLISDCC ASNEQGSVGIGPSEPGAGYNFLVCRLLR PLEKHSIRVGVTQFSRCCLSPPSLTRKG NSLTPCTSRVRRCLALLQLTLSELPHCP VPSV
9488	23389	A	9557	463	40	PIKVEDPEPVKKPKPEQRSIKEMPFITC DEFNGVPSYMKSRITYNQINDVIKEINK AVISKYKILHQP KSMNSVTRNLYHRFI DEETKDTKGRYFIVEADIKEFTTLKADK KFHVLLNILRHCRRLSEVRGGGLTRYVI T
9489	23390	A	9558	338	104	NFKKKKKRRTKKKEIRTEEKGRGANKKT FRGPKKKETRGSNRSPEGKKNHGAKKEG ERRPKKKKKKKKLARYDFTCL
9490	23391	A	9559	1	152	NTCVCVCVYTGFCVHAQVAHELSSNNLP SSASQSAGITGISHAWPGFGF
9491	23392	A	9560	517	238	SGPGESVPHPSAVRTRPAKKPGSQCLL QSAFPLWCSSRRTTWAEERKLTETFGV SGRFLRGRSSRGGRGGNGTPRRNPT SHRAGTGRV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9492	23393	A	9561	709	280	NTSPALTAPCGRPRGIRFMQCWARVPAP SSACPAWQLP\$LCRLSTVPAPHPSPA QPCELSQHHRGGLEPALPGTRQRLCSRT WHRCVRFLPGAQEAGELGPAACATGRLP VSHSTDEQAPGLTSLHQEPHSTARGGT ATH
9493	23394	A	9562	3	130	YRGFCHVGQAGLELLTSGDRITSASQSA EITGVSHRAQPQMS
9494	23395	A	9563	409	160	NPGVKRSPCLSLSSSGGYWSMPPCLAYY KKKKRRFLKDGGLTMLPRLASNSCAQQF SHFGLPQSWDYRHEPLHIAQFFLPSLL
9495	23396	A	9564	1	241	GICLGSNIGSGWMTSSLCPNYSNTLNQ NLLSTTKPFPVPSVGTNCGIEPWSGVT SGLGKMLFLYYYYLLLSQMT PQS
9496	23397	A	9565	2	215	IHWNGWMDGMDGWMGSCVRAVTGPGT SSPHTSTCGHAVCVCVCVYTCAHVFL ALFGVEKNNYFLWKA
9497	23398	A	9566	244	117	DHQLNWSVFISFSFKVIKARKNKKGIL NPDSSMETS P D F F F
9498	23399	A	9567	414	77	FGGVFPGLVPPTLWLPVRVPPPAFCL GELSPPPFFWRKGLAPLLNFFSPGQR GFPSGGKGRPLPRPAGFPGFVAKPPF RPPGFSSTPSDCGGLPFFFFFKKKVF
9499	23400	A	9568	418	198	PPVSLTEVIVSKSHKAEVFNWMPGTLE HPEGDNMYMEFIEVLTEALERVLLVRGG GSEVITIYSYPTLNARA
9500	23401	A	9569	549	415	RQENRLNPGGRGCSEPRSCCCLAAWATE GDCLKKINNKKPKNEQK
9501	23402	A	9570	546	1	KLECRGAI TAHCSLNLPGPGDPPTSATQ AAGTGTCH
9502	23403	A	9571	415	215	SRLRKKIYIYIMCVVYVICVYICIV VCVYICIVYICIVYICIVYICVYIY MHEFITFFSI
9503	23404	A	9572	374	138	LAASAAIQELFKRISEQFTPMFRKAF HWYTGECDMEFAEARSNMGLVSEYQ QYQDATAEEEGFEAAEEVA
9504	23405	A	9573	370	233	GSPPVRSVHQSGVSLSGTQVDEGVRSGS KRMVAPPGGRYNITSL
9505	23406	A	9574	3	399	YSSPGPIALALRDPCHAGGSPNSLSLSP AQGHPARAQGGPQQGPPSHLGSDLRP HVAHTRGALHGPAPAPAPAGGSGSGV AASMCAPRPGRAGGTLSVLTAAHPAS AGCAHRDAYVCKAPGRAVF
9506	23407	A	9575	314	48	SILPHSDPERCFSTIQPEGTIHTAAPLD REARAWNLTIVLATELDSSAQASRVQVA IQITLDENDNAPQLAEPYDTFVCD SAAPG QVSN
9507	23408	A	9576	505	264	IFVVEMEFHHFGQAGRLRLTSGDMPASA SQSAGVTDMSHCTRDPDTPFNFKELPGAV VTFLLCGMQVGRDELEDDWMAWS
9508	23409	A	9577	508	314	PATWKGCLSNFSSYLTKPADFIEHQVLS WEQVPDGGFFIFNERFKSFVVVLNNVAF FVCKYKLL
9509	23410	A	9578	512	1	RMREAFSPGRLPRGAAPLRGPAGTLVP WMPTPGECWLSLSVSAAGEKPKYKSCVCE SAFNKDKLKRHMLIHEPFKKYKCPFST HTGCSKEFNRPDKLKAHILSHSGMKLHK CALCSKSFSSRAHLAEHQRAHTGNYKFR

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						CAGCAKGFSSRHKYLKDHRCLGPQKDKD PV
9510	23411	A	9579	3	487	WDLIYVGRKRMQVEHPEKAVPRVRNLVE ADYSYWTLAYVISLQGARKLLAEP LSK MLPVDEFLPVMFDKHPVSEYKAHFS LRN LHAFSVEPLLIYPHTYTGDDGYVSDTET SVVWNNEHVKTWDWRAKSQKMRQQALS REAKNSDVLQSP LDSAARDEL
9511	23412	A	9580	1	840	SKYLYDEGEEEEVFNDENGAAGGVAVPT LNALERGFLSAMDWHLYTDPREIFEVLS WLESCVAEQQRWRGWYTTDL CVLLEQ PTWQALGSLCQRLVKLSCLLAVAYVSS VALAVASVAVIHQSLGLSCTPTPGPPDL GLTSRCLLEPCI PSVPQCLPSLANVSSC LEGSMLRSLWGSLLASLT PPLPPPPDP PAPPTLLHNCHLCQKLQSDSPTCHACLH PNRTVPTALSSPWHTYGLAPPWPWSPV PLSLPQPQCSLFSVMELARLKS FVFPFG
9512	23413	A	9581	2	158	IHAGFISVSVLDNIIYICMVCVCVCVC AHMCACISEHITHAPRLPEVFTYTP
9513	23414	A	9582	3	144	YTAGVISVSVLDNIIYICMVCVCVCVC AHMSACFSEHITHAPMLP
9514	23415	A	9583	503	3	GKCVCLSAVWGSLLSAFRGSLSVCC LGQ FVCLSAVRGSFSVCCPGQVRCLSAVRGS VSVCLSAVQGNVSVCLSAVRGS LFCVLL SGAVCLSFCLLSGAVCHLCRAPTPCLSR SLAHRRCNVNVCBMTQLISVSYPFCWGW WRHRNNIHLQKCLRILMAYTGQGGP
9515	23416	A	9584	2	1358	AGLDSLHKFPQVKIEKEKVYVRASKQALQ LQRTKVMACISPSAGYSSSTNVLI VIG AETLRQEGFSDRIVLCTLDRLHSYDRPK LSKSLDTQPEQLALRPKEFFRAYGIEVL TEAQVVTVDVRTKKVVFQDGF KLEYSKL LLAPGSSPKT LSCKGKEVENVFTIRTP DANRVVRLARGNVVVVAGFLGMEVAA YLTEKAHSVSVELEETPFRRFLGERVG RALMKMFENNRVKFYMQTEVSELRGQEG KLKEVVLKSSKVVRADV CVVGIGAVPAT GFLRQSGIGLDSRGFIPVNKMMQTNVPG VFAAGDAVTFPLAWNNRKVNIPHWQMA HAQGRVAAQNMLAQEAEMSTVPYLWTAM FGKSLRYAGYGEFGDDV I IQGDLEELKF VAFYTKGDEVIAVASMNYDPIVSKVAEV LASGRAIRKREVELFVLHSKTGDMSWLT GKGS
9516	23417	A	9585	360	239	QCRKGLGKLV SFGLGIWSLIDVLLIGV GYVGPVHGSSYV
9517	23418	A	9586	160	1156	MPRLTFAPKGPWHPPTSLHPGQVTDQTT WWLFQBLPTPSENSMPPGLSTPTASQEG AGVPDPSPQPTRRQIRLSSPERQRLSSL NLTPDPMEPPPKPPRSCSALARHALES SFVGWGLPVQSPQALVAMEKEKES PFS SEEEEDVPLDSDVEQALQTFAKTSGTM NNYPTWRRLLRRAKEEMKRFCKAQTI QRRLENEAALRELEAGVKLELALRRQ SSSPEQQKLLWVGQLQLV DKKNSLVAE EAEIMITVQELNLEEKQWQLDQBLRGYM NREENLKTAAADQAEQVLRKLVLDLVNQ

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						RDALIRFQEEERRLSELALGTGAQG
9518	23419	A	9587	419	130	RRDPHLPRIMGRTRLNRKNAETRINAQL PLTDKGRMARHVLDNSGEWVTKRQVIL LHTELESLLEYLPLRCGVLTGLAIALSL LYMLTHYLLPYA
9519	23420	A	9588	2	399	FSCEFNMENQCPLVVEPSYPDLVINVG EVTLGEEENRKLQKIQRDQEKERMRAA CALLNSGGGVIRMAKKVEHPVEMGLDLE QSLRELIQSSDLQAFFETKQGRCFYIF VKSWSSGPFPEDRSVKPRHV
9520	23421	A	9589	19	205	LYCLVEWHDLCSLQPLSPGFRQFSCILNL LSSWDYRHMPPRPTIKLSSYSSIKLIYY LFMLVL
9521	23422	A	9590	500	407	KLTVNEVRSVKRSQLPESFMCKEKLNT NII
9522	23423	A	9591	727	236	RRSRGLEGREALALCPDGGSHLLCRRTD SSFSFMAFFFTFMAQLVISTIQAAGIPG WGVCGWIATISFFGTNIGSAVVMILPTV MFTVMAVFSFIALSMVHKFYRSGGSFS KAQEEWTTGAWKNPHVQQAQAAMGAA QGAMNQPTQYSATPNYTSNEM
9523	23424	A	9592	381	278	HPSVYKVASGLKEGLSLFGILNRCHCKW GEKLLR
9524	23425	A	9593	412	156	SQRCLSLGCHEHLANAYATIIICDNGFSA LLGPPLPGWIYDIAQKYDFSFYICGLLY MIGILFLLIQPCIRIIEQSRKRYMDGAH V
9525	23426	A	9594	263	50	KHAAPPASLSLSLLHHGQKRACFPFAF CRDCQLEGSPAMLPVQPAKLLVLVBQV CLLCALLIPPSGSRI
9526	23427	A	9595	432	309	GTFSERGPPLEPRSQVTVDVFCQEMTDK CTTDEQPRKDYT
9527	23428	A	9596	457	29	TLLPGWITAQASEGEIGASLPSSLPPLL YLPWSRCSPSGALTHEACPTGQRSSSA LLPSLPQAPPFGCGMTGLRPLPSPSVGC CSAPSQLLCPTQLPPAPESSEGGCSES RCVANVKYTRDLGDFLEKCTNGEASALE YP
9528	23429	A	9597	864	407	PSRRLSPTGRTHGSSAACAPPPRLER RSRTSRPPWGPPhASARTQRACTWYS RSWACSCSWITSRPSWMTTKRTCMIFST IPTTPRTALWRGLSLWKDAWLLTRLKLA PSSPTSMPTTTCTACSSWTWTCGSPAR WASTPMPSSTT
9529	23430	A	9598	421	145	LTQHNGDAAASLTVAEQYVSAFSLAKD PNTILPSNPGDVTSMVAQAMGVYGALT KAPVPGTPDSLSSGSSRDVQGTASLDE ELDRVKMS
9530	23431	A	9599	1013	604	PGRPTRPDICLLERMEEQVKNVMKTPR EELYNIEKAFAEVERQELLASNKKWEQA LQAHNAKELEYLNNRMKKVEDYERQLNR QRIWDCEEYNNIKIKLEQDVQILEQQLQ QRKAIYQLNQEKLEYNLAGEEER
9531	23432	A	9600	409	191	HHVGQAGLELMTSSDLPSLASQAGITG VSHCARTVYGLSIVFSSHRGFASVRTP PSNENFPDRPISIAHP
9532	23433	A	9601	367	1	PPRYSPLGGVRRGGVPPGPGVLAPPPFK GKPPFFFKNPNLPRPGGAPYSPFFGGV

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						GRGISFNPGGQGSFGQKKPPGPPRRGTG GFFSKKKKKKSTKLPVTSHTTTCWFLPE ALDLELDPLY
9533	23434	A	9602	1722	394	GWNGSWNDNLVDTSPDKRDLQDICRRY MEDLKKICFYRELNSKTTLKVFHTSFHG VGHDYVQLAFKVFQKPPIPVPEQKDPD PDFSTVKCPNPEEGESVLESLRLAEKE NARVVLATPDADRLAAELQENGCKWV FTGNELAAALFGWMMFDCWKKNSRNADV KNVYMLATTVSSKILKALKEGFHFEE TLPGFKWIGSRIIDLLENGKEVLPAFEE SIGFLCGTSVLDKDGVSAAVVVAEMASY LETMNTLKQQLVKVYRKYGYHISKTSY FLCYEPPTIKSIFERLRNFDSPKEYPKP CGTFAILHVRDVTGYSQPNKKSVLV VSKNSQMITFTFQNGCVATLRTSGTEPK IKYYAEMCASPDQSDTALLEBELKKLID ALIENFLQPSKNGTSGRSCLGVPPNTV MTLCGAYGNRATRRNCHTLEPCG
9534	23435	A	9603	14	356	DFVERTQYTHQTHTHTSHAVRLSPRP VQSRPEASQTGPTRTKPALGPAHPSPRG APCPDDPGSLRMLGYGSRASHNSRRGRW GHGRCKDQRAMGPHSHMWEALPPGALS SP
9535	23436	A	9604	477	264	LVETGFLCVGQAGLELLTSGDPPTSASQ SAGITGVSHRTWAALSTPTVLNHYHLYF LEVPHHPKLKLSPH
9536	23437	A	9605	1	378	EGINFSDNLRRCCVMVGMFPFNIRSAEL QEKMAYLDQTLPRAPGQAPPKALVENL CMKAVNQSIGRAIRHQDFASIVLLDQR YARPPVLAKLPWIRARVEVKATFGPAI AAVQKFHREKSASS
9537	23438	A	9606	417	254	MVSLTQELCPVAMRVAECHNKMLSNVAE RVTVPNFRIRGALLEQAGQDIQNKLE
9538	23439	A	9607	404	272	PPKELLESQPIRVVDWWSLGMALMYDMLT GAVGAQLKAACIIGLC
9539	23440	A	9608	409	205	HMNGSLGSGDIDGLPKNSLNNISGTSNP PGTPRDDGELGGNFLHSFQNDNYSPPSL PCSWSLFYSLPF
9540	23441	A	9609	449	263	VWICPCDPFASASQSAGITGLSHHLKPC WDYRLEPPRPAHCFCFYSFTMRNRNLLS LVKYSR
9541	23442	A	9610	366	75	TPGLKRSSCLSLMSRWGYRIEKKRTIIR SVVEAIKEQDGREVDWEYFYGLLFTSEN LNLVHIVCHKKTTTHKLTCDSSSIYYPQT RLKRRQPVVRKQ
9542	23443	A	9611	1	801	PGYCGSWVFTCGALRQLSGGRDLRSGAR MGNALRAHVETAQKTGVFQLKORGLTE FPADLQKLTSNLRITDLSNNKIESLPPL LIGKFTLLKSLSLNNKLTIVLPDEICNL KKLETLSLNNHRLRELPSFTGQLSALKT LSLSGNQLGALPPQLCSLRHLDVMDLSK NQIRSIIPDSVGEQVIELNLNQNISQI SVKISCCPRLKILRLEENCLLSMLPQS ILSDSQICLLAVEGNLFEIKKLELEBGY DKYMERFTATKKKFA
9543	23444	A	9612	179	329	KGLAFCPFPGRGGGPPPLWPPPPSYKK IFGLKTPKSGALSPPPPPPGNF

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9544	23445	A	9613	410	298	PRFTPFSCSLRSSWDYRCPFPPRANFL SLSSVLHGT
9545	23446	A	9614	1	130	NPGSHCVAQAGLQLLSSGNPSASASQSA RITGVSHCAWNTTI
9546	23447	A	9615	1	146	NTWRLHMVPRVSNFWAPGILLSWPPKI LGLQKRATTMEGPETITSIN
9547	23448	A	9616	552	26	RLSIRNLLTHAFFAEDTGLRVELAEEDD CSNSSLAIRLWVEDPKKLKGRKONEAI EFSFNLETDTPREAVAYEMVKSGFHESD CKAVAKSIRDRVTPIKKTRKKPAGCLK ERRDSQCKSMGNVFPQPQNTALPLAPAQ QTGAECATEVDQHVQRQLIQREPQOHC SSVTGDL
9548	23449	A	9617	420	48	FSQILRASVEFDSFPWDDISESAKDFIR HLLERDPQKRFTCCQALRHLWISGDTAF DRDILGVSVEQIRKNFARTHWRKRAFNT SFLRHIRKLGQIPEGEGASEQGMARHSH SGLRAGQPPKW
9549	23450	A	9618	190	285	RQGLTMLPWLVSNSWPQVVLPLWPLKVL GLQV
9550	23451	A	9619	392	308	SPIKPKIPLSAPRKNTNSVKYRLKFRFG
9551	23452	A	9620	166	23	FCNPIPSSLPSSLPSPFISPLPCPLTPF LPCPLPPLPFLSFMILTTF
9552	23453	A	9621	49	374	DRRGIRIMAAALFVPLGFSLLGTHGPGS AAGTVFTTA*YLGSKILLTCSLNDSATQ VTGHRWLKGRVVLKEDS\LFGRKPEFNV GPHPPNGDKSSFVFPFPPSPCPLTF
9553	23454	A	9622	85	472	SHVFPEPLRLTLTLHSMVBPETRPNTIY INNLDNKIKDELKKSLEYAIFSQPGHNL DILVSRILNMMGQAFVIPKEVSSATNSL RSMQGFPPFYDKPMRIQYAKTYSYIIAKN KGTFLLSC/DRKLIK*TPQ
9554	23455	A	9623	170	2	IFFFFCFERGSCTVA*AGVQWRSYSL* S*TPG\SSNTASATSVAGTIGL\HHAB
9555	23456	A	9624	2	469	RRLCSDRGLQRSLSGMSAAVTAGKLARA PADPGKAGVPGVAAPGAPAAAPPAKEIP EVLEDPSSRRRYVRGRFLQKGGFAKCFE ILDADTKKEEFAGKIVPKSLLKPYHR*K MFMEIFIHRSIGHQHVL*FHGYF*EHDF MSELEL\CRPRSLF
9556	23457	A	9625	661	1393	ASPPFSQTTAPAGCSAGEVSLA/GLCL QERRLVDVAGFSIFIPSRVLDHPQPSKA EQDASIPPGTHEALLQTALSPPPPTRP VSPQKAKEAPNTQAQPIDDEAS/RWG RNPG*CS*SGSPHQWPLPHLP*GRL*A* PSPCCPG*VG/FVHSPQARRRPITTSIS QRSWKFWPKPTVPRETSGGPWAMPSPSM PSRASISLSPRTSRKQPRPLTLGCCVW HVVHTDGERATCGDVRRRAHHSR
9557	23458	A	9626	1	286	PTMAKLIALTIMGELALFWNHQASYQT RLNALREVQPA*LPNCNLVKGF*TGSED F/EILPGLTFISSGLENPWI*RLDP/N SPGKMLLMDLNE
9558	23459	A	9627	173	491	EGPLPLESSSNWQADLDKKSRELLWKT VYLL*LNQLPYNPNVNPILGINPREHT C/HQEMCTRIFIATLFTKAKA*K*PRCP *AREW/IK*/IWNHIIIEHY
9559	23460	A	9628	351	1	VLGDAIQSRRGSSRKAGSYLLSRSP/CS

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						EGGRGGCWAANLGTMSVASGHGAWVPR ELTS*AWPEPGPAGQREGRPPTPCPPT CAHGPPAQF*PRGKAAYPG/CLGLQWPD *SAFNP
9560	23461	A	9629	599	11	KMWR**H*AKSQIRNAIPFTIAHK/RDL KSLKIQLTKEAKDIYNENYKIPL/NBIR DVTNKNKNIP\CS*IGVLYSTYKYKCTC LVNIYL
9561	23462	A	9630	226	1	KCDNLGYSTFFFFFPFFFEIGSYFVA QVGV*WHNYSNS/DASAFQVAGTTGVCH HAQLIFNLFVEVGSHYVAQA
9562	23463	A	9631	241	1	VSGCPLPRG*RPPQPQSPPTPGTSD HPCTPCR/PALRR*SP**LPCLDLPPAS GPPSTSGNSTGTMTQT*PKLNSSSS
9563	23464	A	9632	201	1027	MTLTPAPGQQQSSQCLWRRPL/PLPPG PDSEEPGSGAAG/PGSSL*SPDLPPAAP PKP*TSS*EMNTVGSTQEGSGLAQRITQ HCPVPPST/RVDILGTCLQPPALCLTS APWLVRMPSPQRSSREIP*RLEAF/SLR TPIFAHSAQPSHQEKEP/PSPR*DHGD* PPP*PPKPTHQTLAQAPRSGQGLARPT LPYPPSPLRVTPRI CRVHV*GHLRRPRG PPSSARRPTWDRVGLPWEDLEVLCR GPAWLLARTSAPFSSLPHTACTGKKITM PF
9564	23465	A	9633	103	379	YHCITIIVLKCIFFFFFLKPCILISPRL EARGIILGH*NLCLT\SQLRLIRKSP LTLEGGVCS DPRSPHCSPAWPTKGNFFS KGKKKILD
9565	23466	A	9634	155	405	VPAFRSVTNISISVSFFFFFETEPGFVTQ AEMQGLDIGNQPPCPKLSSFA*ASQVM GTTGPRH/HC*ALIFLVKTGFPHVAKTW F
9566	23467	A	9635	4	423	GAMRGDRRCRGRGFRGSRGGPRGRFRPF VPHIPLDFYLCMAFPRVKPAPDETSFS EALLNRNQDLDPNSGEQASILSLVTMT YEIDNLTVAPGTLVDLIEERQGGPYIK GTMTT*RH/SVADLTVLILQILTTWESVA S
9567	23468	A	9637	2	492	GSRAIGFGLAHLERHLIKIWLASIVR* DLA*LMNWSG\SHKDLAGKYRPILEKAI QLSGSBQLQAFKAFESMVNENVS LVIS RQMLTDFCTHLPNLPDSTVKEIYHFTLE KIQPIVISFEEQVASIRQHFASIYEKKE DWRNAAQVLVGIP*TGQKQYNVDYKLE TYLKIARLYLEDDDPVPAY
9568	23469	A	9638	1	417	VVQGLGLVMGSPSRRLQTKPVITCFKSV LLIYTFIFWITGVILLADGIWGVSLN YFSLKDKATIVPFI\LIASGSAIILFG ILLCIFSV*HYVPV*LLLVTFI*LLVFL NKWWISPHFLITFNLYLLFDIIDNSS
9569	23470	A	9639	125	451	IYRKPLKSIRRVGGLHLNKFPPFLKQI WGWARGLMPC*HFGRLLKGDCLTLGIGD /SRG/RDHPALQPRQSKTILSLKINK IGWAQWLMPGIPAPWEG*AGRSFGAGI
9570	23471	A	9640	670	927	GHVLLPRRAGCAQPGTGPARAAPAQVR LPGGGVQPSGPGGRAGQGGRLRGT*AGG NPGTGF/GGPHASALLPSEAPGSLPS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						QER
9571	23472	A	9641	115	460	TSWIFLIICVGFPGGGGARVPLCHLSP RLECSSAIRARCGDFPGSSDP*ASAS* VAGTT/G/SCHHVQLIF
9572	23473	A	9642	1	431	AMRAEVLVYCCRGALASGCVAFRARY\ WVLIIVDVPDNEQANASIIVKLTDSFTE QADQLTAEVGKLLGE*KVDAILCVAGGW AWGNAKFKSLFKNCMLMRKQSIWTWTF SHLATMHLKEGGLTLAVAMAVLDGTPG MIGD
9573	23474	A	9643	154	408	IIMNAQSVEEDSILIIPTPDEEEKILRV KL*EDSDGKYGSKIWNHLPENFRLL FKHVGILD*SGLY\EILTKF*ILCVLCY Y
9574	23475	A	9644	3	403	YSQFFGGPKLEDPIRPGVFSQGEHRGH PFQIF*KVGLNGARGPFPVLGKVKCKD NLKLGQGGCSRVEMHPTSAWAIEDPV LKKKKRQR\BHQCSNEQKHTN
9575	23476	A	9646	3	399	ARAMVLSPADKTNKGAAWGVGAHAGEY GAELERMFLCFLTTKTYFFHFDLSHGS AQVKGHGKKGADSLTNAVAHVDDMPSAL VALSDLHAHKLVEGPNCKLLRH*LLVT LGG\HFPWLTPGGIAFLEKF
9576	23477	A	9647	22	407	APSAWGMCHFTEDKATITSLWGKV\NV EDAGETLGRLLVVYPWTQRFSDSGNL SCASAIMGIPKVKAHGKKALTSGLDAI* HLDDL*GTFALQSELHCDKLHVPDENFK LLGNVLVTVLAIHFKE
9577	23478	A	9648	243	2	QIATTTLPGSGEGVGRDLGSSSRHSQ VESVKH\PRDLAQDA*GHGSAPRPLCPP PAQSWHCLRGPCLAHPHTLCEPSR
9578	23479	A	9649	283	196	SYFI*IIITTHSLI\ISIIPLFFNQIN NNLFCSPPTFSSDPLTTPLLILT*LLP LTIMASQRHLSSEPLSRKKLYLSILISL QISLIITFTATELIIFYIFETTLIPTL AIITR*GKPTPLIQ
9579	23480	A	9650	10	354	QLRVITRLTVNN*TSA*SRGVSY*AH \SSDALHL*RELTEQRFIVSVNCAIAHC RHQSASEDHVKLRNEVTEFAQTWDADES AENCDKSLHTLFGDKICTVATLRFTYGE MAD
9580	23481	A	9651	2	404	AFGTTKWVTYISVLFCLSSAYSRGVRL DAHKSEAAHRFKDLGEENFKALALIAFA QYLQCCPF\EDHVDLVNEVTEFAKTCVA DESAENWDKI\LHTLFGY*LCVACFRE T\YGETAAC*AKHEPVEDE\CFLR
9581	23482	A	9652	83	396	NIPGVGGGVPIPLVWKYNISHTQR*RE PYIQLRSGNWSERMHVAR*QRHHP YYI\LLQAQLSMA\SDPANVMDSVITA GVLVA/SRRARRISKLGHRI
9582	23483	A	9653	67	954	REGNHNTERNCRRPQDTGPTQ/RPGPP PPEVPWQDASSAPTAAAPVGKLLPS*G PPGSASCQGR*TLGSVHWL*GSPPLSPS AGGRALPYGPAQGGSQGHWENTGRGTPL PGSRET*GHELTGVEHQHKAPEPQA GQPRLCPPWQSLPPT\ARSPSWSQGERP
9583	23484	A	9654	1	252	RPPQLLASDSLPPSRPPSPFPPSLLSLR PPLSRSLCLSHYLCPLSLIQLTSFPD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TFSPKSTTSGPPQPEDSPSS*PPTPSP P\PPSLSSLPSSLSSAPPF/YHVSVP TISAPLYP*YNS*PHFPFPFPRKQVHL ARPSKPTAREPWTIRRI
9584	23485	A	9655	1	394	SLRTYCFVIEVICFLYL/FIMYSIS*G I*LLMNFTILCIGY*LLQYFFVVKSP YFNFIPIFILFLYLICLLVF*LIFFDL SYF/MCLRLIIFNLFY*LFLLYSICLWN MVLILISKLF*F*FCGRFALIQ
9585	23486	A	9656	122	371	SPYLLLLQGGVSWIVWLLNVESTNSSPL FPETGSHCAVQGGVQWCGRGLSQS*TPG /SQS*VAGITGMCHHAS*LEKFFVEMG
9586	23487	A	9657	425	3	KTSMMNSIVPHISITPLNVNGLNVPLKR YRIAB*IKIHQPSICCLQETHPTKDSH KLKVKWE*IFHANG/QGVAILISDK/T DFKATTVK/RDKEGHYIIKGLVQQENV TVLNLCAPIGTALKFKIK\QLLLDLRNEI NANT
9587	23488	A	9658	179	373	VESWLLWGSQSFLFRPLTD*MRLTH/I MKGNNLESKSTSLSVNLQKHPHRNIQN V/AQNIWVSWNS
9588	23489	A	9659	103	373	LKHVLRCLQSERKLHYLFNIDQWGFY TWDDLYECISSKFTTHFFSFL/FFSF* SQGLALSPRLDCSDAILAHCEFLGSS HAPTSAS
9589	23490	A	9660	216	424	TDINVTTTKTIKPLDENIGITLYDLGLGS GFLDMT*T/AQVANEKIG*WDFIRNLKL TCIGHYHEVKKTNPW
9590	23491	A	9661	276	2	PRIGKLPTNMIEPLIIEKMLINLAMRPH LSPVRMAI/IKIKSNRCW*GCREKGI\ IYHYWWECKLVQPL/WKSSLK/FIK*LP IDLSPVPAIPLL
9591	23492	A	9662	239	356	ICIKRRK/WSGTVAHTCNPSSLGGQGGGR IA*VQEFQPGQQ
9592	23493	A	9663	1	340	RHEMLTPHAFGAMKRVTFISLLFLFNLA YSRGVISRDAHRSEDAHPIDLV*ETPK ALVMIAFAQHLQQRPFEDHV*LLNE\VT EFARTCVAESSAENCDKSLHTLFGDK*C TV
9593	23494	A	9664	759	1039	KRIPFGRPRRVDHLRSGVRDQPGHDET PS\LKIQKLAGGGICL*SOLLRLR*E NHLNPGSRGCSEPRSCHCTPAWATE*DS ISKKNKTKIS
9594	23495	A	9665	1	355	ITDLYSMFHFG*VDLATITSLWKGNEQ KAGR*TLERLLDVYPWTHRFDSFGNLT SASAIMGNPIVKAHGKRVLTSLGDAMH LDD/LKGTFAQLSELHCDTLHVDPENFH ENPCDGS
9595	23496	A	9666	364	3	APNIPPSVTRIPALLAFRSQCLGSCPL PLATEPVGLLLSMSFQAAPCFTWWVTEA WLTGISWPPDFLISLLCI/HINYNAVIF RKYRPRVGAVAHICNPSTLGG*GGWIA* AQEFETSLGN
9596	23497	A	9667	1	357	PISNAMRHLGQETATITSLWGVNVVD AG*ETLGRLLVIYPWTHRLFDSFGNLS ASAIMGNP*V\KAHVKKALTSLGDAIKH LDDLKGTFAQLIELHCDKLFVDPENFKL LGNVLAT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9597	23498	A	9668	24	369	APRPDAMGHFTEEDKATITSLWGKGNVE DAGGETLARLLGVYPWTQRLFDSFGNLS SASAIMGNPKVKAHGKKVLTSLGDAI*H LDDLKGTFAQ\LSELH*DKLHVDPENFK LLGK
9598	23499	A	9669	12	365	LLLMGGERK*FLETDSAPCEDAMNTVEM TTKNLE* SINLVDKAVA/SGFERIGFNF EKSSTLGKMPSNSIACCRIFHERKS/S MWQTSFLSYFKLRQA/PPAATTLNDHQ PSALRQDPSP
9599	23500	A	9670	346	2	YFYDPSWLSLNNMFFLFKRPQNFLLKEGT LTFPFKGFGRDLSLFFWPPYKLFNLKSF L/CKFLEI*RYFFG*IIFFFPFFFFFL RQSLTLSPRLECNGTISAHCNLCPLD*S NSP
9600	23501	A	9671	121	364	HKKKTAGRVQWPLLVIIPALWEAKEADCL SSGVQGGQPGQHSKTPSLP*PSKSWDYRC TPPHLASFCNFFSFFFGRDGVLLCCPGW P*TPELKQSA/CLGLPKWDY/RARATA PGLLFF\FMLKYVLVKPAVNIANAN*KE LSEPDVKNEICFV
9601	23502	A	9672	437	223	EME/FSLLLPGLECNCTCLAH*NLRLLG SSDFPASASPVAGITGVRLHAQLELYFL NLLGFFFIISLVVYLS
9602	23503	A	9673	100	338	KSRPSAVANLTPVIPALWEAEAGGSPEL KQFSLSLSSRDHRFATPC/RG*FFIFF VEMEFHCVAQCGFELLDSSSPPTSA
9603	23504	A	9674	161	1	SFLWKLCRLRGAPSCMRQOLA\LL*DVSQ LGY/SGVRDPLEEAVCFPSDLKLRAGR
9604	23505	A	9675	304	1	VPPLASQLGDKRRIFQKKKKKKKNKDK IHIIISIIILKKFDKI*YSLIIK\TL*KL GME*TYLNI IKVIYDRPTASIIISGEKL KSFPLKSGR*QECPLL
9605	23506	A	9676	111	346	SKEGSKEGSLEIWGFLVLAFFPPFPFPF SFFFF*RQAGRPRLECRSMITAHCNLE LLGSSDPPASAS\QVAGTTGPTSP
9606	23507	A	9677	3	349	ARAGRIIKDLWLGFPPPPPPFPYKKTPL PTRDKGGGKLQTAKKNPHFPVKREKKP PPGTRGGKNPPGNPFWGFGPQRFPPGG KTFGGGAHPDPTLG/PSPQS*KRPF GK RGPPF
9607	23508	A	9678	38	368	QASLLKESESERKSPTSLTSLQKLG MIR LCEGMSKAKAD*RLGLLH/QVSQLVNT KEKLFKEIKSAISVNTLMIRK/RNSLTA DMDKVVVAVIEDLSSQNNPLSQSLIHSK A
9608	23509	A	9679	187	345	PFILFFETESYSA*AEQWCDLGS LQT PPPG\SSNPPVSALWEARAGGSR SQ
9609	23510	A	9680	192	468	ERTSLFTIHLKLLTITNSAAMSNH*V FV*T*IFLSLGQMPKSVTAGSNGQSLFR FFK\NCQTLFHGGCAMLH/SHTQLNAIP LFRNLWQHLS
9610	23511	A	9681	141	367	GSWAASPCSCCTMDFAKESFTVVDYVLL ENCPNMGDYVVAPQFMTDNYVRVTQLNW DVGVTQ*KDYI/SSERNL
9611	23512	A	9682	193	3	IFGERR*ILKIYKLTGHVGLRL*SQILR RI/RLNLGGGGCSEPRSCHCTFVWATER DSISEKKEK

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9612	23513	A	9683	1900	1988	NLVHFEHFPSPSLCHIF/CSRD RVSPY*PGWSRSPDL/RYP/CLDLPKC WDYRRESPCPASSRFLNPLYF*NTTLW Q*KTIPLLF*SGDC/S*FF*YNFLAHTS STMVNSGISRNSRPVFKLADKAPSHSPL SILAFGVVEFF/NLGSLLQPLK*ASH LNCLSSWDNRHAPPCPDNFFFNIL*RWG FPILSRMVLNSW/PLCSLSTSAQSSG/ ITGVSHCAGPILVF
9613	23514	A	9684	69	358	ILIVKVFFPHTQKPNFVLRSLQSIQOM LLPBRKWTHAQKTCVSSENTERCHEKQV ITSHWLGMAHSCNPSTLGGGGWIT*G QVFET/SLANTVKP
9614	23515	A	9685	66	344	IGEKLLTLDKHRNWVLETE*APGKDSVN IDEMT/TR/DLEYIIN/TDKAVTGFBRT DFNFKSSIRGQSL*YSII/CAKGSQKQ QISLVPIPKLPQ
9615	23516	A	9686	269	1	PKIQNGHCKTLPKNPSQSDTKTFPLFTS GSSPQPHKLSFCFSAGPTLPSKTQLKIH L/WQGTVPVHAYNPSTLGSRRGRIT*GQE FKTIQ
9616	23517	A	9687	229	361	DRYYKSHFKPGAHAHAC*LVLASFFMC YRAIMINK*HLYHRKL/VYQVIRH*KYR D/I*THVTLTTTL*DRYYKSHFKPGA AHACNPSNLGG*GG*II*GQEFKTS LANMA
9617	23518	A	9688	318	46	KLYALNDMASNTCKEYDNLQYYRYKIY KRLIQHD*VEPIPEME/NWPN*/RKS I NVIHYIHSLEWERNYMIISLDVADVSDK IKLTFILF
9618	23519	A	9689	168	3	GNSNTMIFFTILYLFLLYFF/LFFIFDM KSHSVARLECSGVILAHCVN*LPGSSNS P
9619	23520	A	9690	192	3	WHKASLSNPQAGCMQPRMALHEAQHTF VNFLKTLWAG/PVAHAYNPNTLRGRGR IT*GQEFK
9620	23521	A	9691	388	1	CRSAGVCWRSTPDPVCLGITSSGCRTAE IVACSFLLWKLHSGAPARCQPELSCMRC /R*TLL*GVSQSGGTGVRDPLKEAVCPL AELENGARRSTALFRASRQDSLKLLKLR PQLPILPGALSQIEGI
9621	23522	A	9692	226	3	WFLLPQVKLAIMTPRLYPNLPFFFF* DRV/CTVAQAGVQWRDLSSLLSLLGSS SSPTSASRLTGTIILQEHAE
9622	23523	A	9693	305	1	NHAITTVN*FGLIRHLVTKAFNSGEVD IV/SIKDPLIALNYTVMFHHDSTHGKF RGTVK
9623	23524	A	9694	320	1	PRDPPASASQSAGITGISHQAWPDMILY IENPKDSSKNPLGLINKYSKVAGYKINT QKSAFL*TNNYLNK*P/MRTIPFTIAT KKKYLETYLTMEVKDLYTENYKM
9624	23525	A	9695	263	1	VRILLFSESLALSPRLCSGVISAHCTL CLPGSRGALSLLSRVDY/Y*VFLVKAGF RHV/GQAGLEFLSSGDPVPSLPDFWDY RCKFR
9625	23526	A	9696	262	359	IRKIHKIWSGVVAHTCNPSTLGGR*TKA HEGSLYCLRVGKIVSNKVGTR*FFRTQ K*V/HLFPS*VYHINGS*SRISL*IRK

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						IHKIWSGVVAHTCNPSTLGGRVGWIT*GQ
9626	23527	A	9697	166	473	TQDTSQPWKNIWISFGSLKVFENVDIHK LYLELDNRHRSWMTDILFFYYF*DGSFT VT\RLECNAGAILAHCNLHLPSSNSPAS AS*VAEVGGTLEPRRLRLQ
9627	23528	A	9698	456	59	LPLWKLHLRGAPGVVRCRLA\LLGASQ LGYSQVRDPLEEAVCPFSDKLHAGRTT TLFKAVRYGHLCLQKFLPFVRLCPAPT GGVFTVRQASMSCDGLLIV*\VSERH*L PKPQQFWELVPKFRPGLKSL
9628	23529	A	9699	4	375	VFCSSVTIVSEIAFLMWLSAQLLVYRN ASDFCMSSLYPETSLSLTKVTQGOAL/H*N G*LT**EQYWKTDQKAVI/CQSTGSS GQSSQAREIKGPGAVAHTCNPSTLGGRG RWIT*GQEFETSLA
9629	23530	A	9700	239	361	RNDTFFFFFTESNSVA\RLQCTGVTLAH *NLCLPGSSNSPA
9630	23531	A	9701	169	1	IFYWKAIFPETESHVSAYAGVQ*SNLGS LQLPSS\GSSDSPISASQEAQTTDAHH
9631	23532	A	9702	37	348	HAKNFDVSLPYTKTHEHFVKEDIWIAN KHVKRCSATLVTKETPPQS/TLKWLKH* PPC*QNGRTGSPIC/C/WWECKIVQLW KIV*PFPPKLSIYL/PY/DPPIILLGI
9632	23533	A	9703	16	339	ARLNTFAMAAC*SERKS/RN/SLTLNH KLQMIKLEEGMLKAVNGQKRLRLYQ/T SQFANAKDELLMDIISATPATV*MIG*Q NSLIADLEKVRVV*LDDQ/TSHNIHLSH
9633	23534	A	9704	276	2	GISRGGLSKPPFFP*DFPLDYLQSPFC KVKRNS/RFRTTKSPLDFFIPPLFFFFF EKVQQAISAHCKLHLP*CHSPASASRV AGTTGTRH
9634	23535	A	9705	352	2	CNSRSDFFQLMMNCFLRWAVSPRVECS/ GVITAHCNLNPDSVDPPTSTS*VAGTT GHTP\HTWLIIIIIIVAGIFLFFFLFS FFGRDGVSPCCPSWSQTSEFRQSACLSL PKCWDY
9635	23536	A	9706	6	351	IWNSRRRPLGGQGGRIQDWPKLHGKTR SL/LKKLQKLARRGRASLSQVLKRLRL TWVDCLSLGG*GCSQP*SH/IHCSPAN
9636	23537	A	9707	76	359	CFLFVCLDFVIFLAYFCN*YLPFPLISH TFFFFLKKGLIFAPGVNLRDQNKFYFTL FDVFFNIYYC*IFFIF/CLVLLPFIFFF FFYCFVMRFIVL
9637	23538	A	9708	342	3	GEELLLMDEQSKWFLE\TPGENATNIVD LTTKOLEYSISVVDKAAAGFBRIGSN*N STLELKTVN/SVPHAR*IFCKRLQSVWQ TSLLPILRN/LP*SPHPLVSAMLIQQS STLK
9638	23539	A	9709	211	350	RQDIALLPRL*SGTITTH/CDPQLSGS SEPPTSASLVAGITGACHYV
9639	23540	A	9710	253	3	VKCFSRHMLIRRSAGGKKHIEKGTLI MSFWVVVVSQSEH/NLCNHAY*SHIKK VWLGTADVYNPSTLGGQGGRT*GQEE E
9640	23541	A	9711	80	324	LITLTMAASMCSNERKSHTSLTSNQLEM SKPTEEGMLKAKTS*KLGLFHQT/SQLV KTKKKFLEEIKSTIPLNAPLMRK*NSL

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9641	23542	A	9712	246	3	QLAKHGLLFFLFFEMGSH*LRLECSL\TALLSKISAHCNLNLPGP\SDPPTSASQVAGTTGACLLAQLIFKNFVVETGSHYVA
9642	23543	A	9713	2	359	AAASTTIKEQDMLKFYFLFYFFETESHPTQVGQVQWCNLCSLQPPPP\GPSDSPAWVTEQDSVSKE*KRKLLIKINVVLQVTTTHP*HSPQHIVRVLVSLN*LNEKINRRVTKSSSKEKDR
9643	23544	A	9714	278	53	KLFRGLNNHRKFQTRCGGLFFFLFYF*DGA/YALSLLCSCGTIMAHHSLDILGSSHPPIASASLAA\GVVRTCSFSC
9644	23545	A	9715	166	402	TLSLKKENISRAWHVPVVSQWKAEBAR*SLVPRSLRL\HCTPAWA
9645	23546	A	9716	168	1	VDCIIMRRSIKSPRRKCRGTISARCKRLSG\SGHSPASAS*EAGVTGVGHDP
9646	23547	A	9717	1	553	TSIRLFFLLSIFFFSRARNRILPKIYCN GVRAGKRGCGGWGTCRGHNTMTWGPQLLLSWGRGMKRQDQGSWGGRGEGDTGCI PPPPGSTSRPWTSPRSPWPLRLHLFASGPPGSSSCSP*LFPLTDSQVGRCSGPDPNPPYHLMKVQPLPALLLPILKPHRFPSLGQ\PDPPSSPPSP
9647	23548	A	9718	13	364	PPNR*RNPLIELTNHSLIYLPTPS\GIS A**NFGSLGACILQITTLGLFLAMHYSPIRLQLAFSSIAHITRDVNYG*IIRYLHANGASIFFICLFLHIGRGLYGSFLYSQT*NGIILLLAT
9648	23549	A	9719	82	351	GEALEPELMPALSH/HAATLLAPLPTT PFVGTKVTIVGQAW/HQAL*SQHFERP RRVDYLHLFSRNGQNPISTENRISWAWWRVPVIPA
9649	23550	A	9720	179	365	FSLPLASLKAQIIDSKPPFSNTLENI*K YEVINFFLYI\IKLHFMNLTSLCFYCHSVCTILL
9650	23551	A	9721	2	320	PIPPGNESSPPTAQEDMQAANKH/IRRYSTSLAIRET/QL/KTTTREPYPATMAT TETSANTTCWREYGESGYSYCWGCKTLR PLCKTVWQFLKKPSM*LAYDPAITLF
9651	23552	A	9722	1	344	PLPTQNWPGQSFLHYFVLLPAVSVLWS SFFFFFWKQILLPRLLEG/NGQNSG*WKFPLPGPSLFCPSFQTSNGYGPQQAR AIFWKFKIKTGPHGVTRGLNFLTSGSAPLGS
9652	23553	A	9723	156	3	VTEAYFILFYFETESHVS*WHDLSGLKS PPPG\SSNSPASASQVAGTTGALH
9653	23554	A	9724	76	337	YLSIYLSIYLAIYVSIYLYPIYHPSISI YVSSIYSINHLPLYFYFSTHLSSTHSSIY LLSISILSINYLLSISLSIYLSI*LSI YDSSIHLSHLSHLYIYLI*YLSIYLSI YLAIYVSI\TIYLSIHLSLSMYHLFIL SIIYLCIIFLPIY/LSTHSSIYLLSISI LSINY/HTSIYLSIYLFVY/HLIYHPT
9654	23555	A	9725	249	436	ELAG*IQDHP/GQHHKTLGLQIKNLAR RGGRHL*SELFRLRQEDHLTPGVRGCSE L*SHHSTP
9655	23556	A	9726	177	3	HLN**FSNLFFETESPSVT\RGIIISAH RNRLPGSSDSPTSASRVAGTTDT
9656	23557	A	9727	272	233	RKNQRIYQIARKRLNEMARISPLRSMII

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						LNVSGLNFPLKRCRLAEWTEKKK\DPIT CCL/QKTHFTG/KDIYRLKIKGWKKIFH ANGSO*Q
9657	23558	A	9728	368	380	RKGQRISLAIKRLNKMARISPLISIIY LNVSGLNFPLKRYRRAEWTEKKK\DPIT CCL/QKTHFTG/KDIYRLKIKGWKKIFH TNGSO*RR
9658	23559	A	9729	294	2	KGNLSPKKNLKNPKVTPQNFGLKDQK TQGPRTLKVSQNKQKPKFK*NLKGRPL KLFPKKKLNPSRSWFYKKKK\INKLD GTLVRQINKKRNQ
9659	23560	A	9730	7	284	SQGLRLRRENYL*FETESHVARTGVQ WRNLSSLQSPPPG\SSNSPASASQVPVI T
9660	23561	A	9731	1	322	RSLLKKRREKKGNQPGQHGKTLFLPK TPKI*KIKKIYPG/RGGTHLSQLLRNL RKENHLNSGGKGCNDPKLGHCI PAQMTK TPFKKGGAKQNGKLLQLIYGK
9661	23562	A	9732	168	2	GFYRKSLCSLVWICFKDFFFFFEMVSR SVA*AGVQWHDLGSMRPPPPG\SGDCPA
9662	23563	A	9733	43	317	LKLPDRDTHCIWLSTTSPFIYFFETES CSVAQA*MQWHDLSLQPPSPG\SGDSP ASACTGMHHHTWLMKCSNFDVPMPL GLGLNSHI
9663	23564	A	9734	8	296	NVVSACSLNGLVKGRSLCLTLNQIL*MT LTTTERFLKAERGQKLGLLHQT/QVNV /AKEIFLNEVSSATPVYEGII RKLNSLI ATMEKACVVWIEDQT
9664	23565	A	9735	3	300	TRPSNSPAALSKCSRRRT/R/TCLTLN QKLEMIKLSKEGILKARGQKLGLLHQT A/QVNV/AKEKFLKEVRSATPVYEGII R KQNSLIANMEKA*VVWIEDQ
9665	23566	A	9736	352	1	PPFYLLNFPPTFFKGPPLIHFFLESFLEN FGFQGAFFKLQNFFAFLSLNPGFLEN PFYFKFPINC\KFLGNTFYCPVLGFF* RSFFFFFFFFFFETESRPVA\RLCSGAIS AHCKLG
9666	23567	A	9737	130	3	KIFFFFFFFFFLRQSLVAQAGVQWC/N* LGSLOPPAGLKRFLV
9667	23568	A	9738	167	3	ISRSVFCFFETESCSVTQV*EQWRNIG SRRPQP\GSSNYCASACRVAREFTGLV
9668	23569	A	9739	140	419	INVKLSRHFFKGNIQSPNKRKAIREI QIS*TDNNKW*GCGEVQYFIHCCMCB MVHSLWKIVW*LLTGL/HIELSDDPAIL LGGIPPEEMKT
9669	23570	A	9740	93	371	KLCNGYYQESKREPTERN*IFANHKTG CISKTYKELQLNNKNS/NPTQKWKDLD ISPQTMKQTAKNQVKRCSTSLVIREMQI YTKSIPLHIH
9670	23571	A	9741	1	288	GTRDHLRSGVRDQ\PGQHGETRSLKIQ N*GCGHGGSCLSQ\LTWRLRQVNCLS
9671	23572	A	9742	296	563	FIKHLNSYMLGQNLATKLSBICKLPFYI EK*IQAGYGGTCL*SOLLRLRHDNCLN LGGGGCSEPKI\HCCTPAWATDGGSVSK KKKSR
9672	23573	A	9743	32	400	DALVPHWSSYPICLDLNLVGLIYLFSDR VSLLVPRLECSDAIMAHSLDLPRLR*S SHLSLPRNWLMEVILVETGFCHVA*DGR

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						KLLGSSNPALA/FLKC/WRNMRKSQL* PLLLGLLSADHSD
9673	23574	A	9744	60	356	HSEVDSIIIPILQGRKQISEVRFORMCE REGGLFISSETLLFLCPAPSCS/HFLTPA Q*SYF*KNVSWLGAUGDTCPNPSLGGRG GWI\RGQBIKTILANMV
9674	23575	A	9745	2	446	PMVNKHVKRCSASLVIRAEQIKTIMRSH CTPNS*M*KTDNTKSW/*GCGATGTPIH C/WMKYKMWQPLWKKAAQOFL/KHIHLPY DPINLLGIS*EK*NHLC/YKKTYYVRI* IAALF
9675	23576	A	9746	257	1	VWLRLSFPSFLLPILSPSSQGDVCCFL MVF*RDGVSLPI PAGVQWLDRSSL*P/P SPGSSSPASAS*VAGTTGMHLHAEPYA SC
9676	23577	A	9747	148	3	IKLCEQFHK*TIHVLNHK/L/WPGMVAH AYNPSTLGGRGWIT*QGEFDC
9677	23578	A	9748	769	1	YPQLFKIAKKKKSNVPIKSIMVSQYGH *ENKKWVLNHKGATLQ/EGKGNFGDTFK VTLKDKIAVAVKTRQERLPQELKLFLL EAKILKQYNHPSNVKSIGVHTQRRPIYV IKELVPGGDFLSFQRKKNELKLVKFSI DADSGWCISKKCIHRDLAVRNCL/VGE NNVLKISDFGMSRQEDGGVYSSSDLKQI PIKWTAPALNYGRYHSESDARSFGILL WETFGLG\VCP*PGMTNQPPQEQVERRY WMSVSWQC
9678	23579	A	9749	607	986	SFSSSSSPEFISYGCDDLPMRDPHFVIT HPAFNLPLFLALGMFFSLFSPPLFIYF LPPPPRPPC*HSPP\PPPLTNSLFVFL PPPPGVPSSPPNTSPPHLPVPRPPSP TSTHLSSPPPPSPH
9679	23580	A	9750	313	339	AR*GLSCSG*S*TPGMQSSCLNLPKCW DYRC/RATVPSLCFVF
9680	23581	A	9751	213	453	NLAVNVDEINLFFFLFLIVTLASKFCS /HLLVGR*FIQSCHYFLFFIFDTESRSV T\RAEMSATVLAHYNLCLPGSPDSSA
9681	23582	A	9752	368	3	PLSSPRLPFPLDPSPYIFLISISIRFL SPFCYFLCVFLSISWGFSLVSQDGSLL SS*SAFLGLPKCWDYRL*PPHPAWRELS FFFS/SFFYLR*GSLSPSLBCSGMIIGH CSLDILVSSARA
9682	23583	A	9753	2	335	ARAGFSGGDWNVGMQSTASGLSLFHCFI S*GELFIILYILLKCYITL*IN*LMFGS FYFRDLQHFRLP/TSIVGKKRPGTVAHA YNPNTLRGRGGWITQGEFETTLANMVK
9683	23584	A	9754	467	120	SQLFGRPRQTDHLKSGV*DQFG/QHCET PSLKIQKLAGRGWV/CAPIGPRLLRP R*ENGLNSGGEVCSEPRSRHCTPAWVRE RDCLKNQNTKSGVLFHSPHQCFLLISNT SRNLL
9684	23585	A	9755	137	368	DGVYLWTHRPYCGLGSLNFGSVIIVLP* VKAYGWMVLTSLGDAIQPLADPECSF\G QLRELRCMDLHVPDPEDFRLLGK
9685	23586	A	9756	172	267	SKSGNKPNHYHLMNGSVRWCIRTIV*QLL KRLTTELPGYPAVAFGLGVYAREMKAYVH MKTYSLQKMT*IFIAALFGIVKKWK*A K*LSPDEWISK/M/WCIRTVEYLLTIRE

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9686	23587	A	9757	56	318	QFWGFSFFFFFCFIDTETCSVSQAGVQ WHNQSWLTA\ P*SDPPAS\ AS*VAETIG MCHHDQLIFFFFKQALCPRGWSAMAQSQ LTSSS
9687	23588	A	9758	179	1	KDTRVSRGNTQDTLKPPFPFPG\SSDSPT SAS*VARIIGVHHNTWLIFCILVEMRFH PRA
9688	23589	A	9759	219	208	NFCNFQMPLYQKILFWVRVSLSPRLEC SGTIIITYCSL/RTPKIK*SS*LSLGVQG CSKL
9689	23590	A	9760	133	371	AMAYQLYRNTTLGNSLOESLDELIO\LR NRVNFGRGSLNTYRFCDNVRTFVLNDVEF REVTELI*VDVKIVSL\DGKQTGF
9690	23591	A	9761	813	3	CGEGWAAGQDQGSRMGSCLPVPRAGRQL GSLFFPAFQVYCSCGTQRSSQSQWHKTE RSLPGNNPAPQDS/ASAPKYQTPGPVLG VQSPLNQQSCHTALSPPRASSSAFFHTTP ATLLHQARTLSLTQGSRRPTTWVLLKMP A*RPRESRH\GR*EWTKRSQARSQRAIN ARPRKALGLSDPAPSLHPSLEDSPKFS LGAPKAPPLPASSPTAQETQQSHISQOP TATGFLGARLCPSPQHCORGGFFGVTP LLLLGEWGVGEHSFPDVLV
9691	23592	A	9762	96	377	RYHTNMAAQIPESDQIKQTGFHHVGQAG LELLTS\FKEFLGTYNKLTET*FLDCAK DFTTRERKSEETTLSEHCLPKYSTMT\H RISLT\FTDNHI
9692	23593	A	9763	164	399	TDEELLRLRDEQ/RKWFLEKIESTAGADAV NIVEMTTGDLE*CINLVDKVAARLERT TNFE/RCSTVRQ/MLSKSIACCTE
9693	23594	A	9764	225	25	KCKITMNST*IE/TVFQDYEHLYVCKL KNLEKTDKVLTIHNFRLNQ*EPEVLTR AKMYKIYNDIE
9694	23595	A	9765	128	218	FFKDLPCDFPKWSHCFTLLLAVYEGFTF ST*LVIREMQIKTP\I*YHFSNRMVIM KKSINCKWQGRGESKALIHCC*ECKTV *PLWKTVMQILKKLIIG
9695	23596	A	9766	194	551	KNFFPLEMEF/SVLLPRLECNGVISAH RLRLPLSSYSPASSSQVAGDYRACTTTA G*ILYF**RQGFHHVGQAGLELPTSGDP PASASQSAGITGVSHCPQLKKSILHETP KGLTGVTS
9696	23597	A	9767	238	3	SFLWKLCPRGAPACLRCLSA\LLGGVS* SGYMGVRDPLEEAVCPFSELEHHAERTT ALFRAVPQGCLSLQKLSAFCSC
9697	23598	A	9768	343	1	RGAAHSRGDCVRFTGFCAPIPVLNHPKP LFPFPV*KSPIERRSLLGPPLKRSKNRF PFLR/VPFRFKNHPEFFFKKIFLFPFPF FFFEMESHSLA\RLSHGAILAHCNLSL PGSC
9698	23599	A	9769	191	2	FRINH*TSH/LRGQKKKKKTSKAIGRK QITKIRA*LNBTQPPESIQRINET*S*F SGKIKLI
9699	23600	A	9770	165	2	GKPPNCFYILNFKKKKGQDVFNRT/WLG VVAHACNASTLGSQGGWIT*AECKTS
9700	23601	A	9771	97	912	VILSTGCSSGPLPGWQSVLHHSLTRCPF SFFLSSPTPEME/FSLLLTRELCNGEIS AHCNLLLLGSSNSPASASGVAGNTGI/C

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						GLHAC*AS*FLYPHSVETGFHHVGSGLG LELLTSDD\RPASASQAGITGVTPRV* PLNSFSRHGLSCFFKETRVLSCCPSWT* TPGLK*SSCLNS*E/C*GYRHTPAHPAQ DMVFIFITY/CPFFVFPL/VYIPRFLF LRWSFTLIVQAGVQWRNLGSLQPPPG/H KQSETPSQI*INKY*LLN*LITFFFSIK
9701	23602	A	9772	3	363	HELSSANEHVFASTFGPTILGLPGVLL IILYPLLIRTSIYLISN\RL\VTQO* LIKLTSKLMIITHNSIGRS*SLILGSLI IIIATTNLLGLLPYSFTPTTQLSINLAM AIPL*AGAV
9702	23603	A	9773	38	385	YLIILDSPEKGLICGCLNCMHSSLLDH LNLTS*SS*MCLYANIHIYVAISCIYFI* F*SI/YIFII*YFYSIAYVYIY/IYIY MYTHAHIMCI
9703	23604	A	9774	13	1350	DRVSLILLRLLECNGSISAHNRNLGLGSS DYPASASQVAGTIGVHHHTPTFALFLV ETGFHHVGQAGLELPTSGDPPPL\ASQS AGITGVSHCTWPHLSTTGKILSSGTICP GIWGQRWWAFLIL\SLPWL*LWHPCLSS IMCLSLFFFLCQ/RCKPLISD
9704	23605	A	9775	376	1	KYFELMYIPVIAICLFNSEVFLNK*QFF NLTSSSGIQNLNRLIISNEVESIIKSLP TVKNLGPDPGIAATF\TYKEQLTILKLF QKHBEARILSNLTSETSITLILRKQPK KVPNEHTVKILV
9705	23606	A	9776	192	2	NVYQPPPVFLYPPGVAGGV*PF*SPPVF RVK/LGF*GSLPFFFFFETKRSVTRL ECSGVILA
9706	23607	A	9777	77	350	WLRKFGSRNSGKLTLYLNYYLQTSFFF FFFKIGV*LSPTLECRGPIWN*NLCPF G*RDPPTLTS*VL\GPRVILEFGFLEKT GFSHPQL
9707	23608	A	9778	133	325	PRWVRFPYLGDCPTRVSEMLGLQGVVFS SSPFFVCFET*SCSVAQAGVQ/WWCDLG SLQPLPLG
9708	23609	A	9779	145	362	RLAFGSCSTCFPLT*TVLYYLI*FNIFF VFEMESLSVS\RLCSCGAISAHCNLCTP AWTTERVDAANSRSMN
9709	23610	A	9780	260	1	QKQKQEKRRKKIFRNKHORDYNEQ*YG /NKLDPEDMNKF*ETRYT*/PNLHQEB IGMLNRPVINKVL*LVIKIPLTKKSPFP DGFV
9710	23611	A	9781	230	1	SSDSKTGSSVVLVACRFFFFLETGSGSV TQAEVQWHDHSSLQPPPPQPPK*/PGTT GA*STLAS*NAEITGVSHHAR
9711	23612	A	9782	20	322	SQHFGNPKGNPKIFRNLEINFFRLRNAD HMLISTDAQKVFQKIQHLFII*TS*QT* TERIFLNLIKAS*KKPTANIILNG*RLN I\FPKTGETKHIC
9712	23613	A	9783	158	379	LVKIIICNSFQYISFFFFFLETKFCFPF QVEVQGNFG*LNLPPLNHNFS\ASAS REPEIPGPPHPG*ILVF
9713	23614	A	9785	54	312	KVDKSTKIGRNQSKMAKNSKVNASSPP KDHNSSPARKQNWTEDELTEVGFRF WVITNSSKLKEHV*PN/GKETNLEKRL DQ

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9714	23615	A	9786	13	613	PGAGWARQHHGV*DPGQHG\KRPSLLK IEKLAGHGGRCLLSPAIGGGLKQGESLE TGGRDCSEPRLCCH\MPAWGNRNKTL SQ /QNKTR
9715	23616	A	9787	794	164	FSFLFCFFFLRWSLTLSPLSCSVTSP HCNLQLPGLSHSPATVS*VAGTIGTCHY TKLS*FF\FDDSL*APFLGVVDTEYYP DPPSSKGLLPHSGQHQHPPAISRAWL SC*VLPPLRS/STSLGQP/RIW*LSKVE V*RGFTFSPTQNTPTNNNCIAPGRVD* SLIID*LQWCDHSSLQPTPVLK\HPPT LASQSAGITGISHHTRPD
9716	23617	A	9788	256	380	YIFRQAKTQGLPPCALFREAVGENTP*V FAC/PKNVLFYVHP*LPG*I*IYQLKIT F*NYEGMVT/FVFRFLPETRSHLSPRLE CSGTITTHCSLELVGSTNSSISAS*VDG NTGVRHNASC
9717	23618	A	9789	22	226	TKINSKGNKELNVRAKTIKLEENIDRN LCDLGLGNCFLD*YCIL*TKINSKGNKE LNVRAKTIKLEENIDRNLCDLGLGNCF LDMPNAQTTKGR\IDKLDIFIKI*NEWL DT
9718	23619	A	9790	288	2	QVWQE*ATESAIHCWVERKAIQLL*KM RWQFLKMTNV\BLPYGSAIPLVGIHGRE LER*ST*NIMFTAPLFIK/T*NLFEW PSPYEQITKMHSC
9719	23620	A	9791	142	361	PPGEGKRVFPTTEPSPRIPSKAKSVSQ DTCTPMFTAALFTIARMNRSKCPSEFE *IKMRCITT/MECYSA
9720	23621	A	9792	305	346	TYEYTDYGGILIL**LITFYDHAVALIIFL ICFLFL/YALFLTLTTELTKTGGDAQE IETV*TILPGIILGLIALPSLRRLYITD DAPDASLTIKSIGHQWY*TYEYTDYGGIL ILNS
9721	23622	A	9793	2	317	SRDRPRVRDR*LFTSNHKGIDIGTRYLLFF A*AGVLGTALSLIRAEIGQPNLIGND HIYYVIVTALAFVIFIDLPILIT\SSF G\SVYVLLILGVPCTAVFLHSS
9722	23623	A	9794	384	1182	RIGKIKG/LCFLFV*WFLKFFFKMEFL PRLECNKI\HCNLLMGSSNSPTSASQ VAGITGMC*F\VFLIEMRFFHVQAGLK LLTLGD/PPRPPKVLGI
9723	23624	A	9795	205	1	GLQIKCTMRYHFAPTKMAITYFFLKRK G\NNKCW*GS/GTEIGILHCWECGMV QLLWKTADAWADAW
9724	23625	A	9796	307	348	QSARL*EAVCPFSDLQLRTGRTTALFKA VRQHLSLQRLLSF\VCLYPAPRGAY RGRQASLSCGGLHPVRASRLCLPKQAW AMVGAPTASLPPCSSISHCCASNQSDS VGYDPSSP
9725	23626	A	9797	193	381	ILLI*IHILLSMISSPFFETGSHSS/V SRLECSGTASAHCSLDLPSSGGSPTSAP *VAGTTGA
9726	23627	A	9799	153	359	FGTYMCFADSYQLSYLVVGTFSWLEEE GV*WCICGSLQPQPPRVK*/FLPSLSLL SSWDYRCAPSC
9727	23628	A	9800	2	396	ARAARAARELEELIKIPFFFFFHWGQIL ALMPKGGGQGGILTYPNPPLPG*NNFPG

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						LTPPRTG INCLGPPGRVNPQIFKKKGGF PPGARGV*NPQPRGTTPPGFPKGR\DKA PHPGPL*TFEKVPRPPNFPQ
9728	23629	A	9801	256	347	LYILLNSLK*LVEKLR*NVVLASLIIR YKVTTKRF**FSKPAQSEELQLLTSA LNF*RYIIISFFFWIQSFALVA*VGVQWC DQGSPPQLPPGFKRFS/CRSWDYRHEPP R
9729	23630	A	9802	109	401	HLRRPCPTPPFALRTSGDQPLSPEARPD SGLLHSPPLTSPRGLNGQCPPRGSTLNFN P*ASIPASPPFSGQPQASQEPVPVASEH PPDT*GDPAQPPP\RPQDFWGPATVPRS QAGQWPSPLPSDFSKGAQWVPVPPTR/PP PSTSTQSRWT
9730	23631	A	9803	371	2	PGFPLFSFPEGNGPSKRQTGD*IRCLF* DGKWECSPEKKKKKTKRKKAVIF/CV PVQTKCIVVEGGEETLVGDV*V*P*\GS FKHVAMFPEK/DCLCTLYEASFRTKES RRVDGFVCVRVGT
9731	23632	A	9804	188	1	FLFFFFSET*SQSVTHAGVQGLEQLSP G\SGNSRASASQVAGITSRRKHSWIFV FFVETG
9732	23633	A	9805	112	383	VFINIRVFRLLFTFSFFFKRGFNLSPRVK CNG*TKGHCIPLDLPGR*SFPSLLTNW DYRCAPPRPNKFFF/SFETGSHSVTQA
9733	23634	A	9806	599	237	FRDRSLTLRLHCHCVITAHCSLKLGL SSELPOASPLSSWDYRHSPPCLANFLFF VETRSHY/ASRNSLGSSNPT*A/FPKCW DWQV*ATAPSLAYWFSEAKLILRLAL KVSDENICTNF
9734	23635	A	9807	168	2	PQQDVFFFFLETGSYSVTKAQVQCDHG SVQL*PPG\STDPPTSASQEATGTHRA
9735	23636	A	9808	225	3	GPLGYLPPYFPQPLISRG*NPSPFLKIS RVFYGT/HYKFEFLFLFFFTESRSVA\ RLECSGVISAHCKLCLPGS
9736	23637	A	9809	541	3	RQLTGINSRRQFQPMNSNYVPIPYMDM IILKTKKSNKYWQGCERTELLHCLWE CKMVQLVWKTIV*QFLNRSDIEFPHDPGI PPL/GYKRKKMKTCLPKLCVLVEP/RM FTAALFEVAK**KQ/PQTPITR*INTMW RIYTMYYSAIPRKTPLIHPA*LDTES II*TEKIQSQETTY
9737	23638	A	9810	213	1	FLCVDVFCNFAELKLALVGLFVCLLFG SVTQAGVQCNL\GSL*PPPPGLSDLPT SAF*VAGTTGVSHH
9738	23639	A	9811	54	388	PARPLPRQ/WDERPNQOPTKKKKRGRN LPTKKKTQNYSHONPVAQRNPGGKTNQK KPKTNPKKKKGGAL*KKTQRGPKQTGGR K*KISPNKGGK*NPCGKLEKNPFSGGE K
9739	23640	A	9812	429	24	RSKGAFFPICPRSSKFSVLQQRQVRIV FQHPGLGESVAR/CRYSQLLGRLRQ*SH LNWGGSGSSEPRSCHCIPAWATRASSIF CNFQASSVEVRRSARKKLFS DILKRHNT INWRVSGLLLVDSYFGRLATPVRTQ
9740	23641	A	9813	149	350	CHFPCHFHTL/CB*EPGEDVTGPIGTFK FPAPGRTDGHHTHTHTHTHTSDPH HLCVWNTLIHFV

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9741	23642	A	9814	66	401	PENKKTIVYRKPIATIIIFNCERLNALPLK LETRP*YLLY*LFNIMLEVLASVVRQEK EINLSIFT*DIVIK/MKIPKNLENKLLK LLSPFSKITGYKISIQKLTSSFLYYGFT V
9742	23643	A	9815	82	1	APPPARFFFFFF*EKPSFPPGGEVQRG VFCPCNT/CFP*G*KIPFL/KPLKKVGF WPPPPGPKNFFYF*KKGGFPPWARGFFI PTPFVPLHPFKKGVKRG*APPPARFF FFFFFL*GRVSLCHPGWNA
9743	23644	A	9816	256	2	QHFP*LPPIPIQT*QHFPQTRSPFQ PPLCQKPFSSPWGSKVVFILLSFFFF* DRVSLCHPGWNAVM*SQLTAASNTW/VK *SSHLSLLSS*DYRCVLS
9744	23645	A	9817	53	411	TIYCSNYVNFVSQHFRLYS*KNCGLC L*FHLFVLQS*NFMQFHM*FCLKI*VDP IITFEV*FTYI*FF*TYSSVSFTDAYNF VKPHR/VYRGPGAVAHICNPSTLGGQGG WIT*GQEFK
9745	23646	A	9818	100	417	DEHSEKQDEPLQRPRLPFPPTPPSS LLLLNHIGQESGLTHVRLASCLNRGFC FDMKERLCLPMLCGRMISDHCSLI/R PG*DKPPASAYQVGETTGTYHRA
9746	23647	A	9819	136	2	IYMGMPQPGAVAHACNPSTLGGQGG/WWI T*GQEFKTRLANMVKPC
9747	23648	A	9820	257	426	IVPGLFLGTGSCSFTHAGVQ*SNCSVQ S*TPGP/SDPPASASRVAGTTGAHKKAW L
9748	23649	A	9821	151	416	LHKLCMLVMESGTAKTPSLSPIFNSVGL ILLLLEYSIDSLC*SVLCCYKEIPRAG* FIKKRGL/WLGVAHACHLSTLGGRGW ITRSGN
9749	23650	A	9822	50	513	RGDPRVRPRVRIIKLSEGMWKAIEGRK LDLLHHTISQVNSKEKFLKEMKSATSV NTRMIRE*NSLIADMEKVLVV*DQTSN IFLVQNIKSKGIGLFLKMRARDEBS/ AEGKLDASKGRFVRLK/EKRSHLHNMKV QDEASVDIETTASYLVK
9750	23651	A	9823	48	406	LIIVVYTLTRWIGHSAYSYPLLRPPYS LRHNEIRPINNPMTASKCSSERKSLTS LTFHLKIKMIKLEEGVSKAKTG*KLGL L/R/QTVSQVNVAMKKYLKEIKSATPVN T*MIRKQNNL
9751	23652	A	9824	143	444	WNKKNKNELADMILWGCCKDTIFMRKL TRDETKYGIPLALRGHSHFVRDGTI/N LDGQVDLS/G*WDGTLHLWDLTSGSTTR RFVVK/TKDVLSDAFS
9752	23653	A	9825	297	2	HRSPTEKTIASIKKTKMITKDLNRQF SKQDKHLTSEYMKRCPTS/LREM*AKTI MRVHLTPIRRAPIKNKN/NKSKCW*GC GETEILVHCW*ECKMVP
9753	23654	A	9826	175	400	GGKGGKNSFLKGGKKTNLGIFGKKPIY GGGTNGANPPPKIKSGSEKKNF*VFFPP FPFKNFFFP*NL*FLGGWPHLSPPQK* V/CFPKIPKLVFSPPLREKFFFPPLPP* NLGPPGF/SFWGPPLFFFFF*RDKF SFYHPGWKAVIAAHFSLELLGSSNPPTS
9754	23655	A	9827	64	622	MFSFFFLDLILNHLFFCFV*MFSFFFLD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LILNHLFFCFVIRQQFSFLFF/ISFFFS FFHCNVNTPELCDFSVCIHSDNSFRFLH LF/NF*HMLCISELR*TLKQSCYSYTK IC**FYSVQLSPLTILY**CKS*QALSI ALQNEFLSV\QYHKMNYITLTIEFSRN KFLSVTFLLPSIFSHNFGISASISIPIL HVYIKNNPIGFFK
9755	23656	A	9828	298	1	MRNCLTDDERKWFPEMASTPGEDAVNTV EMTAKDLE/Y**YINLVDKAASDFEMID SNFERCSTV/NKMLSNSTACYRENFHER *GQSVQQTFFVRVGERV
9756	23657	A	9829	361	1	FLTGTQWKG/DSPFNTWC*DH/WNIHRN LDLYLIPYIKINLKQLTGPNLRKTIKL PEQNIGENLCDL*LSRERYSTKSITRIR KL/DTLGFIIKIKKCKISKDTIRKR*ATD WEKIFANHVLKG
9757	23658	A	9830	402	2	RFHHRFSFVLFGPFAKVAFFIGAKNFIS NHYWAGVFPFWEKKNKIDSFLPPFSKNP ILGELKA*F*NFLF*GFQIFF*SLFFCP FGGK*IPGVFSFFFFLVFFEIGSHSVP \RLKCSGTTTAHCSLDLGLSSN
9758	23659	A	9831	2749	3215	FCQ*IKMYVMCICIYNFRRVYLCIYTYL HTHTFTHTHKHTPTQIPEKDS/QCSLSD LKGHSL
9759	23660	A	9832	3	386	KLRQLQNTSAMAAC*SERKS/R/THL TLNQKLEMIKLSEEGMLKAVIGQKLGLL YQ/TSQVVNAKEELLKDIKSATPVTAM IGKQNSLIVLEKV*VV*IEDQ/TSHNI SLSQSLIQN
9760	23661	A	9833	1	370	RRCRWPPDPSTRTVGRQIGKLVTHRPVTF QERGCFFPLTRQAGSHHGGAFAQVISP TKSISPCGRGGSRL*SQHFGPRPMQVDHL R/LGVQDQ/RWPICGQYGETPA\LLKLP KISWAWWLAPVIPA
9761	23662	A	9834	125	409	GOENRETWKIVHLV*VLYT*HIKRLNCF SHFI*CYQPTASQAHVHDSNDSSSTHV\ N*NSRWPGTVAHACNPISLEG*GGWIT* GQEFETSLANM
9762	23663	A	9835	223	1	PKPKMGTF*PPMEGS*MGPPHWEKMGF FLKKKEGHPFFFFFEMESRSVT\RLC SGA/TISAHCNLCPLGSSNS
9763	23664	A	9836	377	515	FILFLRQVLTLLPRLEYSGAIVAHCSL\ AF*G*SDPPASASRV
9764	23665	A	9837	274	1	AGEWHDQICVFKIPLMKNGLHGARGVQGE SWKERNQQV*DRQKQNLSDS*IQT*R/ M/WPGTVAHAYN/PSTLGGQGEWIT*GQ EFETSLANMVK
9765	23666	A	9838	553	114	GAGVKTHPGHKGKTLFFFKFFQKLPQGV GGKTLPSPLSRGLGRENSFHPGGKGSNK QSSPPSPFG/WGKKGGGLPFQKKKKKEK RKKGKNGVAPSEPLKYSN/WQATWG* RKLLNDTMRVQPTKSRMQKILQDKGPVN GIFTKTGRL
9766	23667	A	9839	36	434	LPFPQCVTEFTIVLISWCYIREDACKNL KHVAITIIINVCIIYICVVCPSSTLYVYMY MLP/HLSDTLTLN*VTLVEMLSFPQCL MFWYHGI*K*HELDVVAHACNPSTMG QGGWIT*QGEYKTSANMVKPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9767	23668	A	9840	268	1	RFPFFFCFLTILFWAPGVVFSNPLGVRA PQPP*IFFPI*KKPSPLIFFFFEKES RSVS\RLYSGTISAHCKLCVSGSQHSP ASAS
9768	23669	A	9841	463	86	LYMHEFISGLFLLFCWSI/WSVLCQYKN CFDDKVYGLDYGNTSQVFT*NSKLIKLY TLTMYSLFCINQTTIKPSEMIQATKANI DK*NYMKLENFCTAKETVNMKMKRLKKW EKVFSIHIPQEVNI
9769	23670	A	9842	37	400	VHSPPFKFWSLYSVLKFPPCSLYFKFL ALYSIFLQMCQHLLV*AFFP*KRGLNSV T\RLFCRGAI SPNCNLCL/SGSSDNWAS LPRKAEAGNSFT/CR*SQVAGNPISIS TRLNQRKTPFES
9770	23671	A	9843	42	407	NCLSFLLITFFFFLFFENKVSFCPOG*/ RGGPFWPHGTLPFRG*GNP*LPGRGE *RGAPPPPGYFWLFGKKRGFPPL/GQGS KPPALKEPPPLGPPKGG\NYKRNP PPP GNFF*LPYQV
9771	23672	A	9844	113	379	LGPVVATSLRGRFLGYQLQSKKH*NYP TVR*GCGEMRTSVHCW*ECKTA*PL*KT VWQFLKLNLTGLPFD\AETPL/LAETPKE LKA
9772	23673	A	9845	284	528	PLPKTMEIMLDKKQIQTIFFLFKFKMGHK IAETTRNIKNAFGPGGTANE\KCTAQWVF KKFCKA*E\SLEDKEA*GHPSEVDN
9773	23674	A	9846	888	1295	LEQGCNLFLLKHS*LGVEVFFVCFRRSF TLVAQAGVKWRDLGSL/HKLPSLSLPS SWDYRPPPLPRLA/NFFVFLVEMGF\TVL ARMVSI*PRDPPTSASQSAGIIGVSHR AGPVAGILMFCRWINSNPKPGAVFKKK
9774	23675	A	9847	88	387	AYRMKIIDRISLSLYTAALWVTLFLFLF LFFFFKTEFCFAPQAGGQ/WGQFKLMDP NPPPPG*K\DFLVSHPRDLGIKAPPQC GQNFVIFYKEKGGWLLTAT
9775	23676	A	9848	298	438	KIPRGAPNPPGGGKIFSPPLGGPIKTPR GALEKKTLE*VRGPWPGEVVKESPRPK LG*QIFWPPGKKPNPPMGG/SLDPPPL ILSRPDP*KKKKKKKKKKGGGPKNP PGGPKFPRGGKNPPPPRGAYKNTPGGS *EKNPFLGGGKKRKQP
9776	23677	A	9849	251	498	AIKKMESKKFW*RHGEIGTLIHICYWEF KMV*PFWKTV*QFLK/D/LNMGLPFD SA FQLPDICLGELKTYVHTENCTQMFMAAL F
9777	23678	A	9850	478	37	ESRNKSHLWSINFQKGLR*LNRGKQPL NK*CRHNSISTCKRMKLDPLYLTPYIKI\ KSKWTKDLNVRARTIKSLEENIEVNLHD LG*GNDFLDMTPKAQTTK*NID*LDI IK I*NFCGSKDTINKVRRQSTE*BKIFANH VADKLK
9778	23679	A	9851	2	378	RLEGLFLCALFCSTAI CMFFFFF* K KRGPFGFGGDPGNFRQLDLPPIKQ FWGP\PPRKAGTGGGPPGANLGFWGK KRVPHGQKGFKE/RNPRGSPRPGPPKG GVAFVFRPKPPGLEQ
9779	23680	A	9852	229	3	FGPYKIFFKKGAPCLENPPVF\HQKL GLGFFFFSFFF*DGVSFLFLRLKCSAA

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9780	23681	A	9853	108	420	ILAHYKFLLPG*SDSAASAS GPRVCVRLSLRDDSLLATEDSLAHTEG DPVTASSHSQAPSLSVHPGAALGVCSWG TGAIACTPEPQKPPQLTPGGRPA\PIAP GLTWEPSPHPPO*RSPPPP
9781	23682	A	9854	2	256	FFIFPLRYVIYCARFQFLSPILYLK*K MD**RRVFQEKWEQAYFFVEV\SPMCLI CNQTLVSKEYN*CHYETNHGENFD*F TEKMDENLLHLTTROP
9782	23683	A	9855	323	3	IIQMANKHRKRH\QSQ**VRVMOKKIIM IHRYPQLWKTSSDKMICCSGYGTTEI FTHYLWECKLLHLLWRMVWL\ILLKPKT DTPHDPALPLLGTYPAECMHMPRA
9783	23684	A	9856	28	385	DGVTQAGTQWGSKFTAA*TA*YQGSIPN AWSFPSPPPVLKTPPPQKK/YPPPKK KIPPPKK
9784	23685	A	9857	436	518	AANRLNIYRHLIYDKD/EHYRIVGKDD LFNKWCWVNI/ASNKEKNLDSYLIPHT K/LNSR*IIQLDVKD*IIKLLDNLYLH DLGDRQKFLGRI/PVFTIKKKIGKFDPM LKLSTFVHQKTPC*RLNSA
9785	23686	A	9858	153	492	RLAGSDPGVADVSVQLQRQKSPCPSWK AVSQAESSSSAGVSLVFLRLLADWMP IPIKEENK\SQSTDLNFNFIQKHCHRN TQNSV*PGGVGPPGTCGPFRRQSSP
9786	23687	A	9859	2	419	TTGKLQVSHKSTYSHFSKKPTHTTKND MKRYSPSL/AIREMQSKTIG\MRYHFT KYG\NNKCWLGCGETETLIYGW*ECKMV QPLWKAVWHFLK*LNIES/PIY**NYS* YISYSWRKTCITIIDPVILLGLIYPREV KTH
9787	23688	A	9860	88	419	TFFFFFGFWLKTCKLFLVQPLFEGGPI LG*WNPPPRD*KNFS/GPNPPGGGE*RA QPPPPGYFLFFKK\GVSPWGGGSKPP TPGNPPPGPFKIRVIRGGPPPPGGRKHF
9788	23689	A	9861	301	401	KRA*GGQEPKVCPPFFYNKRVGNSPPK KFKKGRRAAFFGLRANKRGLFVKKGKKI WVGKVGEPIT/DPFKEFGGR/LPEKDG LV
9789	23690	A	9862	220	415	KIMGGAQIFRGGGFFFFLEGWEKNFPG VSFRKFFFGGVFLPPPP*HKIYFSS QRQYISLGGGGRKTPPPKNFLKDTPK LFFSHPSKKKNPPPPRKIWAPPMIF*I PPPIIFFFFFFFFFFFFFFFFFFKN*P/S FFNFKKPIFKTFLSPPFKVFPPPKKK KNPPISYRRWPLAI
9790	23691	A	9863	116	366	GQEFETSPAMFCFETESCSIA*AVVQWH DLSSLQPLPPG\SGDSPASASRAAGEL EPRIRRLQSVEITPLHSSLGNRVLHL
9791	23692	A	9864	619	295	FFFEFESLPLPRLECNGAISAHNRRL PGSSDSPASAGLL*SQVAGITRLRHHD *LILY/FLVEMRFRVG*AGLELLTSGD PPSSASQGAGITGMSHSHAGHYGKIF
9792	23693	A	9865	12	432	IADRRLLFTNHKDIGTLYLLFGA*AGVL STALSLIRAELEGQPGNLLGNHINYNGI GTAHAFGIILVIVIPIIIGGFGN*LVTL IIGAPDMAFPRINNISFGLLPSTLLLLL TSAILEARAGTC*TVYPCLA\GGYSHLG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						A
9793	23694	A	9866	30	380	LFSTNRRGIGPLYLLFGA*SGVLGPALT LLI*AE LGQPQYLLGDDEHYNDIDTAHA FVILFIVIPPIIGGFGD*LVPLIIGAP DMAFPRIN/NISF*LLPASLLLLASGI REGRSK
9794	23695	A	9867	256	395	EVLRKSEKSFETVCIINNRC/WPGMVAH ACNPMTLGGRGGRIT*GQEF
9795	23696	A	9868	458	2	PKKRFFSQKPPRGFYSAPLKGKNIYFPP PVNFGPPKDFFKGPPLEFFFFFFFFFFP RFFFFFLEKG*KF*NFFFT*NMVFFYIS /CSKKPPFQFVLTPIPF*KVPKPVWFFW DFPIPFKKIFFFFFFCDRVSLCHPGWSA VARSLTASPRV
9796	23697	A	9869	144	425	IPLCSRIYSFGPC*FSLISSSSCLSPFL SIPLCVLS**T**YLFYISMREIYKTR TKGIYPGAQRNSLYTH\FSIEVQSTIKA ERFWPGAVARACNPSTLGGRGGQITWGO EFE
9797	23698	A	9870	138	401	DLRLKLNLSKNIIRLQGTVESSVLTIKE MQIKAKVRYNLI PVKIKR/SGNDRWW*G CGERGTLRIC**ECKLVQPLWKTWWSFL KKKKK
9798	23699	A	9871	179	441	PSGGKGIKGP PPPPKKIFGNFFFLKKK GVPPGPPGGPKPRPLETPPPNPPKGGEY GGGP\WPPPPIP*FPKGPFKKGPFWTN RGNP
9799	23700	A	9872	57	435	FTQMRKNLKNNSGNMCK*GSITPLKDHS NPPAVDPNQNMFEIPGKEFKK/SDY*V TQGDTRERCKPT*VLKTI LDMDEKCSKE MDILMKNQSELLEKDTFRELQNAMESE NNRLDQVEERITELE
9800	23701	A	9873	228	443	FSSKFILISVFLFLETGSCSVAQAGV QL*DYSSLQPQSPG\SGNPPISASQIAT TAGACLHALLIFVFFV
9801	23702	A	9874	349	2	KKPKKKNPLPKNFGFFSPFSP*KFFFF LKGFNFRGFFPNFPKKKFFSKNSQL VFPLPPLKKKIF/CPPTPVKFGP/SQRF FLKGPPLFFFFFLLDRVWLCYPGWSA VARSRIS
9802	23703	A	9875	405	2	KKASRMENVRKKKKLEMIKLEEGMLKA NIGQKLSLLAKQQVNAKENLLKEIRSA IPLNTQMIRMQNSLIADMENIL/VVWI/ EDPTNYNIPLSQSLIQSNALT\FNSMKT ERGEAA*EKFDAISG*FMFKERS
9803	23704	A	9876	355	394	THPYYSHQEQSP*P/LTGALSALLKTS GLAM*GHFHSITLLILGLTNTLTIYQ* WRDVT*RAYQGHHTFPVQGLRGIIL FITSEVFFFAGLF*AFYHSSSLAPTPQLG GHWPTGITPLNPLEDPLNTSVLLASG VSIT
9804	23705	A	9877	47	85	TIYIHCVRİYACEVCVCAYIHCYGP AHLTEQNL\KPARTQSPAPQKNPPLPV DLVSI SLDRQAQDVNLNHYRLGNTCRD VLPKVTCLRL/NFFPCLPILEELQBL P*LENIPLFPQPIDIYTYMAYICV
9805	23706	A	9878	2	389	GRGQFPPEFFYFFWGGSLVPSTPNKKK LGEVLGGGWSNRAPKGWGGGFPPIILAF

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						KPKGPFPGPKFVLKFSNVPPLLFFPKMRG PLPKGGGFLPFFFFETKSRSVTQPGVQ WCNFGSL*PPP\TGSSNS
9806	23707	A	9879	351	1	FLGFSKNFNFPFPQKWPFAFFPKSHRAR VNEIFS/RLSVINF*GLTKPQRLFFSLL NFSS\PIPPFQPPSRLIKEIRFSTFLTP ENSKIKKPLFFF*FFFF*DRVTLCCPGW SAVVQSR
9807	23708	A	9880	123	387	SFLWKLRLPSGAPTCMRCLLA\LLGGVSQ LGYTGVRDPLEBAVCPFSELQRHAGKTT ALFRAVRQGCFFFAFYF*TELFPCY/CSG RVGG
9808	23709	A	9881	341	659	SFLGRVQWLHACKSQHPGRLRQVDHLRS GV*DLPGQHDETLSLLKMPK/QKLARHG GMCL*SQLLRRLRQENHLNLRGRCNEL RSQHCTPAWATEQDSISKTKTKK
9809	23710	A	9882	216	1	PKFFWVLRDSQIFKPGFGPQGF/CGFG NPQKKKPGFWGLG*KKKGFFFFFFFFFF LRDGISFCCPGWSIQW
9810	23711	A	9883	2	244	GRVGAVGRREGENFIKCDLPPPPPEGK QQNLCKFLTGFSLPCQDKKP/CFFV*KK KKKKKKKKKKKKKKKKKKKKGGGA
9811	23712	A	9884	310	2	IFLQTLFPNTFENSLSEYCIIFSEYSFI **KQ/TNFILSSILLYI*PSGSYISNL *Y*ELFSQNLQYQHLWI*KKWGLGAVA HTYNPSTLGGQGRWIAWSPG
9812	23713	A	9885	242	358	KTWVLYMNI*MANNHME*CSLPLVIREM *IKTPVTVH\TVGMAAI*NKK*NITR/C W*ACRETAVLVYCWEFYTQPL*KTWVL YMNIE/IPCDPAIPLLGMYLKE*RPGTV AHTCNPR
9813	23714	A	9886	360	2	LLKLGFPPWAKKGGKKRLWVEGPLGKPP GGFCQKLFSPGGGPKGFSPSIIILPKG *PFVWGPPEVF*KKRPKLKKKFRPTFS /Y/LFFFFETESHVA/RMECSGAILAH CNLCRLGSSD
9814	23715	A	9887	236	347	IKGFFFF*TESHSVT\RLCTST/SAHC NLCLPGSSNSP
9815	23716	A	9888	310	3	NFFFFFFETGSCSVTQARVQWSDQ/GSLQ PRSPGL\SDPPTSAS*VAGNLKFLSLC SSL*SLEIS*DTKKSQVQITDDLCTYTVV LCLFFEMESHVVQAGVQWH
9816	23717	A	9889	119	391	APAYWNPHARDSPPFFF*TNPPFFPQVG GQWPNSGSPQAPPPG/SPPP/YASASK ISGAPGAPPPGPNFFSFFSPTFFSR DGVSPYEP
9817	23718	A	9890	195	3	DGVSLLLPRLECNGTILTHCCLSPV/SW DYRRLP*RL/V*PFLFLVEMGFHHVAQA GLELLTSGDHP
9818	23719	A	9891	3	378	RDGERNMLALGTASAKALKYSLSLSPR LECSGTIISSHSLNPP/GLKWSSCLST SSWDFRPAPPHLAKKTQQ/HATFF*EG ESPYYAQAGFKLLASSSPPAFSLPKCWD YKL\DRHAW
9819	23720	A	9892	231	1	PKFFFPKFFSP*N*KPFFQISPAKIQKI RVYQS\HKKFFSFFFFHGVSLLLPRLE CNGTISAQCNCLSGSSDSP
9820	23721	A	9893	2	347	APARQENVVCVVCVCMVCVIVVLRHC

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						EVLCFYKMLGKKRSIYAY*LVY*YIYIH MCVYIYI/YIYV/YMYIYTVCIYTH
9821	23722	A	9894	28	382	TAHLEAGATGYRTFLLPAIGLLCLPWVL DDGAGQTAQ*SMLLDHAMLLAHLRAHELF I/DYYEFEEYIIPKDKYSFLHDSQTS FCFSDSIATPSNMEETQQKSNLELLRIS LLLESW
9822	23723	A	9895	93	386	FWKTI SHYFYFKYFSCSILISPSDLPTIC ICMFHLLKLCQSSEFLHLLLFVWLVFET QSHSIKQPECS**LSAA/CHLPSSDPP
9823	23724	A	9896	174	1	TLDWGPRKKNFFFFFETRSRSVTEAGV Q*HNHGFLQPPAG\SSDSPTSASQADA W
9824	23725	A	9897	251	386	LQRLCSGTI/SAHCNLCILGSSNPLAS AS*TAGTTGTLTGDDVDS
9825	23726	A	9898	127	393	GHMGTLTGSPATLSILALFFWGGRISTQ LDGINKS\FSLFLYFLRHCSLSLRLE*S GAIITYCRLELLGSGDTPASASQETGTA GTCHT
9826	23727	A	9899	3	334	KLRIGQLNTSAMAAC*KSERKS/R/THL TLNQKLEMIKLRREGMLKAVIGQKLGLL YQ/TSQFVNAKEELLKDIKSATPVTA*M IGKQNSLNCLEKSCVVLIQDQTG/HNI FLS
9827	23728	A	9900	356	1	GRKPFSHLPKATLLPMGPVLGRRALMG PDSRPGVPVSCSLVLLTPLAPLPLTARE SLCPCPPS*TPQPSVNP/H/GKLARRSP CVVSGRQSLP*AEIVPLHAPPALGDRDB TPSQKKKK
9828	23729	A	9901	118	343	IPYAKKKKKQENVLRFIHVNLCISNWF FETGSHFVTQG*VHWCNLSLQ/PNLQ GSGDPPTSASRAAGATGVQH
9829	23730	A	9902	321	50	SLRTRV*RPSPAPG*NPFLKPKQIFQG GG\ESPLSQILKRVQENSYNLGGKGFN *PKLPPCPLTWATKRTSPPKKKKKKNYR TWETSVS
9830	23731	A	9903	317	8	NCYDPSNGIVIPLLGILPKSTK\T*VRT KTCT*MLIVALCII TKWK*SKCLSTDK QVNI*YIHIMEYYSPIKGRKY*HTLQH /WMNLBNIS*KRLDIKPHII
9831	23732	A	9904	287	3	RGALNGRGGPRGVKSPGFAPFKLQLKPP GTFLNPK\QFPFFPNPPF*KKGAFPHFF LPLF*SFRWTEFYSVT\KLECGAISAH CNLCLSCSSDSRA
9832	23733	A	9905	2	406	PRVRTSSRSRATALFFFFFVFFWGKG EIWAPPLKNC/IPPEKFCYFGGAPGAG LPPPPGVIFSLCRVVKKKKKGAPP VLGKKKKTFFTPKGGTFLTLGGF*KKSL FGKTLWLWGGPLLLLKNFF*EKFR
9833	23734	A	9906	1	296	IWVGATECIFKNNPTIWHQETHFTCKD TYRLKV/KGWKKIFHTFTNGNQK*AGI AIVISDKTDFKSKTIKR*KGHY/IMTNG SIQQGDILDWYKSNCSF
9834	23735	A	9907	474	41	FMEYLTLSFIHVLQ*FIHCFVHLFIHS FFYALMKSLIQ*FIHLYSCF/ICIDLLI SSCIYSFIYALVKSLANLTHSFIHTFL Q*FVHLFTPLLCSTHSSIH*PSHSLT FIQLHLFPHALVSGFIWSFIYLFCKINV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FLIDK
9835	23736	A	9908	286	84	LKPPPPFFFFFQANFLCFIRD/GFHHVG QDGLPLLT*SASHGLPKCWDSCRALR PASPLISGPHQTI
9836	23737	A	9909	316	63	DQLVRSIGFEALMSPIFFQMEF/SLS LPKLECNAGISAHRNFCLGSSDPPASA AV*/PMANLLKLCASVSYCTELVLNLH WIK
9837	23738	A	9910	370	461	F*F*FLFSETESHVA\QLECSAMISGR CNRLLGSGDSPATREAGAQESLEPRRQ SEPGLCCHCTAAW
9838	23739	A	9911	294	28	PGKNSTVQKEPGKWFCEMKFTPGENAVN IV*PTTKDLEY/WINI/DKTVAGCERTD SNFERSSTMGKML\SNSIAWYTEIFRGR KSQLMGI
9839	23740	A	9912	307	463	CKL*TLNNDVIVGSLIVT/TCTILGV LIMGD/RLCMCGEKEYLGNLGTPLSIL
9840	23741	A	9913	377	28	REMLTVKPLAPSFRRWSRAYRAIFFITP TWVSKSGKVTGPLFLHIFPPGP/CPGL PIFFFIKTGTRFFFGWFFFERVSLCC PG*MECNAGISAHHKLRPLGSRYSPPASA SEFHR
9841	23742	A	9914	384	725	HLTAIRMTVIKDTENSKCERGC\KTLMH SCWEYERVQPLWKTRW*/LQQVE/LPS PCDPSIP/LLRMPK*LNTD/CKRMC/C IPTSIAALFFVTK/SWKQ
9842	23743	A	9915	187	3	QPHKHLGLDNIYIFFEIGFCSVAQTGVQ *RDHGSLLQPRPP\GSRDPPTSGSRVAGR PRQENG
9843	23744	A	9916	15	167	DGVSLSLPRLECNGAILAHCNLR/LPGL K*FSCLRLPSSWDYRLPPHPAHV
9844	23745	A	9917	345	477	YCSRTSLPL/TLKKGSA*PGAVAHAYNP SILGGRGRWIT*GQEFK
9845	23746	A	9918	460	42	HQRPKVDKTKMGEKRSRKTGNSKNQSA S/APPKERSSSPAMEQSWTENDFDELRLQ EGFR*SNYSELKEEVRTHGKEVNLEKK LDEWLTRI/SNAEKSLRDLMEITPKA*Q LPPERTNLSS*FNQLEERVSVMEDEINK MK
9846	23747	A	9919	282	21	AAGYLQPSFEFWLHSLGSRRLPISVFPV

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9851	23752	A	9924	254	3	RGRQAWLSCDGYHPVRPSRLCLPTQA PGGFYFPGFLPPLGFPKGF*RLWPFC PATFFFLYQISKFPFFFGKYQKNFFFF FFFPESKRSRVT\RLCNGAISAHYNL
9852	23753	A	9925	309	1	YTPTIMLLGIYSNELKTNVHMKT*I*MF TATLFLIAETWKQPRCSSLSEWI/QQLW YIQT/BIYSVVRNIK/LMKTW/MKLK YILQSEKTQSEKTTYI*FQLYDI
9853	23754	A	9926	237	2	RWNFNFTQLILKCIFLRTKFFS*VSK*N FKYFLGFWFFFLRQGLTPVT\RLCSG TISAQCNRLRPGSTDFSASASQE
9854	23755	A	9927	244	1	KPQCLWRK*D*WHNTQKLDVEKGKPLIH YWERKLV*PLWKT*VWRLMR/NLKIPL YDVIPLWGNYSKEMK*LCQREDSRA
9855	23756	A	9928	2	644	IVQVDQKIRLNHCLQETHFKCKYTYRL KVN*R*VYHVNIQEKALVAIDGAYFR ARKITRDKERHY/IMIGSMLQKD
9856	23757	A	9929	1	364	GTSGTRPINNTTVFSGKSSERKT/R/TH LTLNQKLEMIKLSGGGISKTDMG*NLGL LHQTQSQVNTKEMFLKEIKSATPLNT* MIRHQNSLIAAIGKVLVWIDQ/TQHNT LLSQRLIWNKALT
9857	23758	A	9930	88	374	ILKACGPCPGNPHPWGPL*GQGGGLQNP SKSPPHPHPRGDP*TWGGTPIGDYGP KLPHGAGLPKKPCSSGGQNN/PKISGP
9858	23759	A	9931	384	2	LCSPRFFYRKIWGGGQSSRLPPFPWKP GGKDCFS*PGVLDPPGEQRGAPCFP*KKI RWG*GAAPVVP*PQEG*/VGRAPLTPKI PAPVSFGCSPALPGEQSETPFFLKKKK KEKSEAMIPPPPGPRA
9859	23760	A	9932	32	359	IFFFLFFF/C*KGPPPPVQAGGQPKT PPWPP*IAKKT*PLSKKKKKKKGAGPP PPPKGGPPPLKKGEGLLKKRFLKKNNG ENFKKKKIWAGGGGNPREPPPPFGGAR
9860	23761	A	9933	138	1	TGFFCCC*SFALVAKGGVQWCDLGLSQP PPPG\SSDSPTYASCSC
9861	23762	A	9934	103	355	LAGQACCS*STSANRCVNHA\PGYANGR CDTITCILVFIRNSWLITPILITMFCY HVG*VRPQEQAPGNRVSLSDLLL\PPVT C
9862	23763	A	9935	29	363	AWSHNAFLFFFKRELAFVPPQGERENN FVSLKPPPPG*SPFSAPNPPKGGNGKPP PPPQLIFFYF*/GEKGFSYNPEGPKPP TLGKPLGF*NTKKICPQPRGLKKGQHI W
9863	23764	A	9936	173	363	PKKRPIISLKRAFN*SNPGD*QKFLKRG PPMGSQFKRGNYPYDKNLEKLCPPGGNK GSG/YHYGL
9864	23765	A	9937	360	3	NQMRKNQSSKTGICKNQSACPPPKERS SSLAMEQSWENVFDELREEGSR**NYS ELKEEVRTGKEVKNEK/NLDEWLSRI S/N*EKSLKDLMBLKPQAQELHGECP SSQFNQLARA
9865	23766	A	9938	194	370	VSNFFFFFTEFCFSAQVGAQGGNFR*L KAPPP\NCCLFPT*ASRVVGTGTCHHS WLI
9866	23767	A	9939	426	1	SQEFKVAVS*YDLTMHNSNSETLSQKE KTKQTKTKQKTY*EGRKHIKRCPTPLI

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						IREIQIQTTVRYHFTHIRI/VLLPQKQN KCWCVRVEKLKPLVRC*WECBTQPLWIT VWW/FLKILNIKLPFDLATPVVCIYQME FSC
9867	23768	A	9940	255	16	RVIYNIYIMYILCIYTPSRLLVEIGFHH VGQDGLDLLTS*SIKLSLPK\CWDYRYE PPCVNIYIYLHIYLIYMSDGVKY
9868	23769	A	9941	206	355	FLQHTAIKNGRG/WPGAHAHTCNPSTL GG*GGRII*QGEFKTSLTNMVEP
9869	23770	A	9942	3	402	HEELNPRSATSSPALVLHVHTIAHTIAF AEGCFQHDFCFSQPENRHIPLVFTTASK VRNIFYLLCRGRGILRFFLVCLKIDPAI PLMGIYPK\KSLYHKDTYIHMFLAAEFT VAKIRYQSKCPSTDD*IKKICV
9870	23771	A	9943	79	328	CIKILLKFLCLFCILPPCLNFFLRQSCS VARAGVQW\SLQP*PRLKHTPTSAS*S AETRGTHHHAHLIFSYNFL*R*VSHVA
9871	23772	A	9944	321	414	VPSWAG\PVAHACNPSTLGGRGGRIT*G QEFE
9872	23773	A	9945	142	480	QEAKSFDFSDSTTMEVMDKKQIRVIFL FEFK\MGRKAAETTCNIENAFAPGAAND *QMRWWLEKFCCKGESELEDEECGRPSE VDDQLRAIIEADPLTTIQEVAKELSID H
9873	23774	A	9946	191	3	FFLPRGGGDSVFKKPKKNGFPKIPFF CPGFPLAT/INFPPIQIFFFFF*DGVS LCHPGWNAV
9874	23775	A	9947	451	461	K*INK*KVKGW/RKEHHANINQKQVDVT IFISDNMNFRRKNKITGDREGRYIIKQ PIHQENIALNVYVNNRVAKYK*KLI ELKKEIHKFTILVGDFNTILSTIDRTTR *KVS
9875	23776	A	9948	186	405	NHTLAISLF*PYKP*AILKLGIRKERE LVC*RDICALMFITELVTAALWNQPKC PSTDK/WKMWYICTMEYYS
9876	23777	A	9949	18	412	PEFRITLILPEKKNLL*LTN*VSKFSGY NINI*TSVAFF\YSNNKISGTGKIVPF TILSNRMKYLGM/TLTKNMKDLHTENYK MLRKENEYQMGNGSWILKINIVKISI LHKVIYRVKFLSNFNAILLKK
9877	23778	A	9950	1	396	LAFDGRAERLKTGFHRVTQDGLELLTS* SVRLGLLKCWDYWREP/PVPGLOWD
9878	23779	A	9951	307	405	GIRVRR*PQGLRPPNDALVFKKMWPP PTN\PRGWGKGWEPPQGPQDPPPOAAP GFLPETWRGPWNSLPTRGAWPPNSNLP WPPAPSRHPAQRAPGPSTAAPPGGGGGE GWDPGRV
9879	23780	A	9952	2	402	YGRPKEGGSRLFVVLTPGPKGETPFFL KTQKITGGGGGGP*FPLPRRVQENSFY SRGGGFN*PKRAPCALTGKKQKFFLKK KKNTPQPKKLPKCRIQY*TQK/SSSLF MGTPGKRQ
9880	23781	A	9953	249	1070	SSFISRFYFICIYLFETRSHSVTKARVQ CCDYN*LQPPPGAQEILPLQPP*SAG\ ITGVAPNTPQLIFYFFVE/SGGSTHVAP RLALNSWAQNIAL/RLPKVLYFTF
9881	23782	A	9954	75	396	GFKGRKRGLEPLNQLKLTINLSEKGLS KANTGQKLGILL/RPVSVQVNPNGFLRE

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						IKSAF/PIEK*VI*KONSLIPDMBEVLG V/WKTKKYSHNIPGLSLTQKRVLTLF
9882	23783	A	9955	181	458	RLWNDGLYNI FDLKLQ/SIEHV*STLLLF ILEPESHVS\RLCSCGAVTTCSSLNIP GWSDSPPQAFQVAGTTGVCNNAWVPSAF L
9883	23784	A	9956	67	430	LAPRLIYSPIKFQWSFMSVRQIQVQSLA IGNFHNPRLPILICHYAFHRIILFQMV RNFILYSISISANKQESKILKYILLYI NLRNWLGTVAHAYN/PSTLGV*GGRIS* AHEFETSQGN
9884	23785	A	9957	77	422	LPLALWASCRPQLCLDTDFIHGPPTSGA ASQFLCFQTMQPTCSSLRYNL*PALV LDHTTSNVVCFRSP/SFFFLPLPLPPA PLP\FFFFFFFDRVLLCHPGWSAVARFQ LTAAS
9885	23786	A	9958	3	422	LHSSLVTEQDSISKKKKKKIFLGKTKK GGPSLGGFFFGPPGFPKIVKKRGALIG FPFFCPKKKPKKPLFFPKPLGKPPRKKG F*IGEPNKT/EGPGFPKKNFVFFSPWG GNFLFPPQKPGGKVGKILLQPKKPPGK G
9886	23787	A	9959	370	2	PFSSWVANFREGDGEKCSVLQGI RFCMF CRYINVTPLVHFPFPISKGTSTFFPLYFF SPEVM/HFP*LPY*FGWALLSRF*/MSL L*LFFSKFPFFPSFFFF*RFHSSPRLK CNGAISAHCNLCLP
9887	23788	A	9960	256	2	AWEETAPLHSHCLGNQARPNHRHAP\ P*LIVFVFSVETGFHHVAQAVLELLASS DPPTRFNLLSSWDYRGLSPQPMRSKSAQ EG
9888	23789	A	9961	269	3	HRQACGQVRSPICWACKIAQPSLQIV RSSLGK*I*SPYDPVPLPLVIYPRELKT \SLHTKTCT*RFTAALFIARRWKQLKC PSIDE
9889	23790	A	9962	268	324	SGTLSH/WIFS*VGIEITMWLKVDPQTK KISLRSABAAIKYFLTQATASIIIRRAI LFNNRLSEQSSITNTNQYSSLIIMAI AIKVGMAFFHF*VPEVTQGSPTSGLLV L
9890	23791	A	9963	341	2	ITFLPTKIIQSNFKTGKRTDSNDLNR HFKREDTQMANKYM*FI*KMQI\KTMR YYFISKRTTISRKTSNIQC*DTWSPGTF INCLLECKMVRLLWKMTWQFLTEVHIHL VY
9891	23792	A	9964	250	2	YHPVNLYFKYISPIDV*FGCFIYIFDYP LCSCFSLHPLVYLQ*L/LFFFFAESH VARLECSGVVSAHCNLRPLGSSDSPAS
9892	23793	A	9965	3	334	RTLRRHIIWLIDPSFE*HLSCFHLLAIVN SAAINIPC/HSYV*THF*YS*MYRGRTA GSYAT/SMLNLLRNCSTLLHRNCTF*PF YH/WE*VPISQSCQKLDFFIFLIIAIS EG
9893	23794	A	9966	179	352	NQE*TEILNRPMNSQIESVIKYLPTKRS HRPHRFTAELYQTY\ILLKLPQKVEGEG LL
9894	23795	A	9967	2	350	THPSINSFIHVFHASMNSLIHLPTHSF SIYLFTKSFIHLFIHFFSFLFLRPSFT

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						PVAIYSFIHPFTYSSIH*FIYPCVYSCI DEFTHSFTHAFIQHLFIH*II/IFIYSF ISFLFF
9895	23796	A	9968	228	558	CHQLRQELAIFTSFVILQLFSGHLDVYM QAWAQRDPKYEDNK*FIEIKKIQFTL ISKRMK/YVGINLTR*VKDLHNENYKTL MKEIEEDTSEWKDISCSWNGRINSVKT
9896	23797	A	9969	196	2	DRKVFFRPLFIIFGLKKRIFLWFFFP /IRGRG*IPFFFFFETESPSRLECS ETISCHCTP
9897	23798	A	9970	245	1	TQCDMCFVIYTHIYISHICYMVYIYIHT RTHTGILFTPKREKNSNTCTCATKDNP/ CMTLC*/HKRRQTHTHTHTHTHTHTH
9898	23799	A	9971	163	380	NHRRQKKNGR/HNGNKYKTVTKMINSNP PITRNNLVNGLKTPIKRQKLSDSIKKQ YPSIYCL*KT/YLKYKD
9899	23800	A	9972	328	1	AKCGFLKKLNIELFNSIPGHSCRT*TM FAAALYIIISKYKQSPSCPSNDE*MNEIW HILTIIGYSAVKKISWG/RWMNLENIARL SGRQRGHILQDSVDMKSPE*AIPO
9900	23801	A	9973	200	3	MASKCSSERKSHR/SITHNQKLEMIKLS EEGMSKAKIG*KLGFCLQ/VIHVVTAKG KFLKEIKSATP
9901	23802	A	9974	111	517	NLEQPLIKRTIANPKIKKINTTILITTI NVNGLNTLT/K/RQRWSD*IFKNQDPTMI /C*KKN/HCKYKDTNLTIKIG*KNIYDA NMLTQIKKKAGVAILI/DKIDFRA/TDI TRAKEGHFIMIKGSHVQEVVITLNVSAH AS
9902	23803	A	9975	342	3	FLATKKIFFFFFPVFPQGPVPLVAPFF WAFGGGPPKWPAPKKKFFGRGPPFENFF F*GFFFFKTGGFFLRFSKKVFFVFFVFF SETESCSVA/RECSGTISAYCNLCPLG SR
9903	23804	A	9976	13	326	ILDHSNRPSSTLTPNAGKDVQKQFL /LCCW*ECKIVNYLGR*L/WQPLTKLNL L*PYDPEILLGLIYQKELKTCIHTVACT *MFIEALFVIKT*KQPRYSSVG
9904	23805	A	9977	74	396	LAPRTQPLPCSPAPLRQCHTQSLPPFL LRLIFYFFCFLKTRAHSAQAQAQ*RDH GSLQT*TPTLACTPASA/VARTTGTHHH AWLIVFFL/IEKVSHSLVCDKT
9905	23806	A	9978	287	2	QPHNSSYTQIFTPKIIKTTPPNLKQNN TTPIKKKTK*FP/PSTNP/SYPSTHPPT HLFIYPLIHISPPSPTHPRIHPPTYLS IHPSTHPSIHPPSR
9906	23807	A	9979	97	332	GNNDLFLYFFFFLETGSHSVAQARVQWC DHSSL*PQPPGSSGPPISTC/RLGLQAC MCHAWLIFFNFCGRSLFLGLLR
9907	23808	A	9980	168	2	STWLRWDYWKTFFKTSKS/WPGTVALTY NPYTLGGQGRHIT*GQEFKTSANTVKS
9908	23809	A	9981	267	1	LKRERR*RRAN/SKTSRRKEIKIRABI TATENRKPIEK/SNKNG*FFEKTDK/I DNPLERLRKKERD*ITKVRNGREDIL*N NDLIKVKKD
9909	23810	A	9982	230	412	CHIYLC/D*PIDGIV*CHIYYFGHKHT HTYTHTHTHTHTHPTC*VSKILLKKRR TCSVCA

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9910	23811	A	9983	229	415	SYVFCRIRFCPLDSLKNKEIVA/SQVQWC VSVVSTT*VAEAGGSLEPRSLRPDWSQ RDPISK
9911	23812	A	9984	2	288	RGYDSTSSAYTVGHFT*EDKATITRLSG KENVKHAGGETLRLLDVYP*TORIIDS VGNLNSA\SAMM\GPRLPKVLGLQAWT TMPGP*KYTHIFF
9912	23813	A	9985	246	3	FLLDYQYCALCCHCFLFNFCNGHFNIL LGGVKHTKFPKYS*KFSVL/WLDAVAHS CNSSTLSGLGWITRGQEFETSLANMVK
9913	23814	A	9986	342	1	FLNFGLTGFFPKGPPKPLGLRDGALPLD PPQFLGVFKRGAFLGTQ*FHF\LEGFK FWFWEPKAFFFFF/CCETISAHCNLCPL GSSDSAASASWIAGITGAHHYARLSRRL RQQN
9914	23815	A	9987	330	1	NRPLNNLVMAKCSSEKRGYTSFVLSRK /LRKMIKLSSESMITVTTG*KLGLLCQT /VQVNTKEKFLMEIKSATPGNKGTVTKS NLTADREKV*VIWIKNKTNHKIPLSQ
9915	23816	A	9988	209	2	IKGSHFPULI*YRKIIIFGGVKGKGGF YSY\LFFFEKGYHSVTQLKCSGMILAP CNLCPLGS*DSPTS
9916	23817	A	9989	256	357	QHRWMNTEMLNYLC*IIVVHF/HTHTHT HTHTHTHTHTHT
9917	23818	A	9990	263	1	IQIRVFENSHLWPSYVHFPHGHSYLFCS L**AFFRH\G*FVLSVHFLKIFLNLKKI FFETG\SHSVAQACSGMISAHCNLCCLG SSDR
9918	23819	A	9991	3	368	SLDPRRSRLHLAKIVPPRSSLGDRAPC LLKKLELFFETGFCCVAQPGVRWCSHGP LQPRIFG\SSNPLTSAT*VAG\IAGMCY HTQLQLAF
9919	23820	A	9992	294	391	SGTVAHACNSSTLGGRGGWIT*GQ/ESQ TSLTNM
9920	23821	A	9993	317	3	TDKELLLRDEQRKCFVEMEFSPGKHAMS NVDMTKDLEYSINLVDKAAVELERADSN FERSSTLGKMLSNSISCYKIFLERKSQ LM*QIPLLLM/FKKLPQPP*PSA
9921	23822	A	9994	193	395	IFWITCCSSLSVLAASPTFFMLWRQLLS LNLNMNQ*DHSLSQSLIQKSATLFSVT AERGEDSAEEKLEASRSWFMRFKERSCL HNIKVGGEAARTDR/AAAASYPENLR/V KDEGGYTK*RIFVVDEIAFCWKTMPST FIAREKSI PGFKVSKDRMTARCGRSL
9922	23823	A	9995	82	420	SFLWKLCPRGAAAYVRCVSA/LLEDVSO LGYTGVRDPIERAVSPFSELKRCRERTT AVFTAVRQHLSQLK\FLLPFVQLCPAH RGGV*RQ*ALLCCGGLSPVQAPLPLCLP TQ
9923	23824	A	9996	376	1	CGRTDAPASTSPYAMTVRFLRPPQPCVL DGLHNCPARAPQEQNSLGEVDKRGPREQ TR\DATAAPPRPLGSPSWICPGDW**CR NSLQGFSLAASVARGRDWALAGLPATVS ARFQEQQKMTV
9924	23825	A	9997	495	982	VQKFLRPNLAPKKHQRKLAENSLQGRLR SLPSPTVWCTMAPPTGVLSLLLLVTIA VCLWRMHSWQKNHW*ASFKKTHD*TGLA EP\SCARKQCSSEGRYTSNAVISPNLETT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						RIMRVSHSTFPVVDCTAACCDLSSCDLAW /WFEGRCYLVSCPHKENCEPKMG
9925	23826	A	9998	401	341	IASKCSTERV/SRSHTLKQKLERFKL*E KGM/SKNEIGQK*ALLYQ/VSQVNAKE KFLKBIKVD\LHAQMIRK*NSLTADVKK VLVVKIDQTL/PLGHSVIQSKALTLFSS MKAQ*GEEAA*EKS
9926	23827	A	9999	30	393	DTTILKLRQLIIGAVATKHWSEKSLTS LNLNQKLGITIKLTEEGLKAKKGQKRG SCQTVGQVMN/SKEKFLKEIKHAIPGNT *MISK*NSL/IADMEKVLVG/WSKVIF *DOTSHNIP*SQN
9927	23828	A	10000	133	1420	EQRRLPVTGPVASLQTLCCFLPRGCSH G*ESAATHPPGPELVLLQLQGH*AGYLG /DFG/PRTATGSPG\PAGVQPGPCLVPQ LSRAAAAG*PDPT*GAIFSYHCKALRA TAARHCPPGC*WPG\PAGSPPGTSRPLS HPSSPSPPWTVGVSSFLNLVLC*ASDA QGHACYPGPVPALAGQGHDSAGGRLGDP GHHWQQAALHG/DQGGPGHQAAGTQPS AQGLGC*ATHPGEGG*VGYQGLPAG*GR SHPRFPITVRPMGRSCPYATVRPGPGSQ GQTPPGLV\PRGAGQNPCCAAPGLSCI QEVTRGWVW*GKKPLGHYPCCGAVRCP S*PHEDTMFKGTGREGCLPPTSPVGVGT QMS\EGSRPCEWLTMTSPWGE*SPRASC AMLHFCPGSRVGGYHGCPLHMGPPQST AGQAGQPHTLDIKAS
9928	23829	A	10001	1818	6682	IKFPEAEEEEIQEVLVLLFRVAEEKENP SRVGNQREYENQVVLYSICNQLRYRNN L/RHVKKDERGYEELLNYSRDHMLLYP YRLDIMVKGFSITPFSYYTGIMENIMN SGHNFTAADCLRLGIGRNQYIDLMIQC RSSKKFFRRKTAGDLLPIKPVEIAIEAW WVQAGYITEDDIKICTWPEKCATDKTV DSGPQLSGSLDYNVHSLYKKGFIYLDV PMSDDSCIAVAPLEGFVMNRVL/NFDYF ETLLYKIFVSVDEHTNVAELANVLEIDL SLVKNVSMYCRLGFAHKKGVINLDQL HSSWKNVPSINRLKSTLDP*KMLLSWGG GESRRPVQEASSATDDTNSQEDPADTA SVRSLSLSAGHTKHIAFLFDSTLTAFLM MGNLSPVQSTGEGEAQRYFDHALTLRNT ILFLRHNKDLVAQTAQPDQPNYGFPLDL LRCESLGLDPATCSRVLNKNYTLVSM APLTNEIRPVSSCTPQHIGPAIPEVSSV WFKLYIYHVTGQGPSSLSSKGTRLRKL PDIFQSY\DRLLITSSG/HDPGVVPTSH VLTMLNDALTHSAVLIQGHGLHGIGETV HVPFPFDETELQEDSC\NMGVHKALQIL RNRVDLQHLGGVVTMLNASSQLANRKL DASDERGKPDLAGSDV\NGSTESFEMV IEEATIDSATKQTSATTEADWVPLELC FGIPLFSSSELNRKVYRKIATHGL*\BKR AFKNLLHSSRKLSLQVLNLFVHSFQEGAS TLDIHTEPSFSSLLSQSSFADMGVPLPA KKFN/SLKIVSY
9929	23830	A	10002	439	1135	MAVDFYNFVTKLVVTTGYLRISFLAYKF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						FSFPFLDLSL/LLSPRLCSGVIPASLQ PLLPGFKRFL/CLSLPSS*GYRRAPPPC PALLYF*VETGFHHVGQAGLELLTSGKL TRLGLPKCWDYR
9930	23831	A	10003	216	572	LTLVSIPTAKQSVTLPIICMLEMRKWL NDTSAF/PII*KVLEPKIFFFFFF*KG VLFCEPFGGREGAQFGLTKPSPSGLKEIFL PNPPGGWKQRRVPPFAGYFCFFIKRRVS LLWRGLPN
9931	23832	A	10004	3	354	YSNNPKDRKGETGINEKTNNKMDLSSY TSVITLNF*ML*/D/KIN*KFVKSP*KK PTLCCLLETYFKYIGGLKVRWKI*H ANTIGKKTILVAILITKQTSLS*YPNKE EHYILIKE
9932	23833	A	10005	187	455	ASIHYSLGVRICITYIPGCIHPGEKSQKC NTCGKNSTQKPELVN/HR*LKGHRCKM* NEGGKTFTRVQSL/ACHKRVYTERKSYK C
9933	23834	A	10006	134	456	IWNLPGLKPCAWKQVTSDLISPDIAFIN AAIHSLSF FFF FFF FFF FFF FFF FFF NLN*LKLLPPKL\SDFLVA*VSKKVGIT GPPHPGLVIWGFKKKGGSPMLPR
9934	23835	A	10007	210	451	CYYTIQTTEQPANDSMLGIKPHVSI LTL NVNNLNTTPKRLGVADWIK/TQDPAFCC LQETSLTCNRTHRFKVG*/WKLIYH
9935	23836	A	10008	169	462	YPCWVDMAKNTSYNKCWQCGEIRILPH CRWEYKMASPLWK/SQFLNK*NMELP*D LPIPLLDIDPKEWKTGVQTKTCR/RMFI AALFPTSR
9936	23837	A	10009	490	724	EMPP*FMEKNFLAPGG\TPPGVNTTRV NPKTAFDPKRSSSPFLEKSQKPLIEGL THLKTILNPLKKDESSEIPVLF
9937	23838	A	10010	306	588	KQFIRAFIEMSWLTPVIVLWDTKADG SGIRDQPSQHGETPSLLKIEKLAGHGA GL*/SQLLERLRQENHLNPGGGGCSEPR SCYCIAAWVTE
9938	23839	A	10011	473	53	ISLQDSTDISTINIPMAFKLSKRKS HMSFSLNQ/L/EMIRLS/EEAC*KPRS QKLGLLSQS*PSCSKFLKETKSATPVN TQMI*K*NSLITNK/LKEVLMVWIKDQI KHTISLRQSVI*CKALPLFNSMKAERGE ESARC
9939	23840	A	10012	184	455	FWLSLIKKPLSSVTQKKINRET\ILLTT KKKKKDCNFLEGGLLIGGSVCRLVYRHY ATLYSVFCVDSSKSERGSVDPTQVPVET *DKCFDY
9940	23841	A	10013	203	453	KEELYISRERKSSTSLLLNQSQK*LIXL SEQAMPNANIGDRLKARPLSPNSHLIKT KQKFLKEV/KCATP
9941	23842	A	10014	237	483	TLIRYIILQGLFSYIPPPFFETESRSVA QAGVQW*DLGSLVPGSRHSPSSASQVAG TTGFHY/HAWLIFCLFCATGS
9942	23843	A	10015	157	875	DDPVRGRGEESAMPSSGRRNRSSVSSWV GSMAGITTIEAVKRKIQLHQADDAEE *AEHLQ*EAEGKRWAEQABEASVNG RIQLVEEELDCAQECALALQKLEAGK AADESERDTKVIBIWKLD/E/EKMEIQ EIQLKRAKHIADEADGKYEEVACKLVII

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EGDMGCTEERAELAESRC*EMDEQIRLM DQNLKCLSAAEKYSQKEA*CEKERKIL TDNLNKSPMR
9943	23844	A	10016	579	30	CGISTKKNKWMIKQNSSELSTCVHNQIT LHKIAMATQWG\KNSFFNK*C/W/EN*V ST/CKKIKLSPSVTCTI*KQYLKWKYL NIKI*QTS*IS\NGGKYDIGLGTNFFLLQ KTKNLMSPS*L*NQMHKEQIEKWDYIK LQNFCTSKKFKSGVKMSPKKW/DEIFEN HIFDRS*FSQYINN*V*NSTKSE
9944	23845	A	10017	44	228	EFVCRVRGLWW\CVVLASQLLWEARAGG SLBPKSLRLQ*AMIM/DCTPPW
9945	23846	A	10018	471	40	PGEGRFQQTRFPPLPPWGPFGGPFKK PKKKRKRKEMIKLS*KPRQANQ*LGLLCQ /TSQVVNAKEKFLKEIKNATPVNTORVR KLNSLIADIETVLVVGTEQDTSHNIPFG QSPIQINILAVFHSMAKQSKATEEKF EARS
9946	23847	A	10019	217	486	KKIS*PVYLSLYLSIYLSVCLSVYYLSI YLSIYLSIYLCIYLSITIIYYLSIYLPV YLSINLLSI/CLSPIYLLTYHLSSYLLS YLPTYLP
9947	23848	A	10020	327	1245	TENQQGVLAALSKIRMPTRLKWFNLN IDYTKFCEAFHVFKRKKKKKINKNIKQL KMPLTKRIYLAFTYSTQ*QONTH\FPL SADETHGKIE/HVLGPKTRHNKPKR
9948	23849	A	10021	329	490	GESPTDNHCRSPKSOVEKIYITPFETES RSVTPAGV*WCNLGSLQPPPP\GTSD
9949	23850	A	10022	3	394	YRVLEVLYGMLNIRFVVLGCSGQAAQ FREGRSCTTACRHPAHTLHAAKMSRRKV SSAKCR*RETPKKRSARWSAKPAP\QSE TKPKKAAGKDKSSTSS\FSSSSSLKAEK GGKBEQAEVADQETKDLSE
9950	23851	A	10023	448	477	SQVFETSLAS*MSKNIL/WAGTGAHTCN PSTLRGQGGQIT*SQVFETSLAS
9951	23852	A	10024	198	455	SLKTNRREIPEDFHGQPCGKLVHSEKPR VRMGQTESKYASLSFIKVLRRGGVRA S/TRNLIMLFQTIEQFCLWFPE*GTLDL KDW
9952	23853	A	10025	469	26	PPRAVQPPFLPSSSLHTCVPLCRTVFSA TSRPDSLLPALQVSAKMSFVL*SSLILP SLGQGFPMASIA PRL/PHRSLRSCVVAA AHSRAELDRHEAFLQCSLGQWPRNDFLF SFFRDRVLLCHPGWSTAA*S*LTAASNS GAQVMEFQ
9953	23854	A	10026	222	489	KKKKKKKKFCFIARVKSNGAISAPCNLC LSGSNYFPASTSLVSGNTGACPLARVNF FY*NL\FLVKMGFHHIGQESI
9954	23855	A	10027	313	2	QDWEISKLYSYCHS*VRL/IFLKRILS LYYILQHSNLNCNIG*LQFESCYIKLAG DKIAFRFLT LKTNHQLGLVAHAYNSSTL GGRDGWIT*GQEFKPSLANM
9955	23856	A	10028	49	388	TPKIRGVFPFGWFLGVFGAFPFPQKDI FYFPTPMGTRLVSPGKKKKKEV*RVLY GLKKAKKIFVLKVKFSHKRGFFGEIQFK KLFKW/HLKRNPFPKKKKR
9956	23857	A	10029	394	231	GRQIASAQEFKTSWGNMAKLCIFI*RD VSPCCPSWS*IPBLKQSACLSLPKY*DY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RC/RNTTPGL*HLLFRCLLITLPSYLPF CKSFKLLYMDI
9957	23858	A	10030	265	2	HDNMRGSDYFPASNGLAVPFKRQVFTIA SNFLEKSPRLAFT*LQVD*ERKAG\ P VAHTCNPSTLGGQGGWITRGQBFKTSLA NMPKP
9958	23859	A	10031	235	413	KAGKLFFFTTEITFKKGGKAGGGGSFLKP HLFGRPGGNNHRVRL*KRGFYKMGVV LKSLPCDSPPLASQKGGVSRKSPPPRP CPF*RLFP*KKKAFLRFIPKKV*ALV/ SLPFIGEGKTLFFFF*DRALLCRPGWNA VAPSGKLSSCLSLRS*DYKHVPCLLA MF*KFF/CRN
9959	23860	A	10032	167	424	GREFDLRMGHMVKPPLSFFFFPFSETMS LSVTQAGVQW*DITALSASWTPVISDSP VSASRVAG\IGTTGVRHHTQLIFL
9960	23861	A	10033	252	3	VEGCLSSGVQDQPEQHSETPSLQKKIFF *LAGHGSML*SQLLGRRLRWEDHSSPG G*SCSEP*SCHCSPAWARE*DPISKKKK
9961	23862	A	10034	175	492	CPTCFVWIFLPCSEQPVQLYMVVHTHTH THHTHTHTHTHA/HLLFSLFSFSLRQG LSLSPTLWRSGL/CGSTQSQSPRLKQF CSPRYSRG*GWRMA*/DPGGRGCSE
9962	23863	A	10035	200	448	LYLHLVQLSPLDFPTPLRVECPVLSL CLSFS*FP*VCFVFLVSLGLF*GRVLLC RPGWSAVVQSQLTAD/SDFPVLKHSSCL
9963	23864	A	10036	229	463	MILGISKISFSLAITLANFPPTLNLFIF LDTGSCSVAQADVQWHNQSL*/SELLG SSDPPTSAS
9964	23865	A	10037	164	422	GLSSQLTDGHLALLRVGGSEVGSREERS EREEAGREREGERRDSRG*ERERERES GAREEREKKEKRE/ERDRBEK
9965	23866	A	10038	1	490	PNQIQNAVLIMISFISICFVSVIFFKSEI YNGQPKFKSFFFF*DESCSVAQAGV/W CG/LQSQQPRPPG\SSNP\PTSASGVAG ST
9966	23867	A	10039	255	446	FFLRQSCYVAQARVQ/YAIHRCSSHSTLQ LPALASSNPSALLAPRVAGTAGMQHNNQ L*YFFRIHS
9967	23868	A	10040	157	390	DHTCPPPSTADYRLS*FLYFLLLLFRRS LALPPMLECSGAISAHCTLCVQETRETD AAHFKAARTIRAPHPAQLTIAFQVQTHV YQDGH/DGSWWCDLRTHPPRS
9968	23869	A	10041	290	30	TLKKRKEFSSVLCPRGYIVLLLHVHQL FFQTGSCSVTQAGMQ/W/CDQSSLQP*T PG\SNPPVVSASQVAGPTGMHGHFLHTE YESRGPP
9969	23870	A	10042	190	929	NHRYISYLTRLVKIKNFANKSWLESLSF TLKHS*/W*CK*V*SLWKTVMHYLVNL/ KDLTFDPAIPFLMIYLIEMCAQVHPEI YARMFIAVLFEIFKHQ\NNPNKLWYIHT RESYKTIKIKE
9970	23871	A	10043	457	724	HFGRRPQVDCLSGVQDQPGQHGVEQSV LKL/KKLAGHGGGAHL*SQLLWRLRHENH LNLGGRGCSEPRWCHFTPAWTTEQDSV* NNNNNN
9971	23872	A	10044	111	429	KPDEDTTGRENYPVFFNTDANLSKYK CMYPCISVH/HVNMYGKIPEMMFT*Y**

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						*LFLSFFFYEMESGSVPRLECSGVISAH CNLSLPASSNPPPGFPR
9972	23873	A	10045	30	220	LGVLVKKNVFNKCYWDN*ISIWKRM/G LDPYLTPTHKINFKWIKDNIITKTLIC CSWMKTKA
9973	23874	A	10046	203	361	TYKLLVIFIVIDHF/LFSFLSFFFRDRV SFLPRLECSGAISTHRNL*LPGSSD
9974	23875	A	10047	198	358	IQRKCTFFFFFEV*SCFVAQAEVQYCG SPG\SSNLPFSASEVSKTIGVVILPS
9975	23876	A	10048	270	272	RKNQRFFFKIARKRLNKMTRISPLSIII LNVSGLNFPKRYRLAEWTKKKK\DP CCL/QKTHFAG/RDIYRLKIKGWKPIH TNGSQ*QRSEFF
9976	23877	A	10050	256	1	GVTNLYFWKNFLNPPFLVKKCENCPIN KVFP*KPPLLKKTLEFSKKKFCGV/HPT EKFFFFFESLALSPRLQCNGTILAHCN LR
9977	23878	A	10051	112	359	SKVSEPTENEVEHNLKV*SFILPLKQY SM**QKKNIH\ISFYKK*ELTWPGMV AHACNPGRLGTEAGRSPEGQEFETSLA
9978	23879	A	10052	346	2	RVSSYTLITLNLNRLNVALKRYRRLNGF PFLKKP*PN\ICCIQKINLIYKSTYSLK VKGWKNH\HANGKKQAEVAI/LFISD KKDFKSKI VKRDEGHVMTKGS IQQ*D RTIL
9979	23880	A	10053	376	6	TRPSQHPDFILLNKCLLFEATPFLVICY SGHRKLRPVAPPPIRGSKSQIIPMPPAVL PRWHLSCLSFRIPSSFF*LRLPRLCKSR /SAWGPVSPHLPQLFFQAISSFFFL*D GILLCHPGWSAVA
9980	23881	A	10054	102	347	FLSFFVDGKLCLEAKIWLAPAVFIVTR VLLLSTL/RQVELRNIYLCNVHIFH LYFCIYLSAYILQTMSLY*HL*YHSNV
9981	23882	A	10055	251	51	ISLVNWLFILENMKLDPYLSPYTKINIR /WQ*DLNVKNGTTKVLSEN*GTIYVMVG WKRPIACQPKS
9982	23883	A	10056	169	342	SQKQYSTCQNVFCVLFLETRSHLV\TT LECSGAIMAYCRDLPG*RHPPTSAS*V DG
9983	23884	A	10057	1	586	AAARPAQGGKARPGLLLRGRVVELRAGF LTAKGAFRWLSQKHVKMSYPQSRGCG GGMGAAGPPSLTVHQELCGAYS PDGTE ALPLASWPRARPSAKAPAYDTAKLPAL IGCGSRRPPGVNPGASSLKPGACVSEGA GPTGTLESAGSRPPTPLPPV/CCPGPP ARADH*FCHVTPQCR*/PPRPSP
9984	23885	A	10058	393	43	HARPGAECERPAEGEARADAFSGRHAC PHSLYCRL*RGPFVHKLHLNKA/RLIKR RKADNIKWCQRCGAPGTLMHC*WDYETM GLLEQTVFSFEIRSHCAAQAGVORNNHG SLQEF
9985	23886	A	10059	228	466	GLLHGPPYIDLPEPVSTTSPSLYHPPIVP *ASPLGPSAILTLFPHSPPPA/PLFSP HVLGSSGPRSLPT/SPTHLPTLTPH
9986	23887	A	10060	293	9	DILQFYTFSPIQ\CPVYILHL*YISLQR L*FHQKYLIGIYFIETWSCSVARLECSG RITPRCNLNPFGPTYPTPSASGVAGTTG VCDFGLPWSR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
9987	23888	A	10061	199	428	TAYCRTLPKKSNTISGSFFFFLETGPRSVPG* RAGG\DLMAHCSFDLPGSRDSPASPRQVVGATGCPCHPWLF
9988	23889	A	10062	191	2281	LQTRGKLFKYKEKGICTKLHRSIIIGKQWKEAVCPPTGQAQSQGGLDPKSREALRGGHGFVPGGGVCGHQEL* LHSDGLKAVHPAGSEPSDPGGVQAAACQDAATGGTFLQPMPEARGC/TATASSRAGPGMDP/REA/GPEAWQLGKARSSWGSSTSGGPAWVFIRDTPSWWGIPGTVSPAGPRCPPPTRPQWEQLGSGRPG* MQTTAETNAAPRAGQERTPSRGPSADPGVSQHVLSHRRSCPKCERRSVPPNG\AGPTLWTELHPSDASVSALTPL* GDVEVGPPY\CEGYIKPGRRTHQHNWLDLDRPAASRTCRKMLELPRV* FLLRLPELAETYSSTPPACAQRPRGTGGG/PPQRCVLMSSGSHQGGAS* KGRDAPSLSGLERPREGGPGWLS/RQPSPHAVQPCCKHMLCLGPAP* RGRGARGVEVPVRASHFPFHGAAWPGDHMSQP* WQMLSRPARGHRPSWQVRRQCTVLGALKPGLPDLKCPGPATAFLPG* GVS/EEHQIPNVSTQLYLQNLPLPREON* RRFPRDLSSGAGPGTG*CGGGGCHALSPTPSRRLRAHSKDNSWAQPLCCWMPAASGC\PGIGCNGVPPVAAS* QAAA*TPPWSESSLPAG*QPSAHRCVTRVPGGRIPHLLAQAVPPDDRAFPNCQASQQLGVHSRPSLSAAGCRQPLAVSGIGCNGVPPVAAS
9989	23890	A	10063	65	453	ISREFLFLETKSLYIMLKSGSIQQEDIIFVNIYTLNTGAPRY/IK* ILLELKRQIESDTVIPEDDNTPLSALNRPSRQK/VDLICTIEQMDLIDIYRTFHPTASEYLFSSAHGSFSKKYYMLGHKICLETFLN
9990	23891	A	10064	100	466	LGILPLQSRPSGGQCTPTLPFVWSLPVPVRCFLHLCWCLPYSGALGSPCHTGLVCWHIPCF* CCGVSP*R\SCLEVHLYTHTHTHTHTHTRFVLM* MRTPLRKGKRQVMRLCGGGGRA
9991	23892	A	10065	226	377	GLAGSPCISGSVSFCSGCY\RGHGIMFICNDCKVFRFCKSK* NCFKEHNP
9992	23893	A	10066	292	458	KVSSICLKMSFLFLFFRTGSHCH*KVSSICLKMSFLFLFFRTGSH/SSPRLECSGMILAHCSLKLLDSSDLTASAS* VAG
9993	23894	A	10067	252	36	TGFNPLHFIIIIIIIIII\FESKSCSHAQAGVQCCDHGSLKQP\PSSSHPTSA* VAGSRNAHQANSTAWPMVS
9994	23895	A	10068	56	481	GILKNCHNLMIKLRMRSCVLMGEQRK/WIY* DESTPGEDTVNTVEITINDLEYFINLVEKTV/GVETVDSNFERGPTVGK\IVCYREIFHEKKSPPMQQL\Y* KFPQPLOPSAATTLVS*QPS\SKQDPLSARRLQFTAGSD
9995	23896	A	10069	263	435	HFSFLSFFF*KTESHSVT/RVEGRGGISVDCKLCRPGSRDSFASASRVPGTKGISQGRG
9996	23897	A	10070	116	474	RGAGAWGVSGRSSPPLSALPIQPPPHLSTPPPLETP/PPVLH* PLKDLGGWGALLA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						Q*RLPG*HSPKPKKKKKKAPRPPYK*GP PKTPVDPDPDGPFLDPPLFGWPPPP\VF LPGERPPPL
9997	23898	A	10071	159	377	KSHMPLTLNQKLEMIKLSBE/GLMSTAE IGQKL/GLLLPNSQVVAKEKFLKEMKS TSPGNT*TIKWPGAVADA
9998	23899	A	10072	180	473	AIETQLLSRPLCLWPSGRFPDAQVANIR VRVAV*GNPLR*VGPAEPGEQRPSPWGF PSIS/WDISPTWSSSASPGLSADCKFT CHYRCRALVCLDCCG
9999	23900	A	10073	98	440	GQLNKLSGPYPENVGTYTLPLVILNPLAQ PVIYSTIFAGTLITALSSH*FFT*VGLEI NMLAFIPVLTKK\INPRSTEAAYKYFLT QATASIILLIAILFNILSGQKKKKKGR PF
10000	23901	A	10074	358	404	PCLYTYHLHNSNST*SLRLVSIIMEIVT SNLHRTVPHSYTPPTQLSINLVMAIHL AGAWIISYPSMIKNALVHFLPQGSPTPL IPILVIETISLLIQ\PREPLAVRLTGNI TAGHLLMHLIGSATLAISTINLASTLII FTILILLT
10001	23902	A	10076	3	419	KWRKKMWCLQKMEYYSS*KGKLLSHVT IWMDEEVMLS/EIS/SVTEGQILFNST YV
10002	23903	A	10077	335	414	DKSPF/D*RFFLPNSNGFLVKMPPSVK RLPFFFFIFPFSFFFFETESRSVT\RLBC SGTGLAHNCNLRLPGRDS
10003	23904	A	10078	279	1	KDTQLPFIQFFPETGSCSVPEAGVQWCD HSSLQPPPP/GSSGSSPLSL*VAGTIGM LIFKIFSRNPLNFFFLRWSLALSPDWS AVARSWFT
10004	23905	A	10079	397	3	KSSSLFQNLHANSSTYSHLIPTLGYIL NHGNOFDPDTL/RDKM*NEFFCTIVCPHY ELPSLEQW/VSLGSLNYDTILPLDLFCK RQGWSEIPYAQDFMTLYQNLTCQT/P QNPPPPPKESSKVELDIIDDPH
10005	23906	A	10080	281	1	IFLGEWGPFFFPQKKSFFFKIPQWVFFT PPYRKIKIFFFLPR*NWA/HPKIFFKRPP PFFFFFFFFFPGFKENCFILLPPKEHI TQAPAWGFAG
10006	23907	A	10081	207	35	QENRRC*RGREGS/GTLIHGWRECQTQV PLWKTWQLLKRLNTEPPYDLAILLLGE FH
10007	23908	A	10082	2	408	IAPLHSSLGDRARLRLKKKKKKGKIRPL LALFFKNQNPFSFKNSHSFYGALMEP/P PPHIPPPFFWKVQPPLFPFRGTLEFPGP IGTCKLQTLGSPG*WDPPCPLPHQSPGR GGLIPGRKGEDPPSFRGLPPPHF
10008	23909	A	10083	195	2	ECKQRQPQLEMVSRFRRSHEPFFETGPR SVAQAGMQWH/DLSSLKPPAPG\SGDLP TSAS*VAGTI
10009	23910	A	10084	219	1	RLKIKLLKIIITTTIDSGICSFKSKCL* H/LKIQNMWLDKLAHAYNPSTSGGRGRQ IT*GQEFKTSLGNMVKP
10010	23911	A	10085	364	413	KKKGGEKGPLLKKER*KTNGQFLVHTNF /RLPGLKYFF/CPPPPSKWGLRAPPPKP GDFFFFFFFFFLVFLVETGFHHVQAGLE LLTS*PIPLGFPKCWDYRRE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
10011	23912	A	10086	200	3	INFILLLLFIFVLLIFETGPCSIAQATVQ WRDHGTLPQPLGLKQAILP/ASAP*VP RITDVHHHARLN
10012	23913	A	10087	154	329	FSLSDFKTYKKAAGHRGSL*YQHFQKP \RRDPLRPVQDQPDQRGETPSLLKKK KKK
10013	23914	A	10088	157	390	NSSSFPPSCGAQ/KSEVKSSSGPHSSS SSG*RGE/CLPLLVSGGSWHFLAYGSLT PVSACVFT*PFMSLSCVYIQISVS
10014	23915	A	10089	305	1	KKKRAQSLPGQKGGRGFSQPVTAGDRSF RPKIRKEALGLGQLGLTDLCRTFPPTAT G*TFSSAPFPG\YPPV*PTKKNTNLN *FTRIKIISRIFSGHEK
10015	23916	A	10090	329	2	RGFPQPLGFWDPGPIISNLGGPPKLNLLK AEIMGYNFCVPPFPFPGGLPTTHFFPPPR NPPF/CFPFTPSLGFSSNPPGFFFFF FFLSRVSLCHLGWSAVA*SWLSAAS
10016	23917	A	10091	84	408	EKKGENKLFWGFLLGLTFLIGGYRFKI FCLVGYFIFIYLFGE/FSLLLPGL*C NGTCSVHHNLPLPGASGSPASTSGEGGI TGMRRHRLY*YLGWRSFALVARAVMQ WHVLGSPQSPAWCKRFSCNLNRRGWY RHAPAPPSLLNIQKIILGFWLAPVY
10017	23918	A	10092	184	359	FQINSSVTRRSFVLAAGVQWRDLGSP LLPPF\GSSDSPASAS*VAGITGLHVGL SHK
10018	23919	A	10093	298	386	KLCEK*ITPIRMATII*KKREGENS\KC W*GCGEIGTLVYCL*EYKMQPLWKIVW QFLKILGIEL
10019	23920	A	10094	310	1	ICMNEMLYKQDFGRITIIIRKIVIFYWI FN*FGH*IRIY*NLLRYKTCML*RG**I NLPQRSFKNLRLKI**W/WPGTVAHAYN PNTSGGRGGRT*DRFETS
10020	23921	A	10095	40	407	EHTTTACEPGGI*IRPVD*MLISWL* HGTITCKMVTLGETGQKPGQISLIIF FFG\TQSLFVPRNGVHCRGPISAR*KLC LPGPPLSPT*AS*VAETTGACYCTWFEN NFFLRLPLHCY
10021	23922	A	10096	189	2	PPFFFFSNLFKKSFYEQGLALSPLKCR GIIIA/HCS/L*TPG/YK*SSCLSLP\S SWDDRCAPPRV
10022	23923	A	10097	260	401	DHLRSGVQD*LGQHGETSLLKVQKLDG RGGLQLIP\RRLMHENHLN
10023	23924	A	10098	187	464	WYMTRCGLGPSSAAHESHHPQQLMN P\PSPPSSAAHESHHPQQLMNPTIPLL SS*IPSPSSAAHESPGRVGRPEFTGGAH GYLHLSPP
10024	23925	A	10099	397	1	FFGGAPCPPRRKGKTPPPPRKLPFPFF PKKFPPLPKNC*NKNPLLGPKKKNRPP PGRFFKGGFF*NPKAPLTNFWKKKK \SPFFKGVFFPPGEPKPPPPPPPPPP FFFFPTPRVRVRVRVRV
10025	23926	A	10100	253	3	NAINRNKMQ*TKTSEWVYADHNATIKQ KQKRKCQVL/WRGCGETETLVACWECQ MEQPAPVEN/W*HFLENIKIQLPYDPAI HE
10026	23927	A	10101	121	404	VLASVVSIFFFFFFWKGLIFSPRLEGG G/LILG*LKPPLSGLGPFSCLTLPGEWE

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						LKPPPPDPGFFFFF*GKTGPPRGQEGLNFLTWEPPPLAL
10027	23928	A	10102	468	1829	IRDTYTONPDKAGYFSCIFFEIEETTM SRKQNKQDSSGPIFDLQSNVLAQGGAF ENMKEKINAVRAIVPNKSNNEIILVLQH FDNCVDKTVQAPMEGSASEVLKEWTVTG KKKNNKKKKPKPAEPPSNGIPDSSKSV SIQBEQSAPSSSEKGGMNGYHVNGAINDT ESVDSLSEGLETLSDARELEDPEASML DMLDRTGSMQLQNGVSDFFETKSLTMHSIH NSQQPRNAKSLSRPTTETQFSNMGMED V/RPRHQ*KS*VPIFEKSVKDLQRCVTS LARYRVVVKEMDASIKKMQAFABLET LINGSRKWALLAEMDKVKAEMEFLLSR QKKAELLKKMTHVAVQMSEQQLVELRAD IKHFVSERKYDEDLGRVARFTCDVETLK KSIDSFGQVSHPKNSYSTRSRCSSVTSV SLSRPSDASAASSSTCASPPSHTSANKK NFAPGVY
10028	23929	A	10103	254	2	KKKDFPLTPLGFGGLKIQLEFFLQKKKN FYPPP*IFPKIFFFFFFWGTQSCPVT\ RLECSDRIPAHYNLHLQSSSHSRASVSH E
10029	23930	A	10104	256	419	KVIELHTGR/CAVGQHVGRPRVDCSS GIGDQPEQHGEPLY*KNAQSSQAWW
10030	23931	A	10105	153	439	TTVTSLCIYVTIYYFRLLSTHAYTHIY THIYV*KLTIKQPQAGPSEGF*KKEF** RRW/WVGTVAHTCNPSTLRCQGGWMT*G QEFETSLANMVKL
10031	23932	A	10106	424	157	SSHLGRPRWVDHLSPGVPDQWQHGETP SL/LKLAGGACL*SQLIGRM/RLSSGGR GCSEP*SHHCIPVWETEQDPISKKNQTI FRMFKN
10032	23933	A	10107	213	3	NYKCEPTPNLNTLKALYFKKLILSPKA* AIKEKID*/IIKIKHYASNIINRMKQ LTEWKIFANHVSDKG
10033	23934	A	10108	300	1	TPKQKGKKSPPREKPPVNLPGKTLF/Y EV*FMNPLK*QKKKNFQGGFFFLICGT VYHQFTSK*ERGVPGTVAHTCNPSTLGG RGGWIT*DQEFETSLG
10034	23935	A	10109	120	421	KKIKKKNKNHMII\SIDAE*AFDKIQHR FMIKTLNKLGPGRHI/KIMKATYGRGG QDGLHTAKK/EPLPLRENKISGKP
10035	23936	A	10110	102	418	TLVCVCVCVCVCVCVSLSVLSLSLCLS QAGVQWCDHSSLQPRPSG\SGDSPTIAS VVGGITGVHCHIWPFTFYFLIRLKLML L**TSSEMALTKMGVHSHGLFN
10036	23937	A	10111	382	2	VNNATMPKSCSTESKSHMSTSNQKLEMI KLSEKMLKAKIGLKLGLLC/QVSQVVN AKKKF*REI*NPTPVNIR/DMQKVLV/V KTEDQTSNIPNLQILIQNKSLTLFNSI KAERSEEA*EKCEDSRG
10037	23938	A	10112	61	427	ENTTYQVQCSIKEEYLQRTLKYSALFQ KHICGLAFLHLL*PKLYHSRNSAESDW IIQLFSVQPNVKEISKHKIGW*RGHACN /RQHFERPRKHDLRLGVRDHPCHGET PSLLSLLKIHI
10038	23939	A	10113	71	399	NVLGKEARSVGWEAVRGQISRVS IQMKW

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						KGLIKGEKLMKESQACICTYFFFFETE TNFIAQAGGQGHDLGFMEPPSPG*SDS PA*APHEQNGL/TGMHNPVIFV
10039	23940	A	10114	362	1	SKKKSWGSHSGSKCHTSFLSYPTKEQKS YLSLFYKCNLQSLTFKELLDFRPVCLP TIY*NKNWP/RDLPKPSFKTLML*NQT L/WPGVVAHACNP SILGGQGWITRGQE LKTIFANTVK
10040	23941	A	10115	314	3	WRERRCAHLMRCASNMAHDKPSRMLNL *KPKMAT/RNTDHDNFW*GHGETILNH YWDYKIM*PLWKT*QPPKMFNIKLPY VSYIQLLGITYPRNLKINIHTKT
10041	23942	A	10116	44	394	PGFORVSQDGLDLLTS*SAHLGLPKCWD YRHEPLRPAGIYSYPAVLVFLSTYRASN IT*MLMTPKPTSG\YSFLLSFRFSSFSY LRDISAYMSLSCLKLNVPKSKPIIFLSP LWLLV
10042	23943	A	10117	398	3	MESCCFMGIEFVLKEEVLEIGCRTM*Y LHY*SLHLRMVKMVTSLLCVFYHN*TIF KKSSVFLYAGNKQL*I*ILENYIYVMIP FTITSRNMKRNLTQDKDMSTETKYKTQ LKEITD*NKWRDTTFMHQN
10043	23944	A	10118	104	386	KVPVWATCGVKMRLAGHGGWRLWTRLP WRLRRDNRLSSGSRGA\AEILPLCHCT PTWVTEHDSITYKY*KKGAPCWRASS*C TLSGHALFFFA
10044	23945	A	10119	258	401	YNYPFLTVMKEKIGAGMAAHACNPSTP GGRGG*\TRGOHLETSPTNMV
10045	23946	A	10120	310	384	GVFPFLTFLYGGIKGGPPPPFFFLF*FA FLFFFF/ETGSHSVAQANCSGSVAHRS FHLPGPGDPPTSAS*VTGTTGICHHS
10046	23947	A	10121	245	479	TSSLYRKIQKRFYMLALEVLKICNTYF MNTERRFPLKFGQFS/FRIISI*FFPFL FPKIYHYFLRDRV*LCHPGWSAV
10047	23948	A	10122	268	469	NSVPWLGVVAHA/W*VNPSTLGGRGWI TRGQLETTANILPP
10048	23949	A	10123	221	423	GOAGAVAHACNPNALGRPRRSDSLRPGV GDQPGQHSKTPSL/LKSDNF*KMGWLG WAWWLTPILPALW
10049	23950	A	10124	73	183	AGGGWALTNVINPT\PESTPFTPCLSY SCTISTASAFRFPQ\STSTAVLTHVRIL KSTPDAPHPPLKIPRARRNIQRDHTLSS NLFYYNHQNLNVTLELTYYDLT*INPTAT IHAIHTMPLFLHNLNCISI
10050	23951	A	10125	342	2	PNLGCPPPRGTKGGPPFFSFHPSI\IG PPNFPSF*RP*FF*MLKSLGVP/SPTGP IPKPPFFPGFKNYFSPPL\PKGPLLKPP RALFFFFFNNRHRVLL\CPGWSPTAGLK RSSC
10051	23952	A	10126	85	442	KKVINIKCW*RVWRTGSLIHCSWG*KMM PHWRAVWQSF/SLSMYLSYEPALPLEG SYPRALRTTCVCTHSRCPSLLELPQA/W NH
10052	23953	A	10127	180	484	KSFFFFSQAQPIKVIPAP*NPHFFGVK RSSCLSFLRKWGPWWPPPPPPPPFFFL IFVEMRSHYAAQAGLKCLASS\VPPPSG IPRTLD*SYPD
10053	23954	A	10128	376	1	WSPGAQLLFISCLYYNLWSLHTGRTPAK

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						PP*GWTLQKTTPLSCPAP*LPPLPSP QQIDLKELVFTAPACSL/PHSPNSSPW PQRWPSVS/P/PVAHPAPRLPPPPVC ARPLWLPEAPLLGIPPH
10054	23955	A	10129	140	454	CLIRSSINSVHNNYTHSTPDRHLGCFQ FLVVTKNAAVSRLAYVF**I*IPYDHI HTHTPAGYIPRHGIAGSQLTNIFNFSS* LSSNSF/QVGCTSYFLPFSHI
10055	23956	A	10130	340	473	AGARHSVLRPRPPLAGSSCPSS/CGGHC VALGVSCPGGGCRAACVPGCCCLLGLP SDVCVC/SVCWGGSGMSRLGGWAAPGF* GNSREGPGNCSSGRKAGLAGGGLGPAAW EQAPDILCCGPGPHWLGAPAQVPLAPPL SPPPCLYGCLYSDRGDL
10056	23957	A	10131	280	2	DSLALLPRLEYNGVNVAHCKLKSSWIRR SSHLSLPKHLDYRSMH/LPGLEIF*YS YCK*CLLTSPYFEFLMNSLEDISSCFIP IRVMPKCRMK
10057	23958	A	10132	244	3	IISTDLISHSWTLYLISSLVYVFLKQHS LAVLPRLDSCGMIIAHC/KLQTPGLKR/ FL/CLSLPST*DYRHTPPNANFYYYF
10058	23959	A	10133	272	3	VGKPRVFPYRIAFNFRVTSILGPHIKK YHFQCRGGKHCF*KAPEFF\FNETG FCSVPRLECSGTIIALCSINLQGCNSP TSVSQV
10059	23960	A	10134	217	3	FPRFRPLVSPALTELQGF/HFLTRGL*K KKPFFLFFFFSETESCISA/RLWGSGM ISAHCNCLPGSSRTRG
10060	23961	A	10135	229	3	KNDYLCWQCGRTETQMLGCWDIK/LI QP/LWKIIWQFLKLNMHLLCNPTLPLL GIYP*EMNVVYHTQTCICTDAW
10061	23962	A	10136	84	352	RRFKTGLATWQNLVSTKKYKTTVRYHL TSTRMDIIKGR*QVCW/RKC/GDKGTL LDC/WMRMLVQPIWKIV*VWKFCRK*KL NLFFPPPPQ
10062	23963	A	10137	280	2	KCVVPEERILREKSQHLGKIKQEGRLN AVVLIQPGQHGGETLSLQKI/QLAGHGA PLRSQHLRRMRREDHLSPGVRSRSEP** LSLHWVTEQ
10063	23964	A	10138	2	386	HIQEQLPNKDSTLNPFLLISILKRKD EKIQMPSKHMKRCSTSLVIREMQIKRS HFPH*VGKILKSANIKRW*MCRKRG\TL ITCW*TYK*TYKLVKTF*RIILQHPLK THQSYYPAPHLKETOQA
10064	23965	A	10139	229	1	TRSYHESLTILHTNHLNCSFFPOAITP *SRFPYSNRA/WLGSVAHTYNPSTLGG RRNA*GQEFKTSNLNPK
10065	23966	A	10140	261	429	LSHLFVALI*LGLVW/SFVVFVFFETGS LPRLECSGVITAHCSLDLLGLSLPTSA F
10066	23967	A	10141	377	34	WVFGSSGPPPPGFKFFSEPPPKNKNR GPPPPPIFFFFCKKGVSLFLPPGGGP /HPFLSPPPGVKPENFFDRGGGGFP*T KIFSRPPPPGKQNFFFLKKKKKKKEHQ IKR
10067	23968	A	10142	208	424	FFSLFMQTFHIHRYFFLAGGGGAGVD RVS/LLSPRLECRDTISVHCYIHLPGSK QFSCLSLLSN*NYRHAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10068	23969	A	10143	1	297	PTSRSPQVSNLNHKSFTISFYLFIDLLSVC LSVSVYFETSLTLLPRLECSGAITTHLS LLSS*GHRHAPPCQV\FFVETRFHNVSQ SGIELLSSSHLPPTA
10069	23970	A	10144	185	488	SGFPRGTTELIGAVCVVCVCACVCVCYK LGYI*NHKRIYI*LLYIYSTYIYNLSL *LSVY\SYVNRNSM*DRSQSI*IFILPK LKTCLNTHTLKNTHEGG
10070	23971	A	10145	283	3	LGWPGRKADGSGKLTIDYGRLDKLVSP\ I*SAISDMASTTKAVLQQRDQYSVLDL AHAFFSIR\NQSQFSFIRDSPQYAFITLP SEEHLSLSDGO
10071	23972	A	10146	146	380	CFLWDNFFFFIFTEKTGSCSIAQAGACT Q/WVGIIISYCSLKMGRDPPTSLSCVA GTTGMPHHAQVIYFFIFL*ROGL
10072	23973	A	10147	275	3	IKGMLKAKTG*KLGLLCQ/TSQVENAKE EFLKEIKSATPVNT/RMIRKRNCILIAEM EKV*VTLIDQTGHNIPLSQSLPQSKCLT LFNSKKAER
10073	23974	A	10148	281	2	KIFLPQPPQEMVFOGFAPPGG*YFLVF* *KQFPFPLGRFVFK/LPGGIPFFFFF FFFFFETESHAI\RLCSGTISAHCHL RLSGSSDPTRP
10074	23975	A	10149	413	139	SLRWVPIFGLLOANKKKFFWILPLS/IR PLFFFSRERGGTLPFPFFFLRNPCKKSF PPG*PPPLKIQFPGKYFTSRPADPFP LFCQPPGKNLNYWGLGPGFPKIFPPPPPL FFFFF*DRVSLCRSGWSKVARS*LTWGK APFTWVS
10075	23976	A	10150	100	431	GPRLTDHLRSGVNPHPGQHGETSFLLI/ HNYSGG*GRKIANRLNPKGGCSEPKSC HCTPSWGKKRNFVSKKKKKKRE
10076	23977	A	10151	134	417	GLAAPLVG/WGKRNPFP*PFG*GEKTGW GPHPGKI FLKKLLFFFF*KGGLSFP GGREAHFWLKKTPPSRKEILPPPPR RGGGGPPPPFL
10077	23978	A	10152	403	2	LAFFILQEVQFCFCNLLHSLRMYSSSTGS KLFPPLASQPHSLYHLTLARAPNILEE LQSPNTALLKYL*EAALKKKS*HITS SL*KVDLSFFLETKPRSA/RLKCSGTI SAHCSLRLLGPSNSCATASQVAG
10078	23979	A	10153	382	297	GLN*ESWSGEGKTL/LHCWWECKFVQPL WKMV*RL
10079	23980	A	10154	209	15	SSPKF*FFFLSPKTIPLPFF*PIFFFTK TP/HFFF/SFFFFVVCVSGSHSVPRLECS GAITAHCSSTS
10080	23981	A	10155	153	422	RTSGKNGNRQIILVTMTNWLFSFFFF PLKTGPHFVIQAGGQGRAHGSLOA*IPG \SGDLLALVSLQAGTAGFHHAQLSFFF KKTGLF
10081	23982	A	10156	257	3	RRLQNSKDCCLFFPLEAPRGATARCQPE LSCMRCLSA/LLGGVVSQSGYMGVRDPHK EAV*PLAELKR*AGRSSAPFKAVRQGC S
10082	23983	A	10157	37	386	DATRFRIINSVGTAEGLDRIEPNDLQ*Y INLVGTAVRRPDRIESNFESSTVGKLS NNIVCYRSFFCERESQLTQQTSMLYYFK KLPLQPSAITTLH/SRQDPPSARRLQ

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						LGQ
10083	23984	A	10158	407	272	HKGGKREKRKRKKKEKKGREKQERRK ERE/RERKKGRKREMKKVNRYSKCTQ** LLSN
10084	23985	A	10159	248	478	VKVVHRLLLDPSVEDPWKSKLGFLQP* /RL*IFFF*NSGLLCHPSWRAVQSRFT GVSTSQAQAILPSFSLPSSWDR
10085	23986	A	10160	458	129	GFSVLNRLDEDELRQENLLMPAV*DPQG QHSKTPISTKNNMNPAGHGGVYP*SOLL RTVRPEDHLY/SNKPCSYLCAPAWATET LSLKNAPSCCSNHYGLSFQTSFHRILMF
10086	23987	A	10161	82	291	YSKTKSLFFAGHGGTCIYSQLPFRQVQV RQEDHANPGV*GCS/DTMIMPMSHCTP AWAA**DPVSKKKKK
10087	23988	A	10162	6	409	LRINILPEPISLSPLTAPAVFMPWTNYS SCDTFSLASMTLLPLHLSTSLALPWSL FLAPSLFQISKHQLYLSFVLLTLSSCYF LNPCFRNHILMNLGRPRQANYLRSGV*D QPQGRGETPSL/LKNTKITWPNW
10088	23989	A	10163	249	415	APPECSLPLLVLVLLVLLVLLVLRWEDHL PGGG*GCSEPKSYHCTSAWVTR/GDPVS
10089	23990	A	10164	1	405	RSEWRLRQPERQSETVKKKKGFFFSR GGGGGKIFGLMEPSPSGLGQFFLFTPL NGGYRPPPLGGPFFFKKGGFPLCGPG GFEPFALGTPPLLFPKGLNFRGGPTPPA RFFFWGVPVFSVFSKPN*NPPVFRGKNG KNRPPKKKKPGRG/WGPPRKFNPFGNKR GGVPRAGNSKPPGPQRGNPPFLKKKKKG PPKGGGR*PPFSRGVNKKNCPEGEBS INPKIFPPPPPREKKKKPFFFLTVSLC RSGWRNLHSL
10090	23991	A	10165	175	404	AIKMWIQAQVPSQCLHGVGFYLPKRVCV KTP*NKRHRQGVVAHGCNPSTLGGRGGW I\RGQRFETSLTNMVKP
10091	23992	A	10166	317	2	PFKNSPLLLNEMTNHLEPTCNYVNV PFLK*HKFLFF*EMESCSVT/RLECSVT IIAHCCCLKLGTSNPPTSASWAPGMIIG MRHCPAPKVCASHASAHASAHAS
10092	23993	A	10167	325	2	KMGKQGHFIKEEIRKANKHTERCSRL AIEEM*IKATVTI/RKHQTKC*QG*RES GSLVHG**KHKIVHPLWKILSVSYKTKH SIIIGYSSVLLGTVLVHSGSDAW
10093	23994	A	10168	245	3	GEPFLFCFPIKKPKVFFCPYFNQAVFFL ETHRGFFEFFFL*KKKKKS/LGMVAHT YNPSTLGSRGQIA*AQEFKTLIGNMS
10094	23995	A	10169	164	1	MNKMSQYTFPYKN*QWGG\SVAHYPNPS TLGGQAMQIT*AKEFETSLSNNAKPC
10095	23996	A	10170	214	419	LS*PPPPFPGFKFNRLRFYGKSKGPP /FMFVALFQKGGFFYQNIPPPVKLEPPF PTILRVSFFFL*DGVLCHPGWNAVA*S QLTASSTSRVH
10096	23997	A	10171	168	1	WTWWLFPFGFSITNNYCSHFSSSLHLAIW LGTVAHACNPSTLGG*GARGQEFETSLT
10097	23998	A	10172	139	3	PAH/CES*PPGLKRSSVSLPSG*DYR/ HTPPH\QLIFVFFVEMGFHQA/SA/FP KC*DYRS\DHKWP*HLK/SFHFIKK* N*LKRYLACSRWLWFLCIRCMV**NLD DLSILYLHLNKFQFLFIYLFEMES

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspon ding to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10098	23999	A	10173	253	2	FPLKICNTLPPQIPSTQGRGLSLPFTIF LLSLILLRPFFFF*TESHSVPECSGMI SAHCSLRLPGSSDSCASAS\QVAGKTCA R
10099	24000	A	10174	300	3	GRAFFFKGLVKWVFLTPNPFPFLLNFL KRVFFLAPSEKVFVFKNWPP*LSFLIFG EKNFFFFFSEMECSVA\RLCNGM ISAHCNICLPGSSDSP
10100	24001	A	10175	117	381	EILRYIVSIRIRRTNLKFQOEELRVNIK NNLSSLGNMVRPRL/ECSGVITAPTAVS APGFK*SSHPSLPSSWDHRRAPLHLDGF FLIETRSHHVAQAGQVIFNVYSKFLLLK FKISPSDPYRNNISQDFLAIGPTNMVPL QPYIVLCACRTKNNKIIDLSEQSSRT
10101	24002	A	10176	194	412	TLKNNLLSLHCLSFVPTDLYQPERLSKP PRPAKKYKFLIL/WLGVVAHACNPSTLG GRGGWIT*AHEFDINLTG
10102	24003	A	10177	100	339	VPVKSLLLCVCVCVLLL*RISDHLPTLY ANLG*CFFSYLVISYS\NSTYCILQRHL LAIQKQP/CSFLRQ/HLVGWLHKKKHTH THTHTHTHKSNTHTHTHKSOLDTGTQ NTTEFLK
10103	24004	A	10178	229	2	KEKYIKSKLHFEARHNGSHL*SQHFGRP RLMDCL/VQDQPGKCGENPYLQKNTKIS QAWWLVPVVPVYSHRASKTLS
10104	24005	A	10179	368	2	SGSSPSTSPQGRPDPLGLPSAKIVLQQL ATIPPLPLCFLKIFHPLTLPLLLLGGE FNLSPOQQDSISLPWFLCYRGPTYKAF FYV*ASVPEKI\FFFFFF*DTVSLCHPG WTTVAQSRLTA
10105	24006	A	10180	398	1	QNIMLYTINTYFICQLKKKTIQWGENF FFNKWC*ENWIPTCKRKNLHPYLIPTYK TNSKWISELNL/KSLKVNRRGGLHDFQF GNGFLGDTKSKTK/AKISKLEFIKIKNF CVLNDI IKKVKRQLIEWKKYLQ
10106	24007	A	10181	252	419	GARFKGSNFTSAGGQGIIFMGPPLKIS RPVF*HRGEGKTPGVTLNRLNLEHPLFA
10107	24008	A	10182	101	380	FCWIYNSWLIGYLFPPFRTLNLAMCGG SCL*SQYFGRQRQADHLSPGVRDQPGQY GETPS/LTKISAWWHVPVVPATQBAEV GGSLEPREVK
10108	24009	A	10183	2	377	PGQVDCFSSGVQDQPDQYGEILFLKLQ KLGGHGG/IR*EDHLSLGGQCKEPRLY HCTPAWTEQYLVLSQKKKKKKK
10109	24010	A	10184	140	3	DGVLLSLPRLECNGAISAHNRN\SPSCDS PASASQAGCCGTC*SQL
10110	24011	A	10185	364	3	SVCPRRLGGVSQSGDMGVDPFEEAV*P LAELERCAGRSTAFFRAIR*AHLSLK\ FTRNHPPPHVPCPRVMSR*FGLLPFFQR CPAQRGEIWRRLAAVALRSCGGRQLQR TCWQLCLHR
10111	24012	A	10186	2	249	SVRLNKNKENTQIRNKKGDTINLTEIKR IIKEYSEQLFANKLH/SLDEMNFLEIR* NPLRPGAEARLVS*RFWRATAIDHMRP
10112	24013	A	10187	270	2	PWAQRGCVFKTNQKIFFGFFFIPLD*P CVFQRPSP\F*VRLIFIGGGFKPFFFFF FEMKSCSVARLECASTISAHCNLRPLPGSS DSPASA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10113	24014	A	10188	428	28	PIFDKG/E*GN*WGRKSI FNKWCWEKCI C/KKLRDSSLTSY/TRINKWIKDLNVR TK/STKLEENIDIV/IYDLGLGIGFLD MTLKARATK/AKIEKLDKIKIGNFYASK DPKKMKR*FIEFIEQGKIFTNHVSDDT SI
10114	24015	A	10189	85	243	DRVS/LLSPRLECSGMISAHCSDFLPG* SDPFTSVPKSSWNRYRCPARKLSFT
10115	24016	A	10190	96	440	LQSNHINTLVNVRNLSSSMKRFRLSDEIF \KKHGPALCCL*EMYKDKGTCTLKIKG WKNIYHANANNKT/GMVLSSGKIRLES N/TVIRVKEG*LVI/INGRLI/QEDLIL LFILNVYAP
10116	24017	A	10191	137	423	AKDLDRQFSKEDIHMTNRYMKT/SGRQ LIRETQIKTMYRPLTPLDLRKSODKKS ***YEQKGTFAHC**ECKLVQPLQKII* TFPKLLKINL
10117	24018	A	10192	221	72	AKVK*VVVFFCFLFFF*DGVS/HVVVAQ ECSGAISAHCNCLPGSSDSVRVG
10118	24019	A	10193	460	121	SDKTKYW*RCRAIKTLTHF*LKSKLVPL L*KTI*CYLAKLKHIVFDSAIP*DTY FR/E*FCICAPKTYSNMVIEALFVPANQ TSKKKNWK*LSCPQIVDNFLNIHLMKYH LE
10119	24020	A	10194	393	2	ATMPYQRIILLTAVHELESPE*MDQFLD TYNLPFRNQEEIENLNSPIMSNEIQSVI KCLPFGPNPGNGFIIEFVHTYKEE/LP ILL*LFQKIEG\ILENSFHEVSIITLIRK TDKDAT*ETHKPISLMNTDA
10120	24021	A	10195	3	353	EAAPMPVKFFQLLEPSGPPGLSMSCLDG CNGYACFSVSLHQSANSIDQ/SIYQSA IHLIIY/VSIIY*SI/YLLL*SLI*PMY VPIYPLSCLSIYLSFMPLSCLSFNNLSI TRHGSML
10121	24022	A	10196	118	395	DFNAGLLPSYQVLSLYFCF*NGV\CHCT P/RLGDRPRLR/PPKKKKKTPPPPLGG SPPGGEPTPTPGVGPPIPPPFEPHPPREN PGCFHPPPKAWP
10122	24023	A	10197	437	160	FGYPRVFPLEALLKRGPGILFWGPNKKN YSSPARGSKI CFFKRGPPFFFFFYFFF* QTESCFVAPVGWQCDHGS LQPQPPG\S SGPPPTS
10123	24024	A	10198	259	3	RQGNHVTHVYSSRLQLILSPASLAVFI QKIYVNLCTYIHIYNLYA*MCICVCICY TCIL\ICIYGLVAVAHNTYNTTLGAKLG GS
10124	24025	A	10199	1	416	IISAHCNLHFPSSWDYSRTPPYPANFCI FSRDRVSPCWSGV*HHLQHSKMLSKK* NKIDMEHGMCL*S*LLK/RAE*DVLRQE NCLNPGGRGCGEPGRHCTPAWATRAKT LSKASYASSSSSPKKKKKSPS
10125	24026	A	10200	369	3	TAPPEFFFCRDGLRTSLIIFPSRATPYS LVTSGSFLPAGAGRGLSLEIRVLDLVQ DGCPCSQAWAAALGGPGWAPFLCFFET ASCSVAQEQMQ*CNLGS LQPPSPG\SSD SPASVVLWTSK
10126	24027	A	10201	314	2	LHHMRPEV*FTPSKLGVTGYMVSNIYSP WRCRAHK*SQVLVSLRHKHLFPLEMESG

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						SEVQL\DTNRCISANCNFCPLPGSSNSPT SAS*EAGTTDSRQPDADAW
10127	24028	A	10202	68	413	KIGILLKTH*PSIC/VSITNF*YNDTGE LKVKG*KNIYYANINQK/KAGMVMFVLD ETDFRAKK/DYQGH*IMIEVSVHKE/E/ LVILNLYASNKRVTKYMK*EDTDIKGEI DKSTTIVGDL
10128	24029	A	10203	351	1	PKFPPLNPANGTTIKIFFKKKNANWFS PRKEKALQKIHKKG/RLLAKEISFLGGF *TDYKTNPDQSQIRTLGEKKKKIRPGTV AYAYNPSTFGG*GRWIT*GQELKTSAN MVGRV
10129	24030	A	10204	2	392	FLEGVLLLLPRLECNAGTFAHHNLHLP PRFKRLSCLSLPSSWDHRHAPRANFV FLVETGFHHVGDGLDLLTL*SPCLGLP KCWDYRH\DHHAQPSF
10130	24031	A	10205	264	2	PLSLNLFFIPLNSILKIFFILK*L*IH GKLHKMYRKV/LV*TSPPSQC*HLR*V *HNIQNKLMGLGAVAHASNPSTLGGRG GWIT
10131	24032	A	10206	281	2	ISPPLFFFLFSPPKIFFSQKHIFLGPPL FYPPPLFFSPPP\PHFLNGFRPVENPMP KIDPQTWAKNKDKGNFPFFFFFFLPPK KNIFFTKTYFFGPPFLPPPPFFSPPK KK/SYPFLKKNSPNPPPS*K*AAISLP PPFFYFFFFFSSFFLENTWKMDADAW
10132	24033	A	10207	340	1	STKKLVQKLGEHTQCWQCEATGTLIHC RWECKLVQPLWK/SAWQILRQ*L*FNMHL PYNPTIQLQSSYSRE\QHTCPYKDLVA ALFTIAKNC*QAKFLSTGE*INKLWCIH ITE
10133	24034	A	10208	136	3	KNRGPPPRSGKFFFLPLFFFFFF*DRV \YPSHPGWSAMVPSQLT
10134	24035	A	10209	327	2	INKKYYEQLYA*KFDNLDEIYQFPGRYN LPKLTQEKANLNRPVSLRETSTINNL PKRKVPDPDGTGELYQTKEEITP/FS TEAKGILPNSFCEVTIIIVRLFLLRQ
10135	24036	A	10210	89	485	EIVPLLRFPFLVIFIASPTTFYTYGFVSG EKSQYKKREKLCDKTLEQSRSLGMHST CGIALHPKREGQMCTLCACFY*FFLKES HSAARAGVQWHNLSSLQLPP\PSSSNS
10136	24037	A	10211	361	462	IQQIGSNTGNI PAMELAKRNSKNINRL AGWNGP*VFAC/PKNVLFYLHP*LPG*I *IYQLKITF*NYEGMVP/FVFRFLFETR SLLSPRLECSGTITTHCSLELVGSINSS ISARAEFLQRGANL
10137	24038	A	10212	62	469	SLLWKLRS SGASTSLRCLSA/LLGDVDSQ SGYTGVRDPLEEAVCLLSELERGAGRTT ALFRAVRQGRLSLEKL\LLPFVQICPAP GGGIYR/GQ*ALLSCGGLCPV*AS**/M CLPC/EA*TRLLKPPPGS
10138	24039	A	10213	197	1	VVTQPNNEWCVTNK DASFQORCTKKIRT/ WPGMVAYTCNPSTLGGRDGWIT*GQQFK TSLANMVKPH
10139	24040	A	10214	31	213	HASLDEGFHHVGDGLNLLTS*STCLGL PKCWDYRHEP/PAPNWWKKFLSSKAFKR *LGCY
10140	24041	A	10215	442	29	PTINPTMACKCLSKRKSHSTSLTNQKLE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TIKLSEEGMLKAEAG*KLDHVH/QVSQI VNAKEKFLKEIKSATSINI*MIRKQKRF IVNME/KKVLMPWTEQDTSNIPLSQSL IRKRP*LFNSLKAERSEEAPEKLEASSG G
10141	24042	A	10216	195	533	LVVFWLRVTYGVAAKMSSGTTIIGRLSW GWRLLHF\KMAHL*GYWWEASVPLHMKLS SCHGTG\SLRVKDPRELRQKLCQCFYDL VLEVITYWHFYCILFIRSKSLSPAHIQSK RI
10142	24043	A	10217	274	494	CVLKGLPFALPWFFFF*DKVSPSPRLE CSVAI/SAHCSLNLGSSDPPASASQLA GPPGLRR
10143	24044	A	10218	142	480	VTIKIYLHPHDTTTPLRQGSRLKEILV SY*QKQVETRPISHVIFFTVISTQFKKT TTRSGAVATCNPSTLGGREGQI/T/RG QEFETSMTNPVK
10144	24045	A	10219	163	464	AVYFSFWRVCEHDLASLYFENSGKRDNK FVFLVLQAQGPAPWRQGEVHKHLLPCVYH FAFVVLTPQPPQSF*DG/QSHSLAR/LE CGGVISAHCNLYLPQSSNS
10145	24046	A	10220	379	469	V*KVQM/WPGMVAHTCHPSTLGG*GGWI T*DQEFETSLADVAKPC
10146	24047	A	10221	211	473	VTWLLFFSIFRASSLSTDSVSYVIAFQ FYFYLFIYFYLFIETESCSVA*AGAQQ CDLCPQPPPPRG\SEEPSTLQMTSGSS NL
10147	24048	A	10222	142	394	GVCQSLLGSLCQLGGTGVDRDQLEAVCP LALEPCAWRTLRLRCCSLQSQAGIF /RFC*SYIHICPPQVLLSSEMGLSIR P
10148	24049	A	10224	77	396	KRKTKSFWTSPGFGLRPPIPKKKKFFN SRGKQGGFGRGSGRGGGSGTSGRGGGY MGKVFGMGQ*NFTGDQGLAKGGFVFL GRTTIGIKGALKRLFA/NEHDLR
10149	24050	A	10225	155	443	GQAREGTLKSQFFPSPGPWPLILPGGV FSPKFFFFFETRV/CAVAQAGVQWCNI DSSNSCASSS*IAITGAHHHTELIFV F*ISPPSQ
10150	24051	A	10226	290	485	KRGEFPVQKKKFFFFFFFETESCTVAQAG VQWHNLSSL*PPPPG/SSDSPAEFPR
10151	24052	A	10227	228	424	KLYQNLHDTLFGFELSHYEEVH*KMLKG SSWBFVMHSS/VSNKCILICSARKKKKK KKKKKKKKKKKK
10152	24053	A	10228	269	454	DLFAASQGHQQLLEELMATTLSTHTHT HTHTHTTPWSLF*SR/SALSLVC
10153	24054	A	10229	255	1	FYIFSKFLYVWLVNVDLSDHICFCIQSV IISCFGVFYYYY\FF*QSCSVVHTGV QWCDRSSMQPQLQGQNDPPTASQVAGS A
10154	24055	A	10230	18	472	GPEEFGTRRERDRERERETDRSRER VRERER*/RQERERERERERER
10155	24056	A	10231	52	361	WRKNYYPQIKITVYLENTKDFIQKLTK CW*G*KEIGRAIHCWWECKM/VIQPVW R/VWQFLRLNMLLPHNPVAVELLDIYPN ELKTHVCTKALYEAGRGGSRL
10156	24057	A	10232	3	402	APRLPLGGWISFSSPMGAMGLNRTGIM GSFFFFFLKRKSPGLGPQGEGRQNLG*G

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NPGPRG*THFFG*TP*KAGNNGEGPPPR GNFGFLKKKGVPQKGQGSKP/RDPRGT PRLGPPKGLE*RGGPPPPAPQK
10157	24058	A	10233	48	470	PGRRFTTAGLGKQEPAAAGPRAPRAQT PLKREAARPSLRHLPEGA*APRSSARSP LLIPAASLRSRRRTCRRLRHFGIITR PFQPGVRLPDSGPGLA/RWACAAVPAAS RALPALRRPL*RRPGHGAPSSKSHGHSR SP
10158	24059	A	10234	169	446	CPPGPAPSHLLED RDPQAGRQSSFYAG WDRWREKTLFLFLRQSLTSPITPFFF \FEAESHSVTHSGMPGVISAH*NLRLPG SNNPPTSAS
10159	24060	A	10235	264	2	KLKPIFKMVFLKIMFMSYIMEVFFFIET GSRSVTQAGVRWHDLDLSQP*PP/GSSD PPTSVSQVGKWHKTWEAELAVSRDHATP RAKL
10160	24061	A	10236	306	3	SQDMVKSPKKKFP*LV*GLTEI*KIRAL VFNNKFFFFFPPETGSGSCSV*\RLE CSGTIIAHCNQLLGGSSNPPASASRVIN SIKKLFANFIVSANPRPT
10161	24062	A	10237	20	469	QCGAIPRRGDHLRSGV*DQPGQHGETPS LLKIQKLSRHDGH/CRRLSEKNGLNPGG RGCSSELRSCHCTPAWATR\GNSVSKKKK S
10162	24063	A	10238	313	3	TRPRPTQGPPhSGGRACLCIFSPHGPPQ TRLSTPVSPSVRPLGFQVLLSARHGFL CQHGMF\PSLFTMSNITLWPGAVHTCN PNTLGGRGWIT*GQEFQTS
10163	24064	A	10239	274	49	KGNPFFPVETGSHSIAQDGVQWCNHS SLQP*PP/G\SSDPPTSASRVAGTTGVCPC EDKLSHILRRCYAQVFMLAG
10164	24065	A	10240	144	454	VCKIKIITYLIVLLEDYIN*FVKSSL*LK S*K/LIQQMWAIIISLPECLNSVCLGKV G*KRCSQQGTVAHTCNPSTLGGRGGMIP R
10165	24066	A	10241	289	178	FNYSIKNNTDGVVWVWCLLPVIALWEV EAIESF/CSRDEIPLSCPGWSPVKLKR FYCLNLP*CWDYRQEAPHPAISIIFDA TVIELFS
10166	24067	A	10242	352	294	PPRTTKMVV*DQPGQHVEAVTLQKMQL VERGGKHPQSQLC/REDH*SMGGGCGSE PRP*PCTPAWVTERDHVSKIK*NKIK
10167	24068	A	10243	293	1	VSLCRESSNSFIWQCPVSHILALCFOR EKKRLDLP/S*MVGK*EIPFLVPLLFLP HWPLLLMK/YM*IFFGGRVSLCHPGWS AVAQSQLTAASVPRR
10168	24069	A	10244	218	3	LERHIPVRPIICDYKVVWRF/HFLRPL HN*FLFSFFSFFFFFETGSYSVT\RLE CSGTISAHCNLCVHLLL
10169	24070	A	10245	185	1	KKQPQQTKNPLNNVKKEGKGQHFFFFLE T*SRSVAQAGVQWCDLGSLOPPPPG\SS DPPPS
10170	24071	A	10246	2	265	AHKKKPAKHIASTFLYGETEARRSMFK AAQLKCGRAGIILFVFKTESCSVAQDAV LWCNHGSLQP*PPG\SSDPADSACRVAR TTSI
10171	24072	A	10247	2	430	EAGGREALDGCGLTGRESGVQRRRDSMG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						CQGTAGRGTRAGKEGPWRPEHLRRPPA SSVLLSWAHLAWVEGS*TGSLCDLEAP GPTLSPWCWSPELQLHV/HHHTHTHT HTHS/HPNTHDTQSLCHQPSFSVSPRA RTVL
10172	24073	A	10248	201	16	TPPGGVFFLGGFFLFFFFETESCCVAQA GVQWCDLGSPHPPASRRPGNRSSI/AAA *GYHFK
10173	24074	A	10249	167	2	GFDPPFEGMLSYLEKEET/WPGTRAHTCN PSSLEG*GGWIT*GREFKTSLTNMEKP
10174	24075	A	10250	92	389	FQPGQHGEILSLYEIKKI*/ELAGCIDM CLWSY/LLRRLKQEDCSST*VQGCSEP* CLSCIPSWVTEQDPDSGRQI*KKKISL GRRGGIFLFLKIWHVFFL
10175	24076	A	10251	221	415	KKKKRGGGRFKGSNFTSPGWRGNIFPMGP PKLNSRAGV*QRRD/WEKPGGPQNCFG SNPPFPFGGK
10176	24077	A	10252	94	383	GKLNRCGIWLLGRCQSPAVSNALWLHR VAPBEEAGEAWAGTSLQLSCKSKITPN KIVY*KKNKI/WLGTVAHVCNPSLGGGR GGWII*GREFETSL
10177	24078	A	10253	249	2	YPTMIFKCSKRSPTSLSLTINQKLEMMK LSEEGMSKAEBS*KLGLLH/QVSQVNA KEKFLKEIKSATPANTGMIRKRNGLIA
10178	24079	A	10254	132	414	NNTYPQGIKIFILNSQVKGMLICCWWECK *VEPLWKA VWRFLK/DLEQNSKEYKL*T WNQPRYPVVDWIKMWWIYFMEYHA\A IKKNEIMFFAA
10179	24080	A	10255	359	3	YSLRHNIEMRPVSNPTRASKCSHERRSV ISLTNGKREIIQEASREGTLKANKPKA KLFVPVRQVVNAKEKFLKEAKSAAPLN\ RMIRKQNSLTADTEQV*VIWIEY*TSHS IPLSQSL
10180	24081	A	10256	283	2	SLQPWKLYVHVFLPKYATYPFGTLPKT HFFHKILPSKAGSDLSIYAMTYSRHI TIFPETESHVTRLECSGAI\SAH*NLH LPGSSNSPATK
10181	24082	A	10257	216	386	PSKNPPPLINPFFFFETDSCSFA*AGVQ WRNLSSLQTPPP\GSNNSCASAS/RIAG I
10182	24083	A	10258	263	1	FSQWLILPSPLSYSLFLRQGFALLPRL ECSGEITA\PSSAS*VAEITGACHAEF LNFFVEMEFHHVQAALKPLGSSEPPTP ATK
10183	24084	A	10259	248	47	IPKSRVKRENRLNPGGKGCN*PRSPPCS PPWVAKQNSLSKK/NKVKIYQNLHTETQ TVHGDIRGQEK
10184	24085	A	10260	159	2	KRDMSSLKLEY*KKE/RIWPGAVAHTYS LSTLGGREWIT*GQEFELSLTNMVK
10185	24086	A	10261	190	405	ASLHMFMYFFFFFFFKQIFFFVPOAENQ WGNLGKRNPPPPGLRDF\PASPPKEAGF RGGPH*PGLFLVF*GE
10186	24087	A	10262	39	293	PSSSTRIYPEDTPLITQKYICKILFIV ALFIFPKHWKLCCKPHIG/B*IKLQCIY TWRYVAVQKNEENLYQLMYNDYQESILV SD
10187	24088	A	10263	282	3	AFYNRFFLKIFFKRGPRGKBBKGGKKEK KKWGKKKKKKFFFFSPGQIFFLGGVFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FLFFFEABSRVT*AGVQWCDQ\SSSQP RPPRLKPFQ
10188	24089	A	10264	196	376	KKGGGHIINFPFHKGYPKPKKFFFF FFEMESCSVA\RL*CSGMI/SAHCNLC LPSSN
10189	24090	A	10265	514	157	GLTLSFRLEYSGMMSL*P*LPG/FR*PS RLSLPSSWVFLMYVHYAQSPCIFYV ETGFHVRVQAGLKVGLRQSAHLGLPC W\DYRCEPL*LTCLI CFTYGLR*RSKPP FFVDGIQLF
10190	24091	A	10266	57	378	RSRIW*DSVILCS*LVSU/VDQSYFY*V TEILEQIKLGSKIMCFCILQLHFLCFL CGSFVGST\IFIFSRNINLGTVAHACNP STLGGRGRWIT*DQEFETCLASMVK
10191	24092	A	10267	1	212	LIQKDTNIYYIKAL*IPNKH/IKISS IVSHYKMQIKIMR/YHTRMAIKRTDKC LYECRETRTLMHCW*GC
10192	24093	A	10268	3	399	MANKHIKIFASLIRMEI*IRATMRE/H *FIPIKWLVLKSKRESNKCQCGRTGI VIHFQRECKIVLLL*KTV*QPLKLNIR LGAVAHSCNPSTLGLRPRVQDPGQHG KTLSLLEIQKLAWHGLHLSPS
10193	24094	A	10269	190	386	FSPFLPLVTILECDKACRGRKSFDFFL LGPSFYFFKLLL/FIFYP*ERVLLCGPG WSTVAQSWLTA
10194	24095	A	10270	166	327	KTNSKTAEVCPLSVITLNINGLNSPIKR QR*TDF*NPI\ICCLQETHFRFKGTN
10195	24096	A	10271	180	1	IFFLFEVETCSVA*AGVQWNLGSSQPP PP\GSSDFQLIFAFVETGY*IMVPSSS CRT
10196	24097	A	10272	273	3	FLGLFSGNPLKANKPVCHLTLPILQRI FFFESEFHS\VAQAGVQWCDLGLKPPP PG\SSDFPGRRR*Q*AMITPLHSSRGDR VRLRLKKK
10197	24098	A	10273	399	27	YHFVPTRMATIRKNN*CW*TCGEIGNL VYCWECK/LV*LLRKIVWQFLK/DVKQ NYHPVILLLSIYRI*FDCLFLCKSHVEM *LISGVRVGAWWEVIGSREWFMSGFTI SSCHQDCEFSQDLIV
10198	24099	A	10274	275	462	KINLVQLDFFVEMESHSVTOAGVQWC HLSSPQPPPP/GSSGDSRASDS*VAGIT SVHQHAGL
10199	24100	A	10275	2	379	RGPGRGLGSGTCFHPGRGGEPIVYQHL F*FFGP\PENYILILPGFGIISH/IVTY YSGKKEPFGYIGMA*AMISIGFLGFIV* AHHIFTVGIDVDTRAYFTPPYHTFEPEG YIISRRRRRTKGFLF
10200	24101	A	10276	2	407	FPSPPSPFASVSLSLSPHGLPLPEHTW FIDGSPTKPNRHSQAKAGYAIVPSISII EATA/PAPFTTC*QAEIALTRALTIK GLCINIYTD/SHILHHAVMG*K/GFLT TQSSIIDVSLIETLLKAFLLPKEAGA
10201	24102	A	10277	203	545	FLWRGQSLALLLRLCECSGILL/AHCNL GPHRFKRFSLPQPPE*LSNW\DYRRLPP CPANFCTFSRDGFTTLGQAGLQLLTSSD LPTLASPKCW\DYRHEPLVHGLTFNRSF NPF
10202	24103	A	10278	250	3	AKWFLEMKSTPGEDAANIEM/TKDLDY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DINLVDEAVAGFGRIDSNFERSCTVVKM VSNSITCYRELFHERKSRLMCQM*LSYF
10203	24104	A	10279	333	3	SLILLFQSMNHTVVRVTFIDQFCVCSN YSTDWLFPPLSPISLRTPYSLRYNIKIR PINHPTMAMASKSSERESRISLTINQK \LETIKL/SEEGMSKAQIG*KLGLLCH
10204	24105	A	10280	251	3	ITSKVIDSNPTTSIITLNLNGLNTSF*R QRL/DWASSPK*DSIICYLQEMNFKYK IFKKIGRRIYYANISQKKVGVAULTPDK V
10205	24106	A	10281	22	226	TKINSKGNKELNVRAKTIKLEENIDRN LCDLGLGNCFID*YCIL*TKINSKGNKE LNVRAKTIKLEENIDRNLCDLGLGNCF LDMTFNAQTTKGR\IDKLDIFI*NFWD DT
10206	24107	A	10282	238	383	DAKRKVSSTEGDSEGVHAHERRSAHLSAK PCPAEVE/AKPQKAAEK*SSSE
10207	24108	A	10283	127	377	RIPGGSALGKEIRQCFGVKGQAEIGKIE MSQPTQEREVVEGIGSQKAAQVDHLRSG VQDQPGQYGETPTLLKIH*LAGHG/GRC L
10208	24109	A	10284	328	370	VGPGEFG*SSGRVSSCCPGWS\PSELK* SAHISLPKCWDYRCQPLRPATFFFKTAS HYVAAQKVQWCNYSYLQPGTLRLKCCIF KKIQVVQVV
10209	24110	A	10285	341	1	KVVCLVLTAPLSGRFSVCLPFLGPPYFLQ HSDIEIKPINYPTVASKCSNERRSHTSL TLN*KLETIKLIEEGGMSKAETGRKLSL L/QSVSQVNAKEKFLKEIRSITPVNT* MI
10210	24111	A	10286	199	329	LFFSFLNCLSPHRIEESY*KEIKSAPPI TPGIPRK*TSIAGKKNVFMWDQDQTNH NIP/LSQSKTITLFSMRAETVEEAEEK L/ERGCFFMRFKERTHLHNKMKGGPVVA HTCNPNTLGGQGRQIT
10211	24112	A	10287	358	387	YTNAALLVY*DPQGHLMGKDSLFNKWC* KNEYSHAKKQNH\P*FSLYTKTNSKWS KDLNVRAPKIKILEKK
10212	24113	A	10288	111	373	SAQCQPDQHGKTPTLRLRIQKLAGPDGAC L*SQLLR*GCGEPRSRHCTPAWAT/EG KTPSQKKKKK
10213	24114	A	10289	197	375	IRIGLCKFII*FLETKLHTVAKVECSA ISAYGTLSLVDSGDSPASAS/RVVGTTG
10214	24115	A	10290	118	371	QCLLMMSPLGKT*MTGRLRQENRLNPGG GGCGEPRSCNCTPAWAT\GNSASKNQ T\KNKQQQQQN
10215	24116	A	10291	214	368	CGYHQKNKKTNPKNKSCWQCGEIGTLM HYWKDHQV/Q/PL*TIQQOFLTRI
10216	24117	A	10292	2	376	PFPLMAQRPTHVPLSASSGTSLLMPST LLWLPWLKHAHVPTVPLSKLFDHTKPY AVSKNNLGALSI*SY*VIPVPPRSRF/S FIRDKPTS
10217	24118	A	10293	1	379	NILHNLDFFKNTTLEPQSSRLQRAVIAP LHFLGNIVRRCFKKKSGWAQWLTPVIS ALWEADVAGSLEFKSETTLGNMMRPCLN FKKKKKKALFAGPGFFFFMGKILFGI AAPF*SSGRVSSCCPGWS\PPELK*SGH ISLPKC*DYRCQPLRPATFFFKTASHYV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						AQAKVQWCNYSSLQPGTLRLKCCIFKKI QVVQDI
10218	24119	A	10294	201	384	GEERLSVQCSAFK*LR*HINISLQTFFF LRRESHVA\RLCSCGVISAHCNLCPLG SSDSPA
10219	24120	A	10295	161	400	VCVIESVKANHLVDEHALKSLSPHLSLL FGV*GVCVCVCVCVYMCV/CVCIYVC
10220	24121	A	10296	1	433	GEGGGGCSGWSGVETAGSRPAPGAEQDL LPAPALGRWQGLNSVCYPAPWPQPNRRQP LALLCAAGLPGQRLCSCGMIMAHSLD LPGSGDPPMSAG\SIAGTTGTCHAW\E PHHVAQGGLELLGPSDWPPPTVLGLQM*A TTPGH
10221	24122	A	10297	209	1	LTFFELLYHHYTLFF*ESGSCSVAQARM QWCDLGLLQPKALG\SGDPPASAS*DA* STGVDYYSWHTCI
10222	24123	A	10298	225	1	REGMPLSALPCTGHAPARQPHSAACSGP KCPWCQSPQPAVGWTV*VCPLPLSPCLC /FCVPQFWHGGPLPLCPFPV
10223	24124	A	10299	212	367	VTAGSGHMCYTWEERLEQSL*KTVWRF LK*LKVELRFDPAVPLL/SIYPED
10224	24125	A	10300	97	406	LHRCTPAWVTERGCLKTTNQNNGQHVE GEACSSRPFTTIC/EEKIHLVCALTEED *RLAETTANTTDIPIGSAYRILIKKLLK PSKLSLC/YVAKQLSPGQLQTK
10225	24126	A	10301	3	422	YRSSSKTFLIIRRGFIPSSFTLLAHLST TLSTLSHFQKGWVKLFFFFFKKGFPFW PPGGGGRAP*F/HGNPPPPG*KNFPAL PRQGGGKKG\GPPPPGQFWFFKKKGVS WGGGAKTPELGNPPPGPPKGGGITGCPP PE
10226	24127	A	10302	330	1421	RTKGRPLLLALPVLVLLFLHLAPFSAPP GPSSLSSTEDLKWTLSPAQSRKLQFQS LHRAGVRDLQWQGRAGELTAAC/WPAP PRPETAULLQGLPC/QEGRLLLESINGF ALVVSAGTIFYASATIVDVLGFHQTDV MHQNIYDIHVDDRQDFCRLHWAMDPP QVVFQPPPLETGDDAILGRLLRAQEWG TGTPTEYSAFLTRCFICVRCLLDSTSG FLTMQFQGLKFLFGQKKKAPSGAMLPP RLSLFCIAAPVLLPSAAEMKMRSAALLRA KPRADTAATAD/SKMRS*LTLSERLPPN *FEIWDAAAGTLPSPFPFGAFDQGHIF CIHTRALRGSTRTRQCIAAALEGASFRN HVEL
10227	24128	A	10303	172	383	KIENKVWQGYEEIETLVYCWCEKMWOL LWKTWVVLKILKLGPP*\DSIIPLLGI NOGTEIRFCRYSNT
10228	24129	A	10304	205	2	NFYPA*KTDFFLVGSLFIYFE*ASHPIT \RLCSCGTIVTHCSLDLLGSCNPASAS HVSGTAGAHHC
10229	24130	A	10305	423	30	LLEGKLTNRKDIRTKTPSVRRHLHSPKV DRTAKMGKKQSRKSGNSKNQSAFYPPKE HSSSPAMEQSWMENDELREEGFRQSS/M SKLKEEVRVNGK*VKTREKRLAKSLTRI TNAEKYLKDLMEKLTSLVLRPL
10230	24131	A	10306	211	387	IFPFF*IKACSVAGGQGRHLGSLQPP PPGLKQDSC/SPSRGVGTGMTYHAQFI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFGF
10231	24132	A	10307	229	382	ERAVVQPG*HGET/PSLKKL*KLSRCGG MCLYSKLLRRLR*EDHLNPRSWG
10232	24133	A	10308	168	417	GSYCFVRRNLLIVKYMRSVHLLFTIMLL YRGD*WYVTQYNFCILQKQEKLIYRIA /HVRNPSSLRGGGG*IT*GREFKTSLAN
10233	24134	A	10309	253	402	KGGGGGVKTPARGNPPPGPPKGGKRG PPPTQKGGF/CFFFKKGRPPGKGTGE RAKENEI PAPGKKEFFLPKPPEKGEIKG /PRPPGQINF*FLKKTGFKGGGGGSKP RPGGTTPPGPQRGGKNGGGPPPPPKGPF FGGKKKKKNPPR
10234	24135	A	10310	182	400	LHVTMIIFWLYLIKNNLNFYTF/CYIF SVATSTFKIVCV/WLGAHAHICCPHTLG G*DGWIT*GQEFKTRLANM
10235	24136	A	10311	371	400	FIWNI*ASNKHKKT\STSLAFRKIQV K\TMRYLSPPTPIRMT/I/I*KSYSSK CW*GCEEIRSLIHCKMIQPI*KT/WQPF KIINIQLLYNPAIALLGNRTG
10236	24137	A	10312	113	404	QRCGKIGTFTHCWWEYKMWQPLWKTOWN LLQRLNIELPCDLAIPILNLYPREMTS IYICT*MFIAALFII/AKWRQP/KCSSA DE/IGKMWHCIMK
10237	24138	A	10313	146	1	FLTQKFFFFFETESRS*AVVQWLDLGS LQPPSP/GSSDSPASAF*VAG
10238	24139	A	10314	157	434	FFFSEIFFFGPGVFSPPFFFIGGPGIFF FCPLKKKILPPRGKKFFFKGP/HPF FFFFFF*EGVSLLLPRLECNAILAYCK IHLPGSSDL
10239	24140	A	10315	277	2	FFTAFFLVPGVFPFPPRFFKPGPGFFF LGP*KKNFFPPPRGK/IKFFFLKGPSPF FFFFFF*EGVSLLLPRLECNAILAYCN LHLPGSSP
10240	24141	A	10316	1	388	KTITHEVITECIWLKVLVLLYFPNCMIY VRMHICVCVCHISI*MDHIVSYKCIHI \LCIY
10241	24142	A	10317	134	399	LGLPGDTRGGGTIENPPFERALNSONG GK\NPLLGPKTRPLGWGLCSTPKFWEKP RVRVVDLN*TTPCLEKRAPWLKAKKTPA FEIRI
10242	24143	A	10318	233	3	EFLFSLICAICL*CALQFSSCFCLAL IELLGSMLLFH/SSLETFQPFLLQIFF /SFFPLFFGANYTYNKPFEYSLI
10243	24144	A	10319	221	8	CDQPKSPPLSGVQMGDILVVLVFFLFLF AF*R*GSHCVAQAGLELPGSSDP/POAT SQVAGTTGMHCTWLVF*F
10244	24145	A	10320	1	407	RSTPDVVLGFTSGGCKTEKRAGCFPLW KLHTKGAPARCQPELSGMRC\R*PLGG V/SQSRMAVKDSLEBAGCPLSELKRC GRYTGLFKGGRLDHLNLLRLCPQTLLCP GALSQEDGSFIYKPLTGAAFLSYM
10245	24146	A	10321	115	398	ADEELLLMNKQIKYLLEMESTPGKDDVN TVEMTKESEYSI/NLKAVAGFERIDSNF ERLSAVGKML*NSITCYKEIFH/RKSQL MSQTSLLSYFKLP
10246	24147	A	10322	137	454	FFSLYFQGGFFFFFLGKFFFFSPGGKKI CPKPPFPFPPPGKGFSPPPPGKAKKK GPPPPPP\GFLEF*KKPGGFLGGFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
10247	24148	A	10323	246	372	LGGKIFFSPAGGKGGPQKPPFP ISIKSYQLW/LGGVAYACNSSTLGGRGK WIT*GQKFKTSMANM
10248	24149	A	10324	415	1	IWGAPRVPPPPFF*NPPEKNFWGPKKK KKFPPPPG*KIFFFKGPPPLFFFFF SETESCSVT\RLGCSGGISAHCNRLPA SSNSPPSSLRMPSTFVLRPHGDLSPQ LSAWVLSWPFPLSLLPDLDFIVQ
10249	24150	A	10325	3	559	GDGITGLSPTISKFLFFVFESISLSPRL GSSGAIMAHCSLTSRREPPCRSINFFVS VITLNVNLTNGKIGRMDFF*MM*YTIQ ICNLQNTHCRT/KDTNCFKMKRRKEIIH ANSNQKRAGVAILIPDKIDFKPKNVTER HRMLVRES/ISQEDVTIINTY
10250	24151	A	10326	24	387	NQGLGARNQKSQRVFLAGFFFESSCS VAQAGVHW*DHSSV/PGSSAPPASATVV VGTGTVHNPWLIF/VFPVETGSH
10251	24152	A	10327	145	396	CDYFGEMFSYLLNLYLCDDPAIPLLPY VPYENENTDSLKDMTDAHSSFIHNSPKL ETKCPGTDEWI*MTKKS DYCKHW*GYRV TGTLLEYEGECKIV*LLWGNV*LF\LLN IYLCDDPAIPLLPVVPYE\MKTRHSKT *PMPAALFIAPNWK/PKCPGTDEWIN TL*HTHAVQYHVAVER
10252	24153	A	10328	94	639	ASISSSIKWDNISFLVGLLGELEIRNI CKAVNMKQALNKWLILLFVIENNVS SSNNFKIFYAYYIAKAVLLIITEHITLS IVLILKKQNNTRAVTKCW\RGGRKRTL IWLVG*ECKLVQPLWRRVWRFLIKVKIE LPYDPT/ILGIYSKERKSVYRK\NICT PMF\VAALFTTARTWKH
10253	24154	A	10329	143	3	SAWFFFQDRVLL*/SPRLECTVSISNHC NLRVPGSSKNYCLSLISIWDR
10254	24155	A	10330	153	389	RQGLTLFPGLVSNFVLPVLSHGLPKC WGYQCYHAWPS*CF*NRSI/WSGTVTHA YDPSTLGGQKPIIT*GQBPETSLA
10255	24156	A	10331	382	422	RYKLDL*KLNTLPYDPTVPLLGNYPKY *T*AF\SKTCT*MFIAAYSQPPKGRSKC SSPNE*INKMWPIYIMR/YSAIK
10256	24157	A	10332	194	1	CKRQCNKEDRNI/CSK**NPTILF*TTK RKG/WLVAVAHACNLSTLGG*GGRAS*A QEFKTSRANM
10257	24158	A	10333	348	1	NSGQSWIMYPLLKKGVGRVSPDPDIVN SISMVWCGGRLFSNERFASLLTIKKKLA GHGGTCLQSLPLGRLRREDRLSQGGG/ C*GYSE*LCCRCIPAWAABGDLWSWSPN SVAY
10258	24159	A	10334	388	2	IPGSPKRGPGGEKKKTFPHYLFLRAAPP LPRFIFPPKPNPLKGGGGFFPPPPKL KTPRLRKKKKENFCPWKKFFKKQTPO RGRFFFFFLRQSFAVAQAGVQWCDLGS LQSPPP\G*SYHPARTRG
10259	24160	A	10335	3	396	LLRPPCSLRHNDIEIMPHDNPMIASKCS SKKKSCISLTLSQLDVIKLSGKMLKA KTGQNL/GLGHLVRTVRHAVNVKEKCLK EIKNAALLNTQMTK*NSLIADTEKM*V V*IQE*AS/HSMPLRQNLIONK
10260	24161	A	10336	165	442	GQPELLILARNFGILLHFNLSIYYRRLF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: In USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						FSIPRYLFIITYLFIYLFYFESVAHSD AQVECSGTINALT*KKNASLP/ASAPRA AGATG
10261	24162	A	10337	33	430	TGSTHASANFCVSLVWTQLISRSSGQGL ARLQLRCLPCCILFFSFFSLVIYRLHSY LRLPWRRICLQVPSGC*QNSFPNFRIO GSLLL*/MQQW
10262	24163	A	10338	284	3	SQHFGPRPRWVDHLRSGVRDQPGHGETL SRETP\SLLLKIQLSGHGSACL*SQLFG RLRQENCLNPRGGCSEWRQHQCPTV*V TEQDSVPKKK
10263	24164	A	10339	414	2	ERAGPFSRKIFFSPPLAKKVKYFPPTP RARAHKRPIFSRYVKKERGNSPDLPWPP FFPSLW*KQ*GPSLGRIFYPV/SWGIFP SKP*GFPGRPKVFCFLG/LPPGPPGGP FFFFFPGDRVSLCHSRWSAVAQSOLTAR
10264	24165	A	10340	211	422	ASLNGGRPSPLAALQFDL*LRAGII FALFKAARQGDLSL*RLLLSF/VCLCPA PRGGAYRGRQAFLSWGGLHPDRASRLFC LPKQAWAMAGAPPPALLPCSLISYCRA SNQDSSGGIGPSEPSAGYKLLVPGLLP AEK\RTIYGGVTRFRGP
10265	24166	A	10341	116	432	SRQMPSTYHVQSGDTKTGEKPCANGN KGCSSILRSLHRKRFPF*SLKALVWC GGACLEAQLRRLRQEAHLSQGVPGCNE L*PGYCTPAWATEP\DSVSKK
10266	24167	A	10342	103	458	SLNVCVLTTLFSSCSPISLPLRGPPYSL RHRNIEIRPINNPTMASCSSKRKS*MS LTLNQKLE\MINLHEECMLKAKTG*NLG LLHQIVDQVNAKKKFLKKIKSAIPVNT QMVRRQN
10267	24168	A	10343	53	408	SFQFCSVFSPLWIFYLLLVFDDGDVQM GFWCGYPFCLLVFLTDTKTLSCRSVGVP CRVRCQA\LLGGASQLG\SRGSGVRDP LEEAVCLLSDLQLRAGRITTLF*AVRQG HLSLQRL
10268	24169	A	10344	265	421	NNFPPSPRRGGGNPGPPPPRFFFFFLK NPGLPFF*VIYLL/YFTLTSPFCLWCYT ISVYCGFVFFFSFFFFFEKKIFFFP RVEPKNRI PVYPKILFPG*NNFPPSPPR GGGNPGPPPPRFFFFFLKNPGL/HPF* KKGAKFPDLINPPWP
10269	24170	A	10345	207	420	WQKGCPTVFMELGVVGPLYPCFLHLWIQ PTSHRKYIHL/WLGMVHTCNPNITLGGQ GGWIN*GQEIETSLTD
10270	24171	A	10346	115	3	APRGAVKKR/RPWMGAATHVCKPSTLGG RGG*IT*GQEY
10271	24172	A	10347	41	421	FTFVSVCVHFKGIFLSFLSFFFEDEVPG SPLGPKRGGGGNSGPNPPPPGLRGSP PPPPQRTGKGGPYPPPGNFFFKFFFRK RGV/PPL*HPGGPQSVT*GTPPPGPPKF NGAQSGGPVWGKNPLF
10272	24173	A	10348	228	1	SKQVKEKYDSFLHKIQKQAT*NRTFFRV TKKHVEITKK/WAGHWAHAYNASTLGGQ GGWITLGGQEFETSLANMVKP
10273	24174	A	10349	405	1	GGFLKRGPPFFFFLRLQGLSLLPRLECSG MTVAHCSNPILDSSNLSLRRSDWYSHQA QLIFLVSF*VLGSHSVAQAGVELLAS/P

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						KCWDYRHEPL/WPSQSQNLNSFFLDGFS LLLSRLLECNAAISAHCNLRLLGSS
10274	24175	A	10350	301	546	RHIFMNLPPFHNLVKII FHCGRKTLFLDI SNPYLKKQVSSSKPNCK/HLKEI*LFLE AKDYWLGVVPHAYNPSTLGGQGRSITG
10275	24176	A	10351	873	1258	FCYQCYFHLLHLLHHHRFSPRLEPPFPF AALPPVPEGRIIPLPCPSSGPRQTTGPG KRRHPAPHRTPAASAASLPARRTLPA PW*PLSFQNTTPGSA\PGGGNQPASGAG GNSRT
10276	24177	A	10352	184	576	GLSPLSHLKMAASSSEISEMKGVESPK VPGEGPGHSEABTGPQVLAVDPQPEA PQPGPNTTAAPVDSGPKAGLAPETTETP AG\ PQQKPRPOTSA* AQEGNQRPTAAPK THAQETVSKPEVSKATAD
10277	24178	A	10353	110	384	VPGSPRKRTRSPQQMERVLAPKTAKKGC RPGDHRSLQNCRDTRARIKWADSVERP PWAG\ PVAHACNPNTLGGRGWIT*GQK FKTSLVNM
10278	24179	A	10354	123	422	RKQIANDKSKLFIINKYLVNVELNSPIK /RERLAGWIRKEKHDPISICHL*KTHLT\ KDTNSLKMEG*KKIYHANNY/QKAGVA ILISDKIDFKFKKKVUREK
10279	24180	A	10355	36	426	PPERFQYSARVCVCFYTECRGLAPKPE CRGAIIAHCLLNVLGSG*SSNLRVWSS* DYTQLIFKLFVQTGSHCIAQAGFELL/S SKDPPTLA/FPKHWDYRH\DHHSW
10280	24181	A	10356	193	3	FQTRIFKISFFPKFELKFKKFFFIILI* ESRSIAQAGVQWRDLGSLQPPPP\GSSS PPASASLY
10281	24182	A	10357	205	377	SPVVFQPYRRLTIPYQKC*LATVCI*VY *FFKLILYPAILLSIIWIWINTSDPL* FSSHITG*LSLIKNVWVGPMGLAHA*N PSTLGG/RGGWIT*GQEFETSLANMVKP
10282	24183	A	10358	51	376	LCRPFQLCHGDRDMDWCPFPEELQDRCS CRSTSMRVAKGTTCPFLKVLQNIYTV*M FCRTFRKHGVVPLATRLV\IYKNSGPV TLQGRGTTYLSCHHGKAGRVCRATQHAA GVVVTQQRACI
10283	24184	A	10359	295	376	ASELTSQSPGSLFENQKKGRCIAFLPC* KCNSEILVHCWGWCKM\WKIVW*FLKTL \RLELVYDPASPLLAIIYPRCI
10284	24185	A	10360	451	1	CQDIKTILRNEQBVLPVPSVTYKQVQK SFVSRRLWWSGCVLCYAFVTEASKTWHH FPYRSPGFWRSGGRQFDS*PKSQADFR APQGPPTPEPEGAERREPEIAPPPTADP SPKPT/HSPPRSGAPPSAPFPLGRAER GVG\PGQGRPRP
10285	24186	A	10361	2	776	FFFLRWSLALSPRLECSGAISAHCKLRL AGSRHSPASASRVAGTTGARYHARLI/L /YLFVETGFHHVSQDGLNLLTS*SACL GLPK\C\WIYRREPPRPAYFIFFLRSL ALSFRLECVQWCDLRSIQAVPPG\LHHS PASASLVAGTTGAHHHTRLVLILL\FY FLRWSVTLSCLRL\AGVQWHNIGSLQAP PPGFTPFSCLSLPSWDYRCPPCLANP LYF**RRGFTMLARMVIS*PRDPPPSA SQSAHDLFIVGQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10286	24187	A	10362	188	365	CPQLHTQSNLINMDASQRYQFELKIQAL/WAGTVAHACNPSTLGRGGWIT*GLEYATSL
10287	24188	A	10363	146	1036	GWAVYQTLQAAWLGPRTESGVSPHGRFSLPHHPPOPTLHAWPAPPLQPEPCVPLREDPFMPESW*LPPSIPAEGVSF*ECDFSRMMMGKGSVPVTPVAPPLGPAPEPFCVTAGCAPMHTPTHTQ\PPHCSIPLPKISFKSKHFY*LLFCKCLSSSVFSLPESILLFIVESVCQPGERCLALNMGWDGKSGRRWATKSQGVMDIAATQTPA/VFSPV/PATSCPAGVSGGK
10288	24189	A	10364	229	1	PLENAKSIYWGKGRLLKNNARLFTVA*S WNQPQFSLMVDWIKK\MWRMYTTESCAAI*R/DEIVSCAGTWMELEAMY
10289	24190	A	10365	186	449	RFFFFFFPKFFWVFGLSPPFFFG/RLGI*EKDGGFFFFFFFPEMASGSVA\RLCSGAVSAHCNQLQFPGSGSLPASAPRVA
10290	24191	A	10366	445	3	RVDNGVRGRYRGKRGRR*TRWGWGHPQRWDQDRSRERPRETGRERAAARRRETEAAETGRRRRERGRSDNRN/RGRPRERIEAGRDAGRER*ARQESWTEKKTARQEEGDRD/RQGHQETRAHKGWGNND*GRQAERSENRRMY
10291	24192	A	10367	1	491	NTAPFPTSLESFAFVVAVQDRVS/LLSPGPECRAI\LTHCC/LRTPG/FKPISHL S/LPS/SWDYRHVPPPLDNLILCRDNVSQSGKLKLASSNPLTSAFPST/YDYRRETGPRASP*TMQPCFMP/RS*SQP*TOI A/R*QSNWGSQ*VLNNRELAFGTMFFGQRPKAF
10292	24193	A	10368	572	40	LHSFRQHFSNTYPQCTPGTP*VTQSLAARPAGLPEPTSASGGAGAVTPPPRTD\PPSVRWSGKKGLDPVLRGGAPRPSANPAPAPQGPAPRKGTECVPTASKTPRPGGRWEPAAPPHAHPGKDLQPPSTLVKECPPEARCPRALTGDLPSGGENRNGLSAFQGGQRRPAQKSGENCEN
10293	24194	A	10370	36	517	PFLFSDIDFLFSFYFLSFFFF*KRGLILPP/GPEGQGGNKG*WPLHPRG*REPPNLTPQTRGNKGNRQTGPVIFGILRKNGFPPFGQGGFKPPGLRBPGLALQRRGGNNQNPYP/P/PGKFF*RTKRGEKSPQPPYNKP NKKFNPAPMEEFSSFKEGRGPSLN
10294	24195	A	10371	60	403	DVEQPKLRSYPTLCKPRSAILTICPWA LQYRSHGLIFGFSWGLSFETESCSVSQAGMQWCDHGLQT/PTDSTSQAQAIDPPASAP/QAAGTTGACHHTCLIFVFL*RWGLAKP
10295	24196	A	10372	358	33	DSLGVPGAPLLSPGVTPHKQWFFRPYTOIKKLGFPPQIFFGFKV*KAPFFFWGFGNLKKKGGFFFFFFFSEMASGSVA\RLCSGAISAHCNLQFPGSSSLPTSAPRVA
10296	24197	A	10373	264	3	RQTSVSGSNDGKSWPPADIDTI\KYVIGNRLITTOQ*LIKLTSKQMITIHNKGR*SLILVSLIFIATTNLLGLLPHSFPTPTTHCI
10297	24198	A	10374	298	384	TLVI*KDGVHTTPHHQOHAYPGPKEYML

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						HKAPLLHSVSRDPSPPFAQSSNCYNRSIK QEPVDPLTQAEPPVRDAGKMGKTPLESEV SQNGGPS/HK*GQYSGDV
10298	24199	A	10375	84	518	IMKLRQKSRSSSLKIMRSKLQHTRAS/GT QLR/PMLGGNFIALN/AHIKKLGRQTIN NLTSQLEKEKQD/RNPKARGRQEIT\K I*AEKKEITET*KKEIQKIYFRV/WFLE NINKP\PASRLIQRMIERNTIRNDKGNV TSAPPDV
10299	24200	A	10376	70	363	PHQKNLVPGLWVQLLGRRTLQSQHPPAP PPSSSPPEVNPVSEVQAAD*LCCIFYDVK VRKCSPTQKKTRKRKKGCLF/CAPGQTR /CLC*KRGEKNLVGKT
10300	24201	A	10377	299	2	YPVAGRGNR*GCGAHALGVGGAMPGLA TISSVSLTISSLCAPPRGGLEPSLPAP HTPPPPPE/P*ASSPSRGEWHLVPPCMQ PGLPPLPPRLSPLV
10301	24202	A	10378	302	3	WPTVATTCSERCSTSLT*NQKLEGTQ LSEEGMSKAEIGQKPGCHQT/VQVVNA KKLLKEIKNATPVNTQITRK\QNSLIA DT\EKV*VIQIEDQTSV
10302	24203	A	10379	125	375	NEYVFLEKSLKLGRVGSCLLGRPRQVD HLSSGAQD*PGQRGKTPSLQNTQKLSRH GGMCP/RLRWEDHLS/SRGG*GCSETR ST
10303	24204	A	10380	458	3	ITISTISKATSFERAPRASRPPFDEWV SQAGPAPLRGWN*GTRRRDWDPEASLK DPRRSGEPEAPL/PLRLML*SRLPPLR WRRRPPPPDSHTSPGNGKSPRVPRTGS KDKRPEALPP*FAAGEPLEANVPVQHG GGSVRSRGSYLTAT
10304	24205	A	10381	327	2	LSAPKKFFQKSLFLGANFRSPFPGRP FTNRFSDLVNPLTKKIYFSHKSSNPPT FFFFFFETGSNSVT*SGVEWRNHNLSRP ESPG\SGDRP*V*HTTGAPYHTWL
10305	24206	A	10382	754	1	NTALETDTTFSGGGGGHQLCVRSRVSGG G*LIMPDLNHPLQQTSGRNQRLQGEVT DPSPGMSGGAQTGPAPRPPPSALRHSG SLQGQP*FAHLYCGTIPYPCYTAPLER APPPPTPTGH*CPGEA\QDELPVCGCSP WPRPPGQAQAGRNKH*FSGQRSSRDITA CSPCSQSKQSPSRPPCVNDS/PGQGPGP KAPAGPPPALPEASLGSHVHCS*VGVM PTRREGHFLVPGKVTLEQAPGGASGGEV P
10306	24207	A	10383	39	433	SHDQTYTEEEELFMDEQRKWFLLMESTP GEDAVNVVEITTKNLEYCINLVDSTVA/ GVSNFERRSTVGQMLSNSIVCYGKIF/R *KR/SQSMWQTSLLF\NKLSQPP*PSTP TILISQQPSMWRQDPPSEERL
10307	24208	A	10384	283	1	NVFSCKPTSSCLISPDSPTRRFSKAD TYRNFMLRRRHTMHHTYMHVHVC TQLCLHLRPH/ITHGLSL/TCAPPVL*R PSFKPLHPTV
10308	24209	A	10385	12	471	SPPWTHGFRYWEPTPPRFSVPHDALGQ FHTALFRLTRRFQQLSSCINISPHTCLEP PCLGLCVGGPLEPAVCNAR/CPP*RGMV SGWKASPLG/CPPTLLPPC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10309	24210	A	10386	287	1	SFCVRSRPAPTSGRTPFPAPPPFPAPP FPAATTPSTAEDGVPG*G/PAPAANCSP HSSQRGSAAMGIPLPQAS/PPAPTAPP SP*SLPFPAPMY
10310	24211	A	10387	336	3	LIEGKLTNRKDIRSKTASVRHHQSPKV DKPTKMGQRNQRKAENS\KIKSASSPPK ECSSSPATEESWMENDELREEGFR*LVI TNFSELKEKTGKLNPAALVCGRSEDQTT
10311	24212	A	10388	15	470	APSPDAMGR\FTEEDKATITSLRCKVNV EDAGGETLVRLQVVYPWTQRYFDSFGNL SSASAIMGNPKVKVHGKKELTSLVDAIK HLDDLKGTFAQLSELHCDKLHVDPENFK LLVNVLVTVLAIHFGKEFTPEVQAYLEK MVTTVANSRLRYK
10312	24213	A	10389	3	438	QTQREPTMVLSPADKTNVKAANGKVAH AGEYGAEALERMFLEPTTKTYFPHPDL SHGSAQVKGHGKKVADALNNAVAHVDDM PNTLSDLNDLHAHKLVDVPMFKLLNHC LLETLDGHLSEFTF\AVNASLEQFTAF EITWLT
10313	24214	A	10390	2	444	TMSFNTLAICLDCLCSTLQPTRSIPGYF SSPLPGNPTPMTSPSSVPMSPNQEVK SPFLPDLKPNLNSLHSSPSGSGPCDEL LTFPVRDGVV/SGALEPAAQPGC
10314	24215	A	10391	405	3	KMILTCLALPAQHCPFSACQTMAPPL PLSIKGAASMSDKLPYKVADIGLATWGH KALDIVEN/EMPGLMGMQELYSASRPLK GACIADCLQITVETAILIETLFLSLGVQE QWSSCSIFSTQEHAVAVFAEAGMP
10315	24216	A	10392	248	5	RLNKVGGHGGNYEHLVYNKLETLQEMYK FLDIYNLPNLSLERIE\NLMRPITSNKF ESVIKHFPPTKISGLDGFTEAFLTN
10316	24217	A	10393	262	3	LPRDRQAGRSQGPVVPQAVGRARKMPF ISYQVYSKNFFEIESCSVTQAGVQWRNI SSMHPPPP\GSSDSPASASQAPGIPGAH HHA
10317	24218	A	10394	287	410	ALKGSSRILIMLGAWLTPVIPA/LWEAK AGRSSEVRS
10318	24219	A	10395	175	1	GGREVDDEIPLVRESTIPHIFFFFFETE SHSVAQAGGQWRDLGSLPSS\PPG\SCH SPA
10319	24220	A	10396	661	963	STLIAFIVISTLFLPLDMTEIYFSLLE IVDTLGEAGFGKVVECIDHKAGGRHVAV KIVKNVDRYCRAARSEIQVLEHLNTDP NSTFRVCVQ\MLEWFEHH
10320	24221	A	10397	1	268	PQTHREATMGLSTADWNTVKGWKGGA HAGEDGAEALERMFLEPTTKTYFPHPD LSHGSAQDKGHGKKVADALTN\AVAHVD DMRNAL
10321	24222	A	10398	33	302	SRGATLIYVDNENGEPGTRVVAKDGLKL ESGPSIKALDGRSQVSTPRFGQTFDAPP ALPKATRKASGTVNRAEESV\KTKGHL VQEHF
10322	24223	A	10399	16	233	PTDYEFNTTYRECGRPRPEFSTSLDLL SQPCRAVYM\VGKNDIPFELRIVDLIT GKSILGFGEPKSQEGDR
10323	24224	A	10400	177	1	KLLDLGQPQSPALAACLEYSGAIAAM\C NLCLLGSSNPPTSASRIARITGVHHAEP

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10324	24225	A	10401	185	419	YVAKDTLSEHLVWKLKSLGRKSESVT GFSCHEPEPSDKTVEL/WQGAHAHACHLS TLGGQGGWITLAQEFETSLDNIV
10325	24226	A	10402	104	3	GIILIPKPGRDTTKKENF/RPLIPIDAK ILNKILAN
10326	24227	A	10403	3	344	SQVMAVAGPAPGAGARPRDLQFLQRF QILKVLFPSSWSSQNALMPLTLLC/LTLL EQFGNYQVGLIPNQYGVGNKDLGEGFK TLTFLAVMLIVLNSTVRSFPLSVSLVLS SPV
10327	24228	A	10404	3	404	ARAQRGDLSATGRNWSPLPPAGLEATV VLRHSGSLMAATCEISNIFSNYFSAMYR S\EDYTLASVPPAATFGADDLVLTLSNP QTSLEGTEKANWVG\BQSQFWPKTQGLD WISFQAEKNKYEASAIQFPFRWDK
10328	24229	A	10405	254	443	NQLSSIMVMFKKIRSFEEFNDPEKVYG SGDKVAG\RLIVEVCEDETRVKAIRILAC GVAKELRM
10329	24230	A	10406	26	461	GEVARRSCCGAMAGTALKRLMAEYKQLT LNPPEGIVAGPMNEENFFWEALIMCPE DTCFEGVFPAILSFPLDYPLSPKMRP TCBMFHPNIYPDGRVCISILHAPGD/DP HGLREQ\PERWSPVQSVKILLSVVSM AEPNDES
10330	24231	A	10407	1	463	QQAAKMAENSGRAGKSSG/T/PARGRGR C/PAEQVIAGFNRLRQEQRLASKAEL EMELNEHSLVIDTLKEVDETRKCYRMVG GVLVERTVKEVLPALENNKEQIQKIET LTQQLQAKGKELNEFREKHNIIRLMGEDE KPAAKENSEGAGAKASSP
10331	24232	A	10408	180	446	KKAAASVSAASGSHLSNSFAEPSRSNGS MVRHSSSPYVRYPSDKPFLNSDLRRSPS KPTLGYPESNSRAIFSA/KNLQD/KIR RLNL
10332	24233	A	10409	1	417	EAGLVTMBEIGILGEKAQDEIPALSVSR POTGLSFLGPEPEDELDLYSRF/KKLQ ELEFLEVQEEYIKDEQKNLKKEFLHAQE EVKRIQSIPLVIGQFLEAVDONTAIVGS TTGSNYVRIILSTIDRELLKPNASVALY
10333	24234	A	10410	305	53	LEAQPHAPPLLGHHLPCWRIPSHLGTCT RPRAMRVQGSSEEGVA/GQAPPLPWVHR GSLPLVRRRPAGKPTGGNAREEKGVG
10334	24235	A	10411	419	2	NNSRKFGNGTLKLVEVEIYPLISEIPD KSELLTPQDKKHAPLPSAVPNPSA/CP DLRPHTTPASPV\PAKTVETRPSAPQG PLPGPVRRPRGRFVRAASPQTSGRPGA PRPPGALREATDAPRAATPPIAALAGH S
10335	24236	A	10412	74	322	MDEMATTQISKDELDELIEAFKVDLSS NGFICDYELHELFMEANMPLPGYKARET IQKMLDGDGRNTDGKIS\YDEFAYVSM
10336	24237	A	10415	1	415	PQTHREPTMVVASADKTNVMAAGKVGA HAGEYGAEALERMFLTFPTTKTYFPHLD LSHGSAQVKGHGKMVADALTNVAHVDD MPNALYALSDLNHKLWLDP/VNFMLLS HCLLVTLVAHLDPDEFTPAVHACLDKLL
10337	24238	A	10416	19	454	APSPNAMGHCTEEDKATITSLWGMVNV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M. eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						DAGRETLLGRLLVVPWTQRFDFSGN\LS SSDSAIMGNPKVKAHGKKVLTSLGYAIM HLDDLKGTFAQLSELLCDKLHVDPENFK LLGNVLVTVAIHFGIEFTPEVQASWPK KMNVA
10338	24239	A	10417	2	395	ALSSSQPSAPMHPFYTRAATMIGEIAAA VSFISKFLRTKGLTSEQLQTFSSQLQE LLAEHYKHHWFPEKPKGSGYSMIGVNP \KMISLILQACIEGGI
10339	24240	A	10418	2	374	LSTPHAFGTGKWTFFISLLFLFSAYS GVPRDAHKSEAAHRIKDLGEDFTALV VIAFAQLLQQWPFEDH\VOLANDVTEFA TTCAADESSENCQSLHTLFGDLLCSRA TLDESHCVQDGRP
10340	24241	A	10419	48	347	DPKAQLPEPLRLVLWQLTYAMAAGSR/TS LL/LAFALLCLPCFKAGFPNRLSLRFD HAMLQAHRRTTAIDTYQEFENLYPKD/Q QYS/FLMTPTSSALDSIPTPS
10341	24242	A	10420	166	1	NFLKKPGFPQKFFQRLPLILTFEFFF\ FETKPHSVSL\LECGGTVAHCNLCPLV
10342	24243	A	10421	2	251	LGCTQHRSQELVAAATSHQTCQASEDV KEI/FARARNGKYRPLKISIEHQLMIG SY/SSQPSDSWDNDYDSFVLPLEDKQL CY
10343	24244	A	10422	251	1271	KEDLSRAPMSGTQSTITDRFPLKKPIR HGSILNRESPTDKKQKVERIASHDFDPT DSSSKTKTSSESRSEIYGLV\QRCVI IQKDDNGPGLTVSGDNP\VFVQSVKEDG AAMRA\GVQTDGRIKVNGLVTHSNHL EUVKLIKSGSYVALTVQGRPPGSPQIPL ADSEVEPSVIGHMSPIMTSPHSPGASGN MERITSPVLMBEENNVHNQKVEILRKM LQKEQERLQLQEDYNRTPAQRLLKEIQ EAKKHIPQLQEQLSKATGSAQDGAVVTP SRPLGDTLTVSEABTDPGDVLGRTDCSS GDASRPSSDNADSPKSGPKERTYLEENP EEQKKG
10344	24245	A	10423	198	569	QRNMVGQRLVEPRRLKPGFINVKSYNIGD WEWHQGFLLVCFFLRWSLALSPRLECS GAISTHCNLCPLPGFKQFSCLSLPSSWDY RHAHHCTQLIFVFLVEMG\FHHVQQAQ GFFSLEKSLTII
10345	24246	A	10424	2	343	PQTQREPTMVLSPADGTNVYAANGKVG HAGEYGAEALERMFLSFPTTKTYFPHFD LSHGSAQVKGHGKNKVS\DALTNAAHVD DMPNALSALSDLHAHKLIVDPVNFKLLS HC
10346	24247	A	10425	31	342	RAAVMPREDRATWKSNYFLKIIQLDDY PKCFIVGADNEGSKQMQRMSLRGKAV VLMGKNTMMRKAI\RGHLENNPALEKLL PHIRGNVGFETIKEDLTEIR
10347	24248	A	10426	196	2	KNLIISQTKKVICPNTLFLVFPKRVFFF FFFETESRS/VSPRLECSA\SISAHYN LCLPGLSDSS
10348	24249	A	10427	1	405	RLECWLEPPHGAGLQGLGWVWSCSVSTG PTMQALV\LLLCIGALLGHMSCQNPASP PEEGYPDPDSTRALEDDEDPIFIDPENK LPEAGSNFGYDLRLRAIMSPTSNNVLLP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						PLMVATDLWDLSELAQQLTESII
10349	24250	A	10428	223	361	EGPTEENMAAKVFES/IGKFGALAVAG /GPVNSALYNVDVGHRAVIFE
10350	24251	A	10430	3	359	LTQREPTMALSPGDMTNVKAANGKCAH AGDYGAELERMFLYFPTT\KTYFPHFD LSHGFAQVKGHGKKVVDALTNAVAHVDD MPNALAALSDDLHAHKL RVPVNFKLLSH CLLVTLA
10351	24252	A	10431	273	1	NHKDGKKQSGKTEKSKNQASPPPKERS SSPATEQSWTENDFDEFREGEFI\ROSN YSELKEEIRTHGKEVKNLKKLDDRLTR ITNAQK
10352	24253	A	10432	211	3	SFLWKFCRLRGIPSHVSCQSA/LLGGAS QLGYSGVDRDPLEEAVCLFSDLKLHAGRT TTLFNAVROGHLSLQ
10353	24254	A	10433	281	2	TNQEKKKGDPNKKIRSGKGDITTDNTVTI IRDYYG/HTYTNKLKN/LBEVDKFLDTY YLPFRFQREIENMNQFITSNEIESVIKS LQTKKSPGPMS
10354	24255	A	10434	219	1	SFLWKLRRLRGAPGCMRCQSA\LLGGVSH LGYSGVDRDPLEEAVCPYSIDLNCAERTT TLFKAVREGCLSLQKF
10355	24256	A	10435	133	2	FPKPPGNFFFFFETESHVPT\RLCSCGA ISAHCNHLPGSSDSPA
10356	24257	A	10436	248	376	KGGVFFFFFFFETESCSITQTGAQWHT \YGLQPRPP
10357	24258	A	10437	250	1	KGTRKELTFIEQLLSAKYWAAGCMHYFR GSGKYSNGYPVFVFVIFSHTESCS\VA QAGGQWCDLVSLQPPPP\GSSDSPGASF
10358	24259	A	10438	354	2	KRGLKKNPFFNPRNMGFEFLKLGPNPKK IFKNCKIFKMGKKKVLGFYKNSKNLKR GKLNPFVIFFFFFFFFLETGYSIA \RLKCSNSGTNTAHCSPELPGSRDLFDS TTQVAG
10359	24260	A	10439	126	1	GMVDCVCLFCFAIKEGREREKERERK RERQREKER/ERERDKERKREERK
10360	24261	A	10440	29	347	IQKPTADTKKFFKKLKYTTRENLHNNK EDRKEGKKEKTTKQHGSSKSLINKTL NINGLKSPIKTHRAE/WNKNDPMLYC IQETPFTYKDTLRL/RIQGWKKIFH
10361	24262	A	10442	405	1	IFFPHPPFFKSFRLSPQVEIQGIFLGP WKLFPFGFNNFS/CPNLPNNLGFKLPP RPSYFFRIFCKKKGF/H/RVYPEGFPPFL ALGFFPLFPFKSWGFGGDPSPSGPFFFF FFFLVAEGTLSEGCRLIRGRWKNLVP
10362	24263	A	10443	122	372	LYNDPISIVQVTLVRRVFFWVLYSANWS LRWKNFLFFSFFKMASDPVAQAGVQWC DLDSLQPP\GL\SDTPTLASQVSETT G
10363	24264	A	10444	171	3	RHPTMAGSSEMFLSGFGCRLTVFVLFE TESCSVT/RECSGAISAHCYLSLPGSSN LP
10364	24265	A	10445	173	3	CMNVVCFISIFLKNIFILETESHSVSQ AGVQW\LITVHC SLKMGSSDPPSSASQ V
10365	24266	A	10446	187	329	SFLWKFCRLRGVPGHVRCSA\LLGVASQ LGYSRVRNPLEEAVCP\PSDL
10366	24267	A	10447	27	226	YSYPVYLLHLIFLCWKCSLYFIYFVFEM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ESCSFAQAGMKWCDLQPLPPG\SSDSLAPASQVAGVDA
10367	24268	A	10448	119	296	SPIHYILVIIICFIHVILLITIFSEVGS HSVAPAGV\SGAIIAHCHNKLGGSSPP VSVS
10368	24269	A	10449	111	363	SLKKLVFFFSIYTHNFFPPFDPTLKNST RHSLYLSLSLSLFLSHSV\SRLECGGTI IAHCSLNLPGSSDPHTSMSQV\AGPTGS C
10369	24270	A	10450	218	1	QRFWGP GPKNVFKNLGSAFFLGRGKLF LEIWGGFFFFFLVFFLRQSHSIAQAGVQ WCD\LNSLQPLPPRFK
10370	24271	A	10451	179	3	GPFLTLFFFMGKFALGREKCHFFFFETE SCTVAPAGLQWRDLGSLQPPPP\GSSDS PAS
10371	24272	A	10452	71	232	SSPLSDLLFNIVLEVLAKDIMQEVH/YK LILIGKDEVKWSLIVDKIILYVKNKH
10372	24273	A	10453	153	3	ARGELYFLEIGGGFFFFFLVFFLRQSHS IAQAGVQWCD\LNSLQPLPPRFK
10373	24274	A	10454	338	221	MGFLHVGQASLKLTSICP\LGLEPKWD YRHEPPRPVIPS
10374	24275	A	10455	214	366	YNYKYLIHYSYLFFIFIFF/NIHYIF FILFFYLTSPIFLSYFFFFITLF
10375	24276	A	10456	155	2	DRVSLLPRLCNGAILAHCHNCLLGRS HS/PRVAGITVAHHHARLIFCIF
10376	24277	A	10457	870	1249	EGPRWADHLRPGVQDHLG\QHGETPSL QKIQLARRGGTC/LCQSOLLGRLSQEN CLNLGDDGGCSEPRLHHCIPTWGD\GDS PKKKE
10377	24278	A	10458	222	404	KQRPGRQWLTPVIPKLWEAELGR\MLE ARTLRPAWAT
10378	24279	A	10459	122	362	LSBDQLNCYPQRLHHFIFLPVITRVQMS HYLCQSCLEHFF/SFFFLYFEMSSSV T\RLECTGMISAHSNLYLPGSSQSSG
10379	24280	A	10460	3	102	AASTLALSPRLCNSAILAHCKLH/LPA FTPFSCL
10380	24281	A	10461	133	339	KLKSFQGSKKPETKANSLDLALFYHNYI TRQCFTSYSNFFGDRVSLSPRLCNGV ILAHCHN/RTPGFK
10381	24282	A	10462	3	193	ASNMMTELKSIPIPLTLNVNGLNAPLKR HRVAGWINDPTICYLQETIFT/CKNNHR LTAK
10382	24283	A	10463	126	314	RLGGSTIKVQRDLSSDRSKPGRFLYTSN SSYVRKGKRNKACFTERVFP/PVNDII
10383	24284	A	10464	1	332	KKNLFLSKDCLSSLFRFSKSPPAIIGPP RGWTPKTRFIGPKAFFFKGSLGRKY HFGLKPVP/CPPLSKTRFLPGVPPFF FFFETESHVA/RLECSG/AISAHCKLR L
10384	24285	A	10465	173	365	RFVCSTIKVLRDLSSDRSNPGRFLSLQI PP\LRKDKRNKAYFTK/RPSPVNDIIST
10385	24286	A	10466	335	3	PFKKFYFKISTRALLEPVFFGKKIRVPP QRLSPIWAPLFRKGPNSFQVNGVPLFF FFFFVRHGLALSSGVECSGTRLECSGAI /STAHCHLCHLDASHPPTSASWVARPTG T
10386	24287	A	10467	818	1008	VHTDVLADILKSINNAEKROT/RRCFLS \WLQGHCPFLTVMQHGGLCGVELGGLPG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PGDFCKRPR
10387	24288	A	10468	111	1	MVSFGRPRQADHKV\GVRDQPGQHGETP SLLKNIRI
10388	24289	A	10469	204	1	LWGPILKIFCQILKTICEGNFRGPTFFI FFFEMESQSVTQARMQWCDLSSLQPLPP GS\SNSRASAS
10389	24290	A	10470	190	330	ERIKKQDLSICCLQVTHFTFKDSQRLKV KGWKK\IFHTNKNQKRIWT
10390	24291	A	10471	162	2	IKGPKRAPPANKGRAFFFFFFETESC SCLQAAVQWHDLSSEPPTP\GSSDS
10391	24292	A	10472	120	3	SWGFFFFF\EVESYSVAQVGQWCDLG SLQAPHVMILVK
10392	24293	A	10473	298	1	RRALPCPANFLYFYFLSLLFFETEFHS \VAQAGVRWHELGLSLQTPPPG\SSDSPA SGEYSANYTGEYSANYTGEYSANYTGEY SVNYTGEYSVNYTGEY
10393	24294	A	10474	1	380	AVTGRAGSMVAPR\PLRRVLVLYQGKLR SMAGNFWQSSHYLQRIIDKHDLLNERQK DLKVLSEEEYWKLRFFTKVIQALCEHL KLKQPGIATATAYPKRFYARHSLKSIDP VLMAPTCVCLASTAN
10394	24295	A	10475	289	2	TQGFPPINNSFYALYPKQKIPFFSDKLF RVKGFKGPVFHYGVKDFKNKDGVEFFIFF FEMASGSVAQAGVQWRNLGSLQPPPI\PG SSSLTTSAPRVAS
10395	24296	A	10476	138	402	ITGRAPPKPFPFLKRGYLSGGLTNIGFSF SFSFFETESRSVTQAGVQWRNLGSRSWL EST/SPDSSNS/PAPASRVAAIT
10396	24297	A	10477	2	336	ARETNDTTQTRLLPANNTMTSRDPYISI LTLNVNGLNTPIKR\KRVASWINKOGLM GCCLQETHLSSHETHNDTHKLKIKTWRK IYQANGKQKKARVV/ILISDKTDFKP
10397	24298	A	10478	51	250	RKVSLEFKKWCWNTLFYCKR\LSLDYTRF AKINFEWITDLNVREKT/IKLLKNIKE NICDLGLGKDFP
10398	24299	A	10479	216	2	GFTRKALSGFFKTGWFWVFPNFKLFFK KNFSERFFFFFEMESHVST\RLCSCG PISAHCNLHLPSSSLV
10399	24300	A	10480	191	3	FSTDGNVNCVLKYSIYIYIYFFFLIFF FEMKSCS/VSPRLCNGALSAHCKLCLP GSCHSPARA
10400	24301	A	10481	135	768	LGGQVLSCASQPVSLFPLFFFLISFLGC LLAFLSACFASTFSCVLGSPETSFSPCL HPPPKVLSSH\PPCSR/CPQPKG/P PLPKHACPP
10401	24302	A	10482	126	333	MVVQORYCVMCFVI\VLCLFLV/VVVV FLW/CSVYIVYWGAVVLFIFFFFFS LLCFAVCLFVWLLDRF
10402	24303	A	10483	240	2	ATEKNMGLGTSVRGLSGSNPSYGRVRER IGGVCLWSQILLRGC/LRWEDHLGLGG GGCSEPRSSHCTPTWVTEQDPVLV
10403	24304	A	10484	136	2	NRPSYIFSFFFETESHVSAQAGVWHD SSLQPLPP\GSSDSPA
10404	24305	A	10485	161	328	EKNFKPYGSCRHFLFYFETESRVA\ RLECSGTISAHCNLRPLGSSN/SPAS
10405	24306	A	10486	193	347	ILFSFLLFYFFETESCSVAQAGVQWHD HGSLRSRAP\SYNAPALDSQGT
10406	24307	A	10487	114	2	GAVVQSEVQWRDSSLQADPPG\SRHSP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ASASQVAGLV
10407	24308	A	10488	314	49	IRRSTERSEPRYSMVCRROQROGGPCL\RSQLGLRLRQEDHLSPIAGDCSEPRH\LACTIONAWATEQEPVLKMSPTLFCFLWPLPCQ
10408	24309	A	10489	291	1	KSPPPPNRRGLTLRSRGQIGNGVSFYFEAPVTDFFIFFQSLVLSTQAGLQWCNLSSLQPLPPG\SSDSPASASRVAPVSQGHATAPQGRQTLSSC
10409	24310	A	10490	226	3	GSRCMPRRRLAHAFPAARMPKRKVSSTEWATEEPPKRRSARLSAEPAPAKVETK/PEKAAGKDKSSDKKVQTKLV
10410	24311	A	10491	2	153	ARGLVFFVYLVEMLTCHVAQAQVKPLTSSEPP\LGPKCWDYRREPRPT
10411	24312	A	10492	123	342	THYLCLLRFFFLDRGFLLLPRLDC/NAPISPNNLRLPASSDSPASASRVGITVNNHYARLTLLFIFQNETLF
10412	24313	A	10493	194	2	IPGWFFKFNFLPLPLFFFFFEMESCSVAHAGV/GSSDFPASASQVAGTTSMRINAWLIFVFPSRN
10413	24314	A	10494	373	1156	KVQLKVYLLFFFLRLSLALLERLECSGTILAHCNLPPSRFEQFSCSLPSSWNYRRPPHHARLIFVL/SVETGFHHVQAGLEL LTSGDPPASA/FPKCWDYRHE
10414	24315	A	10495	181	3	SFLWKFSLRGVPGRVRCQSA\LLGGASQLGYSGLRDLPLQEA VCPFSDLKLCAGRTTTLFK
10415	24316	A	10496	156	2	AASTTRLGDRDQPGQHSETPSLLKIQKLG\SGGGHLRLRQENCLNP\GGRC
10416	24317	A	10497	157	300	IQSWFNILKSIHVTHHSNRK/EVNHIVSTDAEKAADKIQHPFLIKKQ
10417	24318	A	10498	3	289	LVKKMLTGSTLGKSYRHSPPFSINQGHNALRKAAG\PLPRKAGY\LQGFSPRYGL\WDGKDLTIHQPDTRGVSLSRISKRGRL/CSCPLGTCLSI
10418	24319	A	10499	138	1	WYGLIYLLLEMESCYVAQAGVQWHDLPQLQPPPP\NSSNSPASSC
10419	24320	A	10500	138	1	WEGLIYLLLEMESCSVAQAGVQWHDLGLS LQPPPP\NSSNSPASSC
10420	24321	A	10501	200	343	LEAHSFLSFFIFIIFFDTKSHSVT\RL ECSAAISAHCSLLLPSSNS
10421	24322	A	10502	84	339	PRDGKRRDKQKQBTGGGHHYKSQLRGLRQEDHVSPPGGRCSEPRSRHCTPAWAT\BSNSVSKKS
10422	24323	A	10503	141	362	EWNCCVCC/CCCCCRRCF
10423	24324	A	10504	198	320	TIKKQKNTGGILPNSYILPPLPLEPGDL\RFLDVDNRVKLPV
10424	24325	A	10505	30	356	GYPNCNPILYMSTVGFTTSLDLDIPLHPILKVCPTHTRALRDLSSDRSNPGRILSTSNSSLY/EKDPNKAYFTK/RPSPVN DIIIT
10425	24326	A	10506	16	375	KKFFKKKKKKIFFFFPPLKNFFFPKRVNFFGRGWPKKSPPKKVFPKFFGGGFKKPLKKKKIFFSPPVKMGPPKGFPPKGGPPFFFFFFFFFFF/LLCLIPR
10426	24327	A	10507	156	2	AASTTRLGDRDQPGQHSETPSLLKIQKLG\SGGGPLRLRQENRLNP\GGRC
10427	24328	A	10508	313	2	QSKWLEESTLGEDAVNIVEMTTKDL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YYRNLVDKAAAGFERIDSNFESSSTVAK ILSNICVC/Y/REILHEGKSRPMWQTSLSYFKELPQTQHSAILTLTSPRA
10428	24329	A	10509	325	1	ECAKBMNAETKRNLAI DATETQRIIRDCEHYNKMENLEAMDKFLDTHNLPRLNHEBIENLINEPIMSNETETV/I/NSLPSKKN SGSEGFTAIFYQRYKTPLILKLFKK
10429	24330	A	10510	126	14	DSSGQVQWLKPIIPV/LWEPEAGRSPEVRSSRPACPTW
10430	24331	A	10511	435	769	PFFKFPPLSHACDGGSLFCRLRLCSCGVI T/AHCKPQLPG/SQSDFPASTSQELGP/ TGACHYTRLICCREVL/HVAQAGLELL CPKDPPTSASQHARDYRH/GHPAQL
10431	24332	A	10512	147	412	RFVCSTIKVLRDLSSDRSNPGRFLSTNS SSLY/EKDKRNKAYFTK/RPSPVNE
10432	24333	A	10513	251	466	QTCTGSPASLLELFNSIATQWELVRS IAGNALKDEND/SAVKMLASLIMSYPKAA AAEDYKADCPPRNPGP
10433	24334	A	10514	286	1	SFLRKFCRLRGVPSRVKQCSA/LLGGASQ LGYSGVRYPLEBAVCPFSLHLHAGRTT TLFKAVRQEHLSLQRIILLPLVGRVGRPN DSRCDRVIGH
10434	24335	A	10515	28	428	RFVCSTIKVLRDLSSDRSNPGRFLSTNS SSLY/EKDKRNKAYFTK/RPSPVNDIIS T
10435	24336	A	10516	263	2	IKKPADSESAGALILDFFPASQTVRNSFL LLTSHSVCYFCYSSPNGLRQQLKIIIPF FFLRQSCSV/SRLCSCGMILAHCNLC LPGSNN
10436	24337	A	10517	62	292	PATLFSGVILPPTNSINAFSGSDSKSAH K/CEMLGTENFNFFTCHTHIIAEHSNST HTHTHTTQTHTHTHTPLLFYE
10437	24338	A	10518	172	2	RGKKIFFPPEKGNLVWNTALPFFFFE TDSHSV/TRLKCSGTILYHCSCLPGSS DF
10438	24339	A	10519	42	194	ILVETF/CLRFVSLNVLKMRFLKLLKK KKKKKKKKKKKKKKKKKKKKKI
10439	24340	A	10520	120	1	IFAKRWPIKFFPPFFFPETVPHS/VAQ AGVQWCDLGSP
10440	24341	A	10521	202	375	SFLWKLHLSGVPVGHVRCQSALTGG/ASQ LSYSGVTDITLEBAVCPFDLKL RAGRTT TL
10441	24342	A	10522	272	402	PKIFYVTWKAWNYYPYTITEYTCSE/IR KFFIHIETKYEDNKGSN
10442	24343	A	10523	147	439	LILYVNYISRKSTVYDSRHPCTYYLIPE KNCKYKHCNFLT/SSSIPPTPSTPSR ASPKKKKKKKKKKKKKKKKKKKARGG
10443	24344	A	10524	7	415	RFVCSTIKVLRDLSSDRSNPGRFLSTNS SSLY/EKDKRNKAYFTK/RPSPVNDIIS T
10444	24345	A	10525	321	442	TSFSFLPFF/LETEFHSA/RLRCGTI LVHCNLCPLPGSSNS
10445	24346	A	10526	477	3	IEGKLPNRKDIHTKNPVSRRHQRPKVD KTTKMGKKQSRKTGNSKNQASPPPKER SSSPAMEQSWTEKDFDLREBGRGSIY SKL/REEIRTNKEVKNFEKBLDEWITR ITNAKSLKDLMLKAEAQELRDECTSR AASANCVAVPQAFDRSHGVQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10446	24347	A	10527	265	411	RFVCSSTIKVLRDLSSDRSNPGRCLSTSN S/SPVRKDKRNKAYFTK/RPSPRN
10447	24348	A	10528	81	390	RFVCSSTIKVLRDLSSDRSNPGRVLSTSN SSLY/EKDKRNKAYFTK/RPSPVNDII
10448	24349	A	10529	253	23	RIFLFYFHSFLRQGLARAEGQPHNSSL QPPPPG\SGDPPASASRAARTTSAYHHI PLFFFRSYCVAQAKIINMLSL
10449	24350	A	10530	10	398	RFVCSSTIKVLRDLSSDRSNPGRFLSTSN SSLY/EKDKRNKAYFTK/RPSP
10450	24351	A	10531	289	423	RFVCSSTIKVLRDLSSDRSPGRFLSTSN SSL/QRKDKRNKAYFTK/RPSP
10451	24352	A	10532	152	401	PHCSHSQVRIQANVHGHRQRTYGSVI PHILPLHLVKKTFSLRDPHFSVSLKKNL VLTCLHLFL/GVTRTPRNDPFVSMMLFT
10452	24353	A	10533	2	515	LDRISSLLPRLKCSGPVSAHRNLYLP/G FKRFCSLGLPSSWDYRRASPRVAKFVFL VDTGFHHVGQAGLKLTTSSDPPSLTY/P QCWDYRREPHLAAF
10453	24354	A	10534	469	566	PTKNTKISRWWCVVPV/IWEAEARESLE PGKQRL
10454	24355	A	10535	354	47	KPKNLPGGGGPPFYSSPSKGGKKIPLPWK AKVPINQILPLPPHPGGGKTPPKKKK KKKKKKKMATVQKGM/PHKYHGGKTGS YNVIQHAVGNAVNTNRIGS
10455	24356	A	10536	1	409	TPKKRFFPKPKGFFPPPKKKKKIFSP PPKFWPPQKNFKKAPPPPPPPPPPPPP FFFFLKSNPPPPPP/SKNPILKPPLPPL FRVFPFKKKKKKDP
10456	24357	A	10537	204	435	TSGSLYKLLGMDLGLGKTTIPKQGGHQ NSS\GWHPEATTG/VNWAFLGLHWDPKA LAHLQLWNIAL/QR/FGKMTKACY
10457	24358	A	10538	208	382	RFVCSSTIKVLRDLSSDRSNPGRFLSTSN SSLFER/DQRNKAFFPK/RPSPVNDIIS T
10458	24359	A	10539	63	409	GWRLTNFPVGKTPSTSGTGLLFIFLLN LMGRLPSSISMKEFRKQNRGQKC/EF MKKKKKKKKKKKKKKKKKKKKIGGAF LKIFRGGNPFPGGGEKIFFFLGGGKSR GGGFG
10459	24360	A	10540	3	1322	RGYAWPNGALPASTVPCGFAACPGFELC SVNGRQAPAGSSGFLPPVPSLCPTHVCR ATPQCKEDSTCISLRRFPWGSETHLLCP APIPSVPGVPCGTFTFQCBDRSCVKTLS ASPLPILLCPPHLPSPDCGLQGPSSR IVGGAVSSEGEWPWQASLQVRGRHICGG ALIADRWWITAACHCFQEDSMASVTLWTV FLGKVVQNSRWPGEVSPKVSRLLLHPPYH EEDSHDYDVALLQLDHPVRSAAVRPVC LPAR/SENREQGLQ/CSWITGWALREG GPISNALQKVDVQLIPQDLCEAYRYQV TPRMLCAGYRKGKDAC/QGESPG
10460	24361	A	10541	154	3	GVGNFFFFLRLWSLTLAGVQVQRSLGS LQP/LTSGSLFRQFSCLSLPSTRP
10461	24362	A	10542	3	406	LMVLWTAHLPALAPGSRSTSLLLAF\ALL CLPWLQE\AGAVQTVPLSLRFDHAMLQA HHAHQALIDTYQEFETYIPKQKYSFL HDSHTSFCFSDSIPTPSNMEETQKCNL ELLRISLLLIKSRLEPVQVLTSMF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
10462	24363	A	10543	3	414	HSSAHAYGTYESSGKRKYLQRPSTABL KKALKEKKNRLLQLQQRKSVTSSSSSR DSSARDSSSERETSTSSSESDTDES SSSSSSSAYSTNSSSFDSDSSSS\SR GRSTSDSSADD/STNEESELE
10463	24364	A	10544	240	509	TFTSFIIGTPNLGEFCCKNNFGI/GKFR MKVACQIETLGILSFFFETBSRSVTRLK CGGAILAHCKL
10464	24365	A	10545	275	2	GCSRPFDTAIPLMGPYPPEKKLLFEKNK /DTCTCMFIAAHFPVAKMWIQPKPSIN EWIKNPVTHIYIHTHTYMCIIYIYTHICV CVIHIYI
10465	24366	A	10546	233	2	WSWMAIQSVLPQTAFTELKNKYSCIQET PILFYFLKQSLPLSPLECSGVI IAHCN /LQ/RPGSTTFPASASKVERTTGA
10466	24367	A	10547	2	420	KKKIPNRGGCLKRDTKAFLLKTPPMLQRR TPPAFPKGGGFLPDFNLPSPKGNPPI YSWERFFPRFFKNIWAPVKANLLSFPF FSIFWRTGSRYIAQAGLELLGSSYPAS CLPESWDSRR\DHRRPTI
10467	24368	A	10548	190	1	AASTFFACVCFRLFVVFETESPSVAQ AGLQWHSLSLQPPPNLG\SGNPPALAS PVAGNC
10468	24369	A	10549	155	1	ARGEKYFLEIGGGFFFLVFLRQSHS IAQAGVQWCD\LNMQPLPRVK
10469	24370	A	10550	223	392	RFVCSTIKVLRDLSSDRNRCRFLSTLN /SLAVRKDERYKAYFTK/RPDPVYDIIS T
10470	24371	A	10551	183	3	WQKLLFLFGTESCSVARVGVQWRHLSSP KPPPP\GSSNS/PASASVA\TGALHA RLIFVFL
10471	24372	A	10552	297	10	TDELLCMEEKRWFF\DMASIPGEDTV NTDEMTKT/DLEYINLVKVSAGFERT DTNF\ERSSTVSKMLSNSITCYRKI/F/ RERKSQMMQTSFSLF
10472	24373	A	10553	509	3	LLTDRTLSCRSVGVPSCVRCQCA\LEEG ASQLG\SRGSGVRDPLEEAVCPFDLQL RTGRTTALFKAVRQGHLSLQRIILLSF\V CLCPAPRGGAYRGTOASLSCGGLHPVRA SRLCLCPKQAWAMVGTPPP\TSLPPCSL ISDCCASSQRDS/VGVGPSKPGAGYNLV VRRF
10473	24374	A	10554	262	453	GWGILTANLLVFGGSLISERIFFSPPL ATGFCVAQAGVQW\LI IAHCSLEFLGS SD
10474	24375	A	10555	112	372	KKKGGGPPFFFFFIFFLIRQKAKLVVL AFNRRGLRKPDIFFYAGVGKIVKKKYS GFFIELVTTCGKNYLMCALAVIDPRDSN IIRS
10475	24376	A	10556	50	358	RFVCSTIKVLRDLSSDRNRCRFLSTLN SSLY/EKDKRNKAYFTK/RPSPVNDIIS T
10476	24377	A	10557	203	350	QLHADKVS RFATHAECRGVIMAYFNLLN PH/FKRSSCLSLWSSWDYRHAP
10477	24378	A	10558	98	387	IQDTDLIRGVYRYRDKKREKDSPPER EGEREIEIKQKKER/ERKKERKKEST HQKE
10478	24379	A	10559	237	3	EVFFKNIFEIESCSVTQARAQQDHSGL

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						QPPTPG\SSSPPTLASQSAVITGVNHH TQSGLTFSQPKQKALGKMCISSGG
10479	24380	A	10560	37	359	RLKCGGPVLAAYCKLEILGSSNTPTSTSW VAGTT/TCHHAQ
10480	24381	A	10561	170	3	RPPFLPWGKKFQGVSPFFFFFLVFFFEI GSHSVP\RLKCSGTITAHCSLDLLGSSN
10481	24382	A	10562	1	388	LPEPLMVLRTANLVAMAPGSRITLL\LA FALLCLPWLQADAVQTBPISMLYDHAM LQAHRAHQLDIDTYHELEETIYPEDQKH SLLHDSQTSFCLSDSIATPSNMEETHQK SNLEMVIRISLLLIETWLE
10482	24383	A	10563	224	392	CVDPILKWFFLRATRCQCPLS\LFNIV LEVLAIRQEKEIKDP/QIGKKEVK
10483	24384	A	10564	185	2	RYFGGPDSPONGKTVFNPLFFFFBTRV\ HSCCPNESNGTISTHCNLCPLGSSNSPA SASQVA
10484	24385	A	10565	175	324	APGYGTYRVILCKILLRRLRHKNHLN PGRGCSEPRSHHC/ITPAWTE
10485	24386	A	10566	3	367	HELLWSTIKVLPYLRSDRSNPGGVISTS NSSL/C/EKDKKNKAYFTK/RPSPVNDMI ST
10486	24387	A	10567	128	391	GETCEGVYGFQQGGKQTKVFKSKKDEG PCSKTWDVGLGSSPQFIFLKKVRFFFFF FETESHVIRLECSGTPTG/HCNLCYPG TS
10487	24388	A	10568	251	485	SFLWRFPPLKGVPGHVRCQSA\LLGGASQ LGYSQVDRPLEDAVCLLSDLKLCAGRTT ALFKAVRQGHLSLQRFLLPLFSY
10488	24389	A	10569	176	3	FVPPILKKMGPFLLKKKEGKPPFFFFSEM ESRSVT\RLCSGA/TISAHCNLCPLGS SNS
10489	24390	A	10570	212	386	RFVCSTIKVLRDLSSDRSNPGRFLFTSN SSLY/EKDKRNKAPFTK/RPSPVNDIIS T
10490	24391	A	10571	134	489	SLFFLPSPDRWSLTQSTEMPPSWKFP REIRSPLLAMLESLLLQPTAFLCPSSLT LLSLKPDLSLRTGSLFLSFFSFLYFEACS VA\RLKPSGTISAHCNLCPLSSSDSPAS AYIVSG
10491	24392	A	10572	1	470	GQSRGIPLLLTLTDLEKPVSLLSVTNLY SKNSAQFSTILQTLSPPATFTPSPIPL SSAYFFFFSDRVS/LLSPRQECGLNLG AHCPRQPPRFKRFCSLSPSS\SWGLTRR HTTTPGLIFCIP/SVEAGFHHVAQTGLE LLSLSNPPASA/FPKCWDHRR
10492	24393	A	10573	242	410	VMLRMQIYFSLHNPIFFFFFETGSHFIA\ RLECSGMIPAHCNLCPPGSSNAPASASQ V
10493	24394	A	10574	236	1	ARTFFIHLKASCGDNATGVLWHRATW CPVLLDRDSLSEVCEILCIHAC/VMR IHEHTHTYIYANTHTHTHTHTHT
10494	24395	A	10575	241	35	RSSYLFIFFNFVETRSVAQPGKLCCSA WAGTPG\SSDPPTSSSQSAGIIGMSLNL FLWLIIIDQAGNTN
10495	24396	A	10576	294	72	FKNFKSPLFSLFFFLILGTRFCYVAQAG LK\SWPQGDPSALASRVAGTRGVHRHTQ LQVSFNYYKVLAMHSGSQL
10496	24397	A	10577	1200	1625	PDGWSYSSGHSWLPPEASNGRAWSSCW

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						VPPQLSPPOAPPSPATHLGPTPPLA/SP PQAPFPATHLGPAAPPPLSSAP\PPPD TLLGPAAPPSSSGDPFRYSP/EVPPQ LSPPQAPP
10497	24398	A	10578	226	325	ERHTHTPHSHTRSHTRLTHTHA/YTHTH ANTHA/YTHTHAHTHFP
10498	24399	A	10579	108	320	TINVFLKVNVMKLSYLRFNTRNCSFFFL AGVQGEDHGSLLQLQPPG/SSCDPPSSAS RVAGTTGAYQHTQLIF
10499	24400	A	10580	1	288	ARGERERERERERERERERERERERE RERERERERERERGLSFFFSRSGGKLV CVC/RPSARERERERHAFSAPPSLQKK KKVFGGREGTHSLFYPPCGNSLRR
10500	24401	A	10581	1	476	REWGLALSPRLECSVVIIAHCSLGSGL KRFSCLRLPSWKDYRCAPPCPSLNLFFV ET\GPHYVAPGWSLLLGSSD/PPPLASP KCRDYRHE
10501	24402	A	10582	210	346	PHCSITHSQVRIQANVHKHRQRTYGSVI PHILPLHVLKKT/FSLRDF
10502	24403	A	10583	316	461	LPNILGVVLEFFVSETGFCSVTHAGVQWC DEHGSLSQSQTFFG\SSDLPTSD
10503	24404	A	10584	172	383	NLDLYLTSYIKINSKWIIDLNVIAKTIK LLE\KNVAGENIPDLGLGKEFLD\KTQK ALS\TNKKIDKLNFR
10504	24405	A	10585	273	374	GGPTEAHTRNPSLTGGRGGAIT/R/QOE FKTSLAKM
10505	24406	A	10586	150	344	KLKCKIITIKLGKISFAVIVVVEIGPHF CYLGWVQW\PIRTHPGSSDPPASASQSA GITSMSHHT
10506	24407	A	10587	199	3	SFSYIRVHLGHIKTRHKASCEVYANCK AKGIITGIKKK/RFWPGTVAHACNPNTL GGGRWITRLV
10507	24408	A	10588	216	1	PRGAPTCMRCQSAL/LGGVLQLGYTG/V RDPLEAVCPISLKRKAGRTTALFRAV RQGRLSLQKFLLPFLV
10508	24409	A	10589	190	3	ISAPQWAAFEKRFIFTYRAPA/LKFMIF FSPFKGVPPFFFTFFFFEMESRSVARLE CSGVISAH
10509	24410	A	10590	369	40	KTERNSININKNDVHTKTPSKGRQHRP KADKSREMRKNQHKKAENSKQNPPSSPP RDHNSSPARKQNMENEFDELTEVG/FR KVGNSSELKEHILTPCKETKNRTRGW
10510	24411	A	10591	114	398	RFVCSTIKVLRDLSSNRNPNPGRFLSTN SSLC/EKDKRNKAYFTK/RPSPVNDIIS T
10511	24412	A	10592	132	1	ILYLWCVCVCVCVCVCVYLLILV/CKVL SCLGEPALSVGAFQMS
10512	24413	A	10593	3	287	IGFITLNVGLYLYLLCYIYVYFFQVNYI VFILVLAVFLKKNRLLRYNTALYNEEVT REKISHYFI/NSYIHTVGKINKND
10513	24414	A	10594	2	363	RAEVGVMAPLYLLLLLSGALGLTDTWAG SHSLRYFSTAVSRPGRGEPRYIAVEYVD DTHFLRFDSDTAIPRMEPRKPWVEQEGP QNWE\WTTGYAKANAQTDRAVALNLLRR YNQSEAGE
10514	24415	A	10595	156	3	NGLELSDDDGCIALFFYFETEFCS\VA QAGVQWCDLGSLLKPQPLGFKPTRP
10515	24416	A	10596	80	306	MDEELLFRDEQRKWFLEMESTGEVAVNI

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						V/EMPIKDLG/YRNLVDKAVPGCERVD FNFEISSTGWVWLTPAIPVL
10516	24417	A	10597	232	389	ILCWVFCCCCCCTETFLVIOAGVHWC DLDSLQ/SPPPGSSDSPASAS
10517	24418	A	10598	463	154	MGQKPRFFLFFHPFYIPFLKQGFSL PRVQGRAKKVPGLASWGQKILLPQPPR /RVQENCLNPGGGGFSEPKIPSPFAN GEKGSLLKLNKKKTKHC
10518	24419	A	10599	208	38	LGPPQGFFTAPPPFFETESRSLAQV GVQWDLGSLQLPPPG\SSDSPGLSKF LL
10519	24420	A	10600	200	3	CQPELSCMRC\RQSLGGLSPSGMEVR DFVEEAVCPLAELKRCAGRALLVRICCS LQSQAGTFK
10520	24421	A	10601	73	427	RVVCSSTIKVLRDLSSDRSNPGRFLSTSN SSLY/EKDKRNKAYFTK/RPSPGNDIIS T
10521	24422	A	10602	193	401	GEVSLSPRLECNGVISAHCNFR/LPGF KRFSFFFL
10522	24423	A	10603	181	395	RFVCSSTIKVLRDLSSDRSNPGRFLSTSN SSLY/EKDKRNKAYFTK/RPSPVNDIIS T
10523	24424	A	10604	384	10	PRRPGGECVHCLGDSLVTDRRYSGLRSS DQTLGSDPMEAVPWSNSLSCSHYRLKPA SGITWGCKQAGFFSFFLFKMEHSV\T RLECSGAI SVPCNLCLPGPSNSPAPGGS LGPRSSRPWTT
10524	24425	A	10605	215	379	RFVCSSTIKVLRDLSSDRSNPGRFLSTSN SSLC/EKDKRNKADFTK/RPSPVNDII
10525	24426	A	10606	1	163	QTHREPAMVLSPADKTNVKAD\WGNVDA HAGEYGAEALERMFLSPPTTKTYFPR
10526	24427	A	10608	283	2	IQKHGLIIRCPQETPFKNNDVGMQKVKG RGEKSI MQIL/YFFFLNS/HLSRPLR/ CSGAI SAYCNLRSLSHSSDSPA/VDGTIG ACHHTQLIFLFLVE
10527	24428	A	10609	144	327	CSWSWFCGCVRVSTLIKKKNFFEMBF S\VAQAGVQGRDFGILKPPPPG\SSDSP ASASRV
10528	24429	A	10610	137	1	HKCPSTDEWDERV/WCMYTKEYCSALT EEIMSFSGKTWMELENIMI
10529	24430	A	10611	201	334	SFFWRFCRLRGVPSRVKQCA\LLGGASQ LGYSGVDRDPLEEAVCPF
10530	24431	A	10612	146	2	KTPLKKGLKRVPPFFFFETESCSVTOAG VQWHNIGSLQVPPP\GSRHSP
10531	24432	A	10613	205	259	TTMPGLSFCTRTKSNKNSFLTLDGSAR VDLFLYLLLFRTIFQNF/CGRDKVLLCC PGWSQTPELKQLICLDLPKYWDHRYEPL CLAYPFALGQNLTKI
10532	24433	A	10614	153	2	GVLMVSDGVLSMLANLFFSFLFF/LFET QSHSI\SRMECSGVISAHCNLCPL
10533	24434	A	10615	213	8	KPPFFPPFFLFFFLRWGSHCVVSGY/C KGTII VHCGLLELLGSSCSPAFQVSGIT GLCYCASIFIFRE
10534	24435	A	10616	146	1	ILTIRDYWKITLFFFFFPKPHS/VLPR LECSGAI SAHCNLCPLPASSDS
10535	24436	A	10617	208	2	NNFWFSSSGKYGYFSSETESRSVTWGH DLYSLQPPPP\GSSDSPASASQVAGITG SCHHAQLILVFIVE

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10536	24437	A	10618	120	2	SFFFFFETEFERSVAQAGVQWHDLSLQPPPG\SSDSPSL
10537	24438	A	10619	162	1	SFHWKLRRLRGAPGCMRCHSA\LLGGVSQ LGYSGFVHPLEEA VCPFSDLTLCAG
10538	24439	A	10620	193	419	TFFFFPETESRSVAQAGVQWRDLGSLH/S QPGQQSETP
10539	24440	A	10621	313	460	KPGLWRGTRSQKQVLFEPESHVA\KL ECGGTISAHCNFC LPRSSDFSA
10540	24441	A	10622	243	505	PTGCPKQEQVQAMLRPVVFFVPETQFN S/VPRVECSGTISAHCNLRFPGRDSPA LASRVAGICRR/CATTAQLIFVFLVETG FCHLVG
10541	24442	A	10623	67	430	LARRTWKNQHSSTHGCDLFFFFFFF LIKKGVFFFPPEGGHGRFFFINIKFLN YKRFFFC LFEDVLMISVGPPLAFFFFF WRGGFSYLLLRV/LTFLALGAPLFAFM FFLFLGSEL
10542	24443	A	10624	3	207	PGGQLGSECSGVRMDVDL\TLKSLIIG ESGVGKSSLLLRFTHTDFDELAATIDP SSVNPARNAAATP
10543	24444	A	10626	151	380	KMLFGQVQWLTPIIPALWEAEAGGSLE\ LRSSRPALKRSETSSPPLPCQKKKKK KFPFRAGQMLEVPPGRVGAG
10544	24445	A	10627	210	3	NFCQVKGFWKQKSSQIKGFGKNKKKGG SFFFFFETESHVST\RLCSTIIVHC SLDFPGSSDPPTSA
10545	24446	A	10628	237	2	LCFLSGASCSPYIDVYTEVNGVNPFTII LTNKTNTFGPLFLIIFPGETESLSIA\ RLDCSGAISTHCKLCLPGSRHSP
10546	24447	A	10629	1	352	RGPLSIQDYISKALFFLLFGFLLLLF FEVRSCSLTQAGVQWCNHSISSLQSPT PG\RSPSDPFASAS
10547	24448	A	10630	48	200	AIKPKNFLFFSETKSSSVTQAGVQWRDL SSPQPPPP\SSDSPAPAN
10548	24449	A	10631	209	376	SFLWKFC LKGVPGCVRQSA\LLWGASR LGYLGVDRDPLYEA VCPFSDLKLCAGRTT
10549	24450	A	10632	141	1	AGFFFFFLFFLETESRFA\RL\QCSG AITAHCNLC LWGSSNYHAS
10550	24451	A	10633	18	522	PLYSLTRHTPREA/KDNLKSTQLLSVI DAISEGPIEGPVDGLKSVLLNSTPVLDT EGNTNISGVTVVFRAGEQEQTPPEGFES SGSETVLGTEVKYDTPITRTITSANIDR LRFTFGVQALVETTSKGRNPSEVRLLV QIQRNCGWVTEKDITIKGKTTSQYLASV V
10551	24452	A	10634	127	2	NLSPLFFFFETGSRSVTQAGVQWSDLGS LQTPPP\GSRHSPTK
10552	24453	A	10635	336	452	RIFFFLFETEALSVAPAVAQWFDLGLSQ SPPP\GSSESPA
10553	24454	A	10636	259	3	GTRIFFFNSSPLSFPPVOKKSVSPFFF SF/LFFFFETESRSVT\RLCSCGAISPH CKLHLPGRHSLASATRNVLRLWRIHA SCA
10554	24455	A	10637	96	413	GDNTSQHSAILINYFIFFFTFLFF/ETG SHSVAQAVRLEYSSVITAHCNFRLRGSS NPPKKKKKGAVLKDPWGGQSLEGLATY YFFPYRGANKNLGDFWEGPLFV
10555	24456	A	10638	180	473	CYMGKAWLVLSNLLTLKKKKKKKKKK

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						KKKKKKKKKK/EMPVKQKNRGRALYKK KKGGRPFPIFWPFFFFFLGGGKKHPGG FFRKKFFFGGGKKKK
10556	24457	A	10639	312	480	ETVDSTSGEDDVNIAEMATKDSSEYINL V\GKVAEAFERTDSNF\RGKMSKSI
10557	24458	A	10640	2	516	MKPLENLSQTASLARGATLLRPVLRRLC GLPGLQRPAAEMPLRARS DGAGPLYSHH LPTSPLQKALLAAGSAAALYNPYRH/E ERPRISTSLDLGKLQSLPEGSLGREYL RFLDVNRVSPDTRAPTRFVDDDEELAVI QRYREVHMDLHTLLGMPTNIIIGETIVKW FEAVQ
10558	24459	A	10641	56	455	PLCSYIQFIYHSKFNSNQISLVHTIPLS KLEGYFSQLYSIYSYLQHFHLLSIFI TVFCIVYWVFVHLISVPMYICVCLCTN VCVCV/CCLW
10559	24460	A	10642	272	33	GRWFLFLGPAKYFLTGGRRPSPDFGGLK INPPFFFFFDTESHSVAQAGVHWNL GYLQ/SPPPG\SSDSPAPAEFHTV
10560	24461	A	10643	285	1	MGNFLKRFFKNEKKFFPILRAHPNFF PGKSPFKTPRRALPLGVPPKHPFFFFF FSETESRSVARLECSGMISAHCNL\NLH LPGSGYSPAL
10561	24462	A	10644	100	466	FLLKFRLEVPSSRVRCQSA\LLGPTSQ GYSVGRDLEEA VCPFSDLKLCARRINT LFKTVRQGHLSLQRFLLPFVQLCPVPRG GVYRGRQASLSCSGVHPVRASPPLCLPK VPPPS
10562	24463	A	10645	260	460	LKPHAERETIDGRLPYYSFFFFFETESC FVAQAGVQWHDYSLPPPP\PGSEGSRA
10563	24464	A	10646	360	504	QIGHICAYVEKTELRLIFFLFFFRQS CSVT\RLCSGTILAHCNLC
10564	24465	A	10647	241	45	WEVEVPRVAPCHILKRDYFYLFLFLF FEMESYSFT\ELC SSAISTHCNLCPPG SRDSPGIPPH
10565	24466	A	10648	76	462	FLWEYQEKAHILWSLFSKLILSRSRFTV KEKVRQKPGILFIYLFIFEMBSCSVAQA GVQWRDLGSLSPQKKKDS/DQSKAITTV EGINSKRGGWTGPHF/HCSLKMIFLI
10566	24467	A	10649	3	359	QTQREPTMELTPADKTNVKAAGKVGAAH AGEYGAEALERMFLSPPTTKTYFPHFDL SHGSAQVKGHGKKVADSLTNAEAHEDYM LNALTALNDLHAHKLWVDQVNFKL\LSH CLLVTLA
10567	24468	A	10650	266	3	TPEKKKKIGGLGAPFGYPKKIWPNNFF FFKKT KFFFFQRVGWAPPPK SFFFFF EVESCSVAQAGVQWRDLDSLQSPPP\GS RGSP
10568	24469	A	10651	278	461	KKIICGFFFD TGSCFVAQAGQQRDLRS LQSPPPG\SSDSLTSASRVVGM SRHMRA VF
10569	24470	A	10652	161	456	VFFPPGENIAFVENKTTLSYHFMFTRMT AAKMMENYKGCWGWTIGSFMP CWLESK RVQSLW\KVVQFFKWLNVKLLYGLAIP TGICPKKLKXYVOGY
10570	24471	A	10653	91	486	PCFNHGT TWYMYFFSLSLILEFVFSLK PVILAYKTFSPFITIRVLLQRRHRQKFV LDGFNGVDQNNILGSICVSLIKIFLTE

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						SCFVAEAGMQWCNIGSLQAPRP\GSCHSPGISPPVLG
10571	24472	A	10654	267	470	NLHMRCEKEQNFNKLSPKDLFGLGWLWF FIPCFWRRILTLSPRLEC/RG/MIFAHCLNCLPGSGHSPASA
10572	24473	A	10655	775	1401	TFPSQIRYGLRKRPNSTLSPRLECSGA ISAHMQRPFGFTPFSCLSLPSSWHYRR PPPRPAICVCVCVCVCVCLVETGFHRVN QDGLDLLTS/S/IPPASA/FPKCDYRRE
10573	24474	A	10656	287	454	LPLIYFLYFYETECHPLAQAGVQWRDL SLQSPPP\GSNDSSASASPTVPTSAM
10574	24475	A	10657	212	64	LFLSKFYFFEMESCSVAQAALQWCDLGS VQPLP\PGSEDSPASAWGYLD
10575	24476	A	10658	368	473	GFIDHTRRRERPECP/LTDEWIKKMWIHT TTEYYSAL
10576	24477	A	10659	358	1	ILAVFCFCGSAPGFEGGKLTFFFNRGRE TFLALVKTPPPGKARGPVFISKNNKIPE FKQPPNPNPNSEFFFFFETESHTIARAG VQWHNLCSLQSPPPG\SSDSPGRWSLQRT EIAPL
10577	24478	A	10660	2	235	KRDLIRHYPRKEDIYMANKYILK\CSLT MHTETLIRTTMKYHLILIKVTIFKKT DNMTAVGVHICNPNTLTGHGRGIA
10578	24479	A	10661	9	538	CVTVRIPSRRPTPLSSDRSNPGRFLSTS NSSLY/EKDKRNKAYFTK/RPSPVNDI IST
10579	24480	A	10662	374	38	SPLWKLHLRGAPGCIRCQSA\LLGGVSQ LGYSQVDRDPLEEAVCFPSDLKPRAGRT TLFKAVRQGRSLQKFLLPFVQLCPAAR GGVYRGRQASLSCSGLHPVRASRPLCSR R
10580	24481	A	10663	268	47	ALIPLSSLTISAFHLLLETVSTSSPKM ECSGAITSHCSFNLDPSSPSPTSASR/V IGTIGARHQALMFIFYC
10581	24482	A	10664	64	451	FSSERKSHMSLTINQKLEMIRLSEGLS KAKVGQKLVRHQTVSQVDAKEKLLKL IKSATPVNIGMIKQHNLIADIEKFGMIW TDCQTSHTVLCORLIQSK/ALTLENSM KAERGKEAADEKLEVRRG
10582	24483	A	10665	355	474	ILFYFIFFFETESCSVAQAGVQWRDLGSL QAPPPG\SRDSP
10583	24484	A	10666	317	481	GHTCPWQTFFFFLFRDRVLLHHPGWSAV TQSWLTAALT\FGPKRSSCLNLLNDWD
10584	24485	A	10667	57	329	VKNTQWGDSEFNKRV\FKNWASTYRRI KLD\LTSAKINSKWKIDLNVRLEIVKV LQVEYPSFKILNGSVLDFVFFYSGIFA LHLMGEHP
10585	24486	A	10668	86	468	ENYKIPLMGGKNFLLEFSPIPPYFFFSR LGLTLLPRLKCSGDHCSLQPRPPGLKRS SCL\GFPKCWDYRNEP/CVPR
10586	24487	A	10669	254	25	GSHICKVPAIYSNTCTSSHEGDDGGVVG GCSSGSTTHPSPVADSFFVVVETVSL/S VTQAGVRWCDLSSLOPPPPGI
10587	24488	A	10670	206	3	YGRPRKLCNIGLKSGLDPTHWGQHRVI SFFIFMETDSRSVAQAGVQWHNLSLHP PPPG\SSDSPAS
10588	24489	A	10671	20	355	GFTSQSELLYSIDPITRPTDQVTIGISA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QSYCRVHVHNRVYDLDVESGHPNGAPAIKGSVCSTIKVPGDVSSGRSNPGRFVSTSNSSLY/EKDKKNKACFTK/RPSPVNDIIST
10589	24490	A	10673	112	359	NKAQQCVHENHFKLKDANTLNLIKVWRNICHSPPNQKKYGLAILNLDKSGFRSRKDTGDDE/HFIKIKKSVIQEDFSIINIYA
10590	24491	A	10674	317	2	TGPGFFPQIWKVFPFPFLKIFFTQKFLVSWFGFKTIKVGPFVFPFGKQPFRFFSPFLGVQAEKFFFFFFFPCERGSHSVAVRLECSGAISAHCNLCPPGFK
10591	24492	A	10675	240	495	DHRPEKTKSSTCQAGEVPLLGLFVPFRSSTDWVRPAFI/MEG/HICPTQSTNSNINPVWKHPHRHTQDNVWPNASPHGPFVKLMHKLI
10592	24493	A	10676	271	484	NEAGQCTRIKSFSSFFETESCSVTQTGVQWHDHGSMQPSLGP/SDPPTSANSSAKQEVVRSLSHNALCNDQASPLPGSGHWKSKQKLSKAAPCAGSSKHKHL/HKECWKHTHTHTHTHTHTHTHTHTKDRFA
10593	24494	A	10677	364	121	FFFFFFIVFEESHAIAQAGVQWCHLSSPHLR/SPPPGPN/DSPASASSAGITTLS SVRL
10594	24495	A	10678	354	539	RWSLCHERLE/CSGTISAHCK/L/RAPGFTFPFSCLSLPSWDYSGARHARLIFFVFLVETGFHHVSDQGLDLLT/SG/TPPALA/FPKGWDYRRE
10595	24496	A	10679	123	853	ASLGVSAPLCIHVSPCPPNGDLGKTWWVGGGFFFFEMEFHS/VLPRLECNGTISAQCSLCLLSSSNSPASARIPP
10596	24497	A	10680	251	30	NFPAPGKLGPPRDSLKTAPFFFFFETGSRVA/EAAPV/W/CDLDSLQPPTLPDS SDSPNSASGVAGITG
10597	24498	A	10681	203	1	DSLTLSPRLECNGSISAHYNLC/RLGSSNSPASAS
10598	24499	A	10682	237	397	LYMCWFRPGFLAHNSHDHGYSLTLSCWGA SGLKKQP/CRLSEKKKKKKKKKKKKKKKKKKKKKKKKKDS
10599	24500	A	10683	8	388	IYWEDIVQGVADRLTSRKHNSKFLGEC LMFGQGFLFFEMDSHSAARAGVQWRS LGSLRPLPPG/SQVILLPSSDSPALASRVD ETAGV
10600	24501	A	10684	201	463	PEKNRKTQKGAPPPFFFFFETGSPSVAQA GLQWRSHSSIQNEPP/GSSDP
10601	24502	A	10685	151	1	CVFVEDIISNFFFFMETESRSVAQAGV QVREHGS/ASRVAETGVVHHAQLFR
10602	24503	A	10686	165	3	NTEIGVWWLTTVIPALWEAEAG/EITR SG
10603	24504	A	10687	292	384	RPPCWIRTSRWCWRYRFDGSTIKVLRD LSSDRSNPGRVLSTSNSSLY/EKDKRNK AYFTK/RPSPVNDIIST
10604	24505	A	10688	161	365	QPSSVWSFRSVICAPADFSGMGLSPELQ QCIVGNFASRYTMTKSSAVLFIILIFSLI FKLEEL/REAPASLVSLFPQMLRIKWE SEQWLVLCDRG
10605	24506	A	10689	286	3	SDTPAWWPRKHVFPFGFFFFFETESRFVTVRLECSSTISAHCNLCPLGSSDSPASG S
10606	24507	A	10690	169	2	

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10607	24508	A	10691	240	406	DGIRRLSFFFFFFFETKGFVA\RLGR GTIWNVNLHLPGRSDSPASASQVAGIT
10608	24509	A	10692	343	3	QVPLNLSLHLKGLMFPFGCINGSLSQFL QFFAQISPYQTGFPSFYKTSIYHNSLHQ YLSLFLPYFIFLFFSFFFLKQSHSVS \RLBCSGMVSAHCNLRLTATSTTQVQVI LV
10609	24510	A	10693	196	3	YDAGHTKKTTLHFPTVYPFVLFWCWWECKM VQPRWKIVRR/FLKKLNTKLPYDPAIPF LSVHQKELRT
10610	24511	A	10694	245	391	KTDYQPGAVAHFGRPRREDHPRLGVDQK PDQLEKPVSTKNTKLWV/SWWL
10611	24512	A	10695	252	389	KTGGKVLFFFFETESRSVAQVGQWRAL RSLQPP\QPGTSDCPASAS
10612	24513	A	10696	385	1	PPNKAKMISSKDNKNLHWGKDTLLNKWC WESWIVTCITMKLDSHLSPTYTKINPKWI KD/LKTIKILGENIKKTVDIGLHK\NM SKTSKAMTKILDLIKLKSFCAKEIISR VNRKSTEWKKVFASYLSN
10613	24514	A	10697	296	430	KHIQARRGGS/CGN/RQHSGRPRRADHL RSGVREQPEQPGEKPHL
10614	24515	A	10698	280	468	DYLCL/SLSIYLSIYLSIYLSIYHQFIY HLFYHLSNLSISSIFFTKWLS
10615	24516	A	10699	15	393	RSVGVLPVRCQCA\LLGGDSQLG\SGG SGVRDPLEEAVCRFPYLOLCTGRRTALF KAVRQGHLSLQRLLSF/VWLCAPAPIGG AYRGRQASWSCGGLHPVRA/SMLLCLPK EAWAMAGAPPPASLPPLS
10616	24517	A	10700	176	1	DWTTNFTTFLYNFKPSSMLPYLSHLFKT LR/MWPGAVAHARNPSTLGGRGWIMRS GDE
10617	24518	A	10701	494	80	FNKKDIHSDTPSEGHQLRPNVETLKKM GRNQCKKGENPKNQASSPKDHNSSTPR EQNWMKNESDELIEVGFRRWVITNSSEL YKG\DVLTQCKEAKNLENRLGKVLTRIT SLEKNHGGLMEVKNIQAQLCEASAGWR
10618	24519	A	10702	264	410	KKGPLFTPPGGGGG/PQKPPGFLNPGG QRDSSFFPPPGGNTGETPPGG
10619	24520	A	10703	125	3	NRGNKGQV/QWLMFVLPALWEAEAGRSF EIRSRDQPRQHGETL
10620	24521	A	10704	184	2	RLRVLAPCRHLPRAPRTWPKRPFFFSFF LFFPQTQSHSVA\RLBCSGAISAHNSLC FPPTRP
10621	24522	A	10705	187	406	LFLWKFCRLRGVPGHVRCQSAL\LGASQ LGSSGVRDPLEEAVCLFSDLQLRAGRIT TLFAVRQGHRLRQLILL
10622	24523	A	10706	82	410	ILRGKFGKHYFNRIWREALRQSLSLFN FIIFSNFLASLHKPEMETELKGSFIELR KALFQLNARDASLLSTVSDFSFCRKFS R/CSKCGQ
10623	24524	A	10707	390	2	SKDCRTAKIAACSFLWKLSRGAPARCK PELSCMRCLSA\LLGGVSQSGGTGIRD PLEAVFPPLAELERCVGRSAALFRASRQE HSLLLKMHPQLPLPSGALSQADGSFIYK PLTGASAFLEMPQOERR
10624	24525	A	10708	229	392	YSWWROMHSAHAGVQWCD/LVSLQPPQ PG/SSDPPASASLAARTTGAGHINQLIF
10625	24526	A	10709	193	2	RYLCYQDHVILLLLLLLLFLRWSLTLSL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						RLECSGTIMAHCSLDS\SSNPPISASQA AGTTGACYH
10626	24527	A	10710	180	11	LLFFPETRS/HVSQTVVQCGMISGHCNL RLSGSSDPPPLASRVAGTTGKHQNIWLS R
10627	24528	A	10711	234	408	MKLIMLKVILFPQIHLQIQPNFYQNIFF FETELCSVAQSGVQWHNLSLQHPPP\G SSD
10628	24529	A	10712	312	470	TGPHCVT\RLECSGAIATAHCSLDFAGLS TSPTSVSQVSGTTGTWMKLETIILS
10629	24530	A	10713	64	392	PKMVIRISSETSLYASLPQMKGQRQK/ CEPQPKKKKKKKKKKKKKKKKKKKR G
10630	24531	A	10714	169	427	NNQKTNNKMVGVSFYLSIIILNVNELNA PIQRHRAEWIKKKKKKK/DPGICGLQ QTLFFYEDP/HDPLRLKIGW/RKYTPS RGTQIK
10631	24532	A	10715	176	410	ARSSWGLHTAVPVAFSLRFLLEIFLDR DTRCSPPAAFFETGSCCVA\RLEGRGA ITAQCSLNLGSSSNPPTSASRVA
10632	24533	A	10716	234	389	NSGNMDRYKDVQNIIONPICWPGTVAHA CNPSTLGGRGQIL/RQGFETSLA
10633	24534	A	10717	190	2	GPFPHPGGFLRGFPVNTIPPPTFFFF FFLRRLSVAQAGVQWCDLSSLQPLPPG P\SNSPCQ
10634	24535	A	10718	201	1	WPLFLPKMFFFFKRFPHMGSPWPVGAQA KKKKIFFFLTGSHSVT\RIBCSGTISAH CSLNLPGPSH
10635	24536	A	10719	195	419	EYHTSLVTCGNPCVYRSNNKLNQTSRRK VITKIRAELNEIETEK/LQSGETKIWF FEKINKTGLELLGSSDPPVW
10636	24537	A	10720	218	407	GKKNLAFKKKKRKEKKKKKSPSQNMNS AKIEARTNIKLVVKGHWKNCIIDA\LQ KAFGDNA
10637	24538	A	10721	231	409	GTQLHLGGFFFSBKELSPCFWF/MFALF EMEACSVT\RMECSGTVLAHCNLRPGT SNSSA
10638	24539	A	10722	40	401	PLCPSESSGNILMASSDPSTPAVPPNPT THPPCLSKSHLPLRPKQGLPSGNLLQL PLTLIPLLGAPVACWQLPQQCTLSTFF FETKSHPVAGVQWCCLSLQPLSPG\ SRDSFDSAC
10639	24540	A	10723	210	14	HVMGLLLLFLNKLTVNNFGWLAGFWCLG FFWFFSFFETRSGSVT\RLECSGMISAH YKLCIPGSSH
10640	24541	A	10724	347	462	TFFFFFETKSRCDIAGVQWCDLCSLP PSS\PDSSDCP
10641	24542	A	10725	169	386	DKKQAKTIKNGKNSFSNKWCWNNCIATG KRMKLDP\YLTYPYK/INSKWIDLSI
10642	24543	A	10726	257	54	PLFFFFKROGLTSLPRLECNGTVAHYN LKLLGSRDLPTSASP\SAGITGISNPAR LFTYLNPTLQOT
10643	24544	A	10727	2	401	NNYDRAETQIYQYMCNLNPTFYCLQETHL TCNDIYRLVKGRREIMQIENKRVGVAI LVSDKTDKPTTVKKLHYTIKGSIQPE DLIILCTYSPNIRASRFIKRIPDLRKEI A/HTVKVGDFSISLNLRSRQNT
10644	24545	A	10728	154	1	PMCSLLGLSKGGIIFFFFEABFCVAQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AGVQWRDLGSLQPPPPG\SSDS
10645	24546	A	10729	34	151	PRPPVPSLLDRGRLQLWRQGLRHRHS NGFIFGGKQIMKLLKNYVRRPVG/VAVA IMFDPDPYPRSWIEDDFNYGGSVASAT VHIRMGSLVENNKS
10646	24547	A	10730	2	408	VFLTLVTRTLICRSVGVWWRSTPDLVCLG ISSGGCRTANIGLYQMLLPDHSSGSFCL RGVPGHVRQCSA\LLGGPSQLGYSRVRD PLEEAVCPFSDLQLHAGRTTTLFKAVRQ VHLILQRFLLRFWLCPAPRS/GVYR
10647	24548	A	10731	274	89	ENIPIVFNPPVCSPLLWQPQ/CHYPKL CKLCLKLHKHRVY\FLFFPFETEPHSV ARLECSG
10648	24549	A	10732	251	1	TFQMMQKCPSHRKIFHNLLDKASYKIVY KEDPFPSSSLSSSVSLKNNFFFLTESC SVTQAGVLWCHLSSLQPPPPG\SRDSP
10649	24550	A	10733	375	1	APFFPLWVRGSPFSPPLVFFHPKLPPL AEILGFFKERKWSIRKPCLFVKVKLV VWPGLELQIFKFIGEPFSPFSLVGRKP NFFLGPVFFFPEKESRVA\RMECKGT ISAHCNHLHLP
10650	24551	A	10734	82	398	SFLWKLRLRGVPSHVRQCSA\LLGGASQ LGYLGVDRPLEEAVCPFSDLQLPAGRTT TLFKAVRQGHNLQRFLLPFVQLCPASR GGVYRGRQASLSGGLHPVRAS
10651	24552	A	10735	2	341	TFCAISWLESGVEDGPRSRISYRISTFF FFFKGAPEPKVGRGRPKGLAPTSPLPGA HGTTLGSGWTPSIGGWQPPPPRENPK GEHPPAPVAGDTFQ\PKKPPPIKLVFF K
10652	24553	A	10736	171	1	RVFYLLAFALFVDTGSPFVSQAGVQWCD HSSIQSQTSG\SNPPASAYRVAGTTGV
10653	24554	A	10737	190	1	EKTTVRKIPKMEEMADSGSNMLRIIF LFLFFETKSCSVT\RLCN/GSISAHCN LHLPGSSNS
10654	24555	A	10738	252	413	GLLGLQNFYSYKVLTKAHLKKCSWLDV AHAYNPITLGGRGW/IQEFQTSITNV
10655	24556	A	10739	101	249	AGSTSRCI/QELSDLLEHLEQENCLNPG GRGCSEPOSCHCTPAWVTETOKK
10656	24557	A	10740	185	403	LGLPVHTMRSNYHYHLCHHHHHLQH HHHCHCHYHS/HHNSQHPPPPPPPP HHHHHHHHLP
10657	24558	A	10741	119	425	IKFHLHSMERTHLFLWNCWAHKQRNCFK ADFVITDDIKQLCPPQSWWTRAGKLPLG AGRGSHMLSHHFWRPRHADILYLGLD QPGQGETPSL/LKNTKSSW
10658	24559	A	10742	112	2	GETFFFETGSSVA\RLCSGAISAHCN LHLPGSSKSP
10659	24560	A	10743	188	3	PPPLFFFFFFFTGSAT\RECTA HCNCLPGSSHHPTSAVQVARTTVCNH AWLIFV
10660	24561	A	10744	176	3	SLYSKNKNPSHLLFLPIPIKFFFFFFET EFRSVAQAGVQWHDLSLQPPPPG\SSD SP
10661	24562	A	10745	250	1	GPRIFFLKEFYPRFVFGKNPAPGGFFS GGKKPGPPFPNPRPIKFFFFFFETFRS VAQAGVQWHDLSLQPPPPG\SSDSP
10662	24563	A	10746	155	3	PPHPPFPNPLPIKFFFFFFETFRSVAQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AGVQWHDLSLQPPPPG\SSDSP
10663	24564	A	10747	157	1	TFRPFFFNPPPLKFFFFFPETEFRSVAQ AGVQWHDLSLQPPPPG\SSDSP
10664	24565	A	10748	157	1	TFRPFFFNPHPIKFFFFFPETEFRSVAQ AGAQWHDLSLQPPPPG\SSDSP
10665	24566	A	10749	153	2	PPPLSVVTPAPLRFFFFFPETEFRSVAQ AGVQWHDLSLQPPPPG\SSDSP
10666	24567	A	10750	157	1	PPPPFLFFPRPLKFFFFFPETEFRSVAQ AGVQWHDLSLQPPPPG\SSDSP
10667	24568	A	10751	155	3	NTFPFFFTPLTPKFFFFFPETEFRSVAQ AGVQWHDLSLQPPPPG\SSDSP
10668	24569	A	10752	86	406	SFLWKHLHRRAPGCMRCRLA\LLGGVSQ LDYSGVRDPLEEAVCPFSGPKLHAGRTT TLFKAVRQGHLSLQKFLLPFVQLCPAPS TGVQEGRQASLSFGGLHPVQSSR
10669	24570	A	10753	364	469	GQFLHSLD/SHWKKSEDFCLWFPHSEN VSAIHQDH
10670	24571	A	10754	250	61	GEKKKKKPRVFFFFFPETEGSVT\RL ECSGVLSAHCNRLPNPNDSPASASRVA ASAKLG
10671	24572	A	10755	66	446	SFLWKFCCLKGVPGCVRQSA\LLGGASQ LGYSGVRYPLEETVCPFSDLKLRAGRTT TLFKAVRRGHLSLQRLPPSVCLCPAPR GEAYRGRQASLSCGGLHPVRASRPLCLP TQALAMVGAPPPGSL
10672	24573	A	10756	252	482	RLPRQPVKRWVAGVRGCCVWGVVSKSLQ RSTTLDWQGPQRRGGPILFFFFETLCH /TRLENGEISAHCDCCLPGSN
10673	24574	A	10757	205	488	PLESLRSLPLGSLSWRTASSVPVICIYY IYIYIYIYTHY/HIHTHTHTHTHT QYIFVCVFLKDRVLLCHPRQSAGARSW PTRTSASQRQEM
10674	24575	A	10758	272	471	YSYVLFIFLIGIESCSV/AFSAGVQWHN HSSLQLQTPGLKQSSHLSP/ASAPVA GTTGMRYHARLIF
10675	24576	A	10759	17	342	GTLSSGAQVLIGRIESIVVGLKPPWALG GCPSPRAVHWLLASSDWRPSLQDGAEGW KKGANGNHKR/GIAVISDQIDFKTKTI KGD\KKSHYVMIXGPIQQBAITINI
10676	24577	A	10760	42	498	EFREGREREKERKTEERMEDRERKA EREREKERQERERERERQRERERERK ERERKERE/RHEPGSL
10677	24578	A	10761	1	305	ASWDDPAHNNNFHIPGGVVAHFFFCRL DCPPWAPRPPAPR/VLL/TPAAAAAAA AASRPEKKRAEENVGAIIPRKRPPRWE RRGPRKGSAPPGRGARRAR
10678	24579	A	10762	364	2	FPQKQNGQYLPLFPKPTGLCGKGKTRLG FFLNYPGKKKKRGRELGFPPFCQIWGT SIYRSGMYFFFFFWRVSLALLPMLC C\RMIRVHCSLDLVGSPNPSTASQIA RTTGTCMCHH
10679	24580	A	10763	152	484	RFVCSTIKVLRDLSSDRSNPGRFLSTSN SSLY/EKDKRNKAYFTK/RSPVNDIIS T
10680	24581	A	10764	208	420	SFLWRFPPLRGVPGHVRQSA\LLGGASQ LGYSGVDRDPLEDAVCLLSDKLKAGRTT ALFKAVRQGHLSLQR
10681	24582	A	10765	319	85	GKLLNNNRCFGSKFGIMFFFGETESPY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						ITQSGVRWHDGSLQPP\PPGSRDSPAS AS\RGITGARKHTQPIFLLVSNS
10682	24583	A	10766	122	3	KFFFFFFETEFERSVAQAGVQWHDLSLQPP PPPG\SSDSPSL
10683	24584	A	10767	240	86	RAPPPFFEMESCSTIAQAGVQWLSLGLL QAPPP\GSCHSPASASCCELMFSKI
10684	24585	A	10768	244	85	RAPPPFFEMESCSTIAQAGVQWLSLGLL QAPPP\GSCHSPASASCCELMFPKI
10685	24586	A	10769	35	296	EVKSPSARQPPRLGSEHLRPAAPSGR EVGGQPPPGQPPCPGGEG/PPPPGSPDW EVRSPSARQPPRLGGEPNSSLRTHGDDD GGFV
10686	24587	A	10770	260	484	MDEELLLMNEQRTWFLEVESSPGEDAVS IQLATRDLEYDLNLVEKGAAG/LERKH YSFERSSTVDKILSHNTACY
10687	24588	A	10771	248	393	TOEGKKLINWPGTVAHACNPSTLGARGG RTTRGQLETK\LANIKKPC
10688	24589	A	10772	239	2	SFLWKFCRLRGVPGRVRCQA\LLGGASQ LG\SQSGVVRDPLEBAVCPSDDLQLRAG RTSALFKAVRQGHLSLQRLLSF
10689	24590	A	10773	158	455	LFFTLCPSSLQHIAMLELGLKGPSTQ PIFWFLQGTETP/HFLVTPVR/CCLPLL KLFCLLVFGMESPSVPHAGECSGVISAH CNLCLLGSTDSSASPSRV
10690	24591	A	10774	166	403	KKTFLGEPLFWGGAKKKKPGKKNPGFFP RG/IKPRVFFSRFFFGPPPKKGFPOKS FFLKSLPGFFLFGGCPPIPPPPPPPPFEM ESCSNTRLECSGVILAHCNLCPLGSSDS P
10691	24592	A	10775	208	1	RLCFFYFRKALLGKAQIKNIAFFPRKGS FFFFSETESRSVAQAGL/LDCSGAISAH CKLRFPGSRQSPAS
10692	24593	A	10776	192	29	IFRKEFPCLNFFLLPFETESRSIAQAGV QWRDLGSLKAPPPG\SRSPASRDTGV
10693	24594	A	10777	275	490	KPGFFLLQMAKVYMIFFPFEMEFCS\VA QAGVQWHDLSGMQHRPPG\SGDSPSCLP SI/AGIPG
10694	24595	A	10778	340	3	LKVPVGKPRSTLLGVKKVPFFGNKRKKF LALFFFPRPPGEGFSTAFIAQKPTPRV VPALGFPKNQSPSPFFFFFFETKSCSV TQAGVQWCGLRSPQMPPG\SSDSPASC L
10695	24596	A	10779	313	1	ANPFGGPGGDPFSSRVFPFGPKNETP FFKNKTATKKTGNKGWAPSPHRGGPK KGPALWDKKGNLWPPFFFFFETESHVS\T RLQCSNTILAHCNQCLPGS
10696	24597	A	10780	116	422	ILEDNIQTITETLLAIREVQIQTLRNH FTLTGMALII/RKTDNNKCWRECGKIETL ICCWRECKMLCNEVGTALEIVWQFLQSL NIELSYDLAMPGFIIFPRE
10697	24598	A	10781	120	418	TQTTGAPQLHLASRWLSRSGGLTSSPQE IPKLFWSESPLGSSKHLQLQVFVCLFV CSFVFEMESCSEVARLECSIVISAH\CTL HLWGSSHFHASARVA
10698	24599	A	10782	134	1	SSFFFLCQTESCFGVQWHDLSLQSPST RAQA\LSLPSSWDHRR
10699	24600	A	10783	2	435	CSHRGSSSSYSQLSGIRAGDLGGGKDI FRLLPTTLNIFAGKESYDVVCVTHRM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LC/SCLFIYMCLCMCVHV/HYIHEACVF MCLCL
10700	24601	A	10784	432	161	FSRAGFH/RVSQDGFDLLPS\CLPPLGL PKCWDYKREPPRPAWKLMCRQVHRKCTW LFIQIGSTLFKTNGLSAVAHAYNPNTW GGRGERIA
10701	24602	A	10785	270	442	NVRLRLGLALSPTLECRGTIMAHCRDLF PGLMQSSHLSHRVAGTTG/TCHHAWLI F KFL
10702	24603	A	10786	12	424	LIQLPRLECSGALICARCNFTY/SLGSGD PPTSASQ/VLKTTGVCHHAQL
10703	24604	A	10787	350	3	DSSSVQTNKGIPGQVLSDLSCAVKASV LVIIPLHNALSSWLVPALFLWKSQVQVK SQQAHSVSGLC/MHYRSHTHATHSPH RHRHTYTYARAHTHHTQMLSAVLPKQ PSGLS
10704	24605	A	10788	155	3	HAFALCIRNRLECNVILAHCNLC/RL LGSSDSPVSASQVNGIAGACHHAQL
10705	24606	A	10789	188	2	RRDLSSLQPPRGQ/MRGCIYTHHTHT HTHTHTVHWGWRHVPKGMKSANG ESGRAK
10706	24607	A	10790	19	405	IRPTISRVERGINSLVASEGQRLPWDGI ACSQGLVVVQQTWGPLGFPSSLGMPHR PTFRDLNSEPAPGVANVSGTLSTPLPGA SHGLLVFFPETESHFVAQAGVSWGDLRS LPPPPPG\SSNSPVSAS
10707	24608	A	10791	157	1	KPGPPFPYGPGLKIFPPFFETEFERSVA\ RLECSGTISAHCNHLPGSSDSP
10708	24609	A	10792	157	1	QPRPFPNRPKFPFFFFETEFERSVAQ AGVQWHDLSLQPPPG\SSDSP
10709	24610	A	10793	83	387	SFLWKLHPGAPACMRCLA\LLGGVSQ LGYTGFRLLEEAVCPFSELKHHAGRTT AVFSAVRQGLSLQKFLLPFVQLCPAPR GGVRG/RQALLSCHRLHPV
10710	24611	A	10794	204	419	KGVYGHSGSFSPAPLACFRDKTLFPVS LWKEFVHSPWCKCTLPQLWKTVMRYLK NFKME\IPYVPEIPLG
10711	24612	A	10795	207	2	RRGFTMLVGQNSLDPSTSRSAHLSLPC WDYRCKP/PAPS/LREGFSYLLBSLLHP TPAPGSHLWALIC
10712	24613	A	10796	2	237	FFFLRERILLALSPRLECS DANMHSCL NLPG/FSQSFCLSHP\SRWDHRMPPYP VKFFGIFVGDRLVLPKLSIYII
10713	24614	A	10797	342	40	DRVFFCSPRLECSGAIARCS/LRTPGL KQSSHLSLPKCNHRCKPPRPARCSLNE SHSAKKWPGQSTDSSACEEVQPTSPFPT VPYPTLLSPSAGHGRGR
10714	24615	A	10798	209	2	CSVLAVILNPECIYVVPWLELLAHDPIP RLVCPKSFFFETKFCVAQAGVQWHDLG SLQPPPPG\SSNSP
10715	24616	A	10799	142	2	IFFFFFEMESRSVARPGVQWSDLGSLPP PPP\GSSDSPASATPSPMQS
10716	24617	A	10800	276	2	ILPIIRNTCCCFLLKESRSCSVTQARV QWHII/GSLQPTPG\SSNPPASAFQA TGAHHHTSLIRNTLIIINWEKNTHKLSG CTSMHFRFL
10717	24618	A	10801	12	364	LHHYKTVSGIYKCLCVLNGPPTRFFPDF LPPLGLPYSLRHNNIEISPINNPIASK

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						YSRERMSCISLTNLQTLVMIKLNEESLL KANDHKLCLLR/SVYQVNAVAYEKFL
10718	24619	A	10802	235	3	HRPSEDLDFFPHWAVMRAPQYPSWDTRE GGPRSFLFLFLFFEMESYSVAQL/BGTI SAHCNLCPLPSSSDSPTSRLCSL
10719	24620	A	10803	349	1	NQTPFFFFFGGTETTSTTLCSS\YGLLI LLKYPEVA/ESASQRDPWEAAVWRWLE GPGSAQPPSAPAKGQELDPVVGQRPVPS PDDHVQWPYTNVALLLEIQRFISVVKRTL TLDTLY
10720	24621	A	10804	365	3	IDVCNVCVRKQYRGFCDQYRAWISFPVY PHKCGWHRVYNTPTPHCETEWLWVILHA QEH/TFSLTGRHTHTHTHTHTHTHTSKL APPASRALFGVAHVEAQKALASPSGGRY LAITMFVQPCI
10721	24622	A	10805	406	96	CPPEFSEESPRLLKFRVGGYLTQVSKC GLGVVRIKVFVFWSEPPKQVTSLFFFSKT GSHSVT\RLCGDTILAHCDLCAPGSGD PPASATRVTVTVGLEPPCPAR
10722	24623	A	10806	58	369	FFFFKGDRAQNNNS/WGERCLLNKGWYDI WISTCKMKSTPYLTTLHTKISSKGLKDL IIRAKRIHLLKKYIGINLHDLGLK\DFL NMTPKTLATKEKIDTLDPIKIK
10723	24624	A	10807	126	1	KEPFFFFFFETESCSVAQAGVQRCNLSS LQHQTG\SSDFP
10724	24625	A	10808	204	415	HLGFDLSLTTCISLSDGLKYKATVFLVFF FERESNC\AVWAEANGPISVNCNRLRPG SGSSPASPSRGVEIT
10725	24626	A	10809	168	2	KISKRPFFFFFFFETGSHVVA\KLECSGV ITAHCSLDLPGSSNPPTSASWVAGTTGT
10726	24627	A	10810	97	389	LAVSPSLSLSLSLSLSLSYLGLPYSLRR SNIETPINTPAEGSVCSSEKRGHMSLS FNEKIEVITLSAQDMSNTKIG/RKLDLL CH/TSQVVNAEEKFLK
10727	24628	A	10811	24	416	LEYIARRYLGVVWLFVFFFLNRQGEKSR GPFKFFPPRGFFSTRNGAPPGGPWGPLP WGGGPPVGFQKQKGGAP\PPKKNRFPK GGPLTQPNLPKTPINPKGPPTRGFFPS GPPPKKGAGPPPIFRVGGP
10728	24629	A	10812	60	435	KKRKNFPQKKISPYFYPLKWFKTPPLWV KNQTPPV/CCFFEAPFSLKPPRGLKKG /WGKNPPPLVPQKKKKDTAGVAILVS DKKDFNPTKIKKDKGHYIMVKGSMQQRG LGCPDANVPS
10729	24630	A	10813	618	1519	FWFGVNCKSVCPFLPVLCFVVCWCER GVLSQRSMGQAQSKPTSLGTMLKHFKKG FKGDYSVTMTPGKLRTLCEIDWPALVVG WPSEGSMDRSLVSKVWHKVTCKPGCPDQ FFYIDTNLQLV/YRPPPY
10730	24631	A	10814	179	15	KVKRLKTPFFFFFFETRTCSVAQARVQW HNHSSLQPPPGPKRS\PTSVSREAGT
10731	24632	A	10815	61	422	NCFPLKGPPLFFFFFFFLLQIIVFI YKFFAFLQMEFRSLPRLDKCNCAISAH CNLSLPSSWDYRNLPRIANFFLFLVET RQPASA/FLTCWDYR
10732	24633	A	10816	170	440	RQGLSLLPRLECSMTTAHCDLKLSSS NPPISAPHIALG/LTGLCHTQL
10733	24634	A	10817	322	443	FIFIFYFFETRSHAVAQAGVQWRDLALL

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						QPPPP\GSSDSPA
10734	24635	A	10818	134	3	KKAHLPPFFFLGTESSHVA\RLCSGT ISAHCNLCLEPGSSVSV
10735	24636	A	10819	76	245	FLLRKGTQGGPLSS/LFNIVRDVLAR AIRL\EKKIKDIQIGKEAELSLFADMI IF
10736	24637	A	10820	233	440	FFFGALKKWKSMTTHKKVERGKRITLNG GGIKAAKTASLKKHLQGWGKVMLMANKL LRGERAW/FPPIRG
10737	24638	A	10821	293	402	RNPFFLETEPHSVAQGEVQWCNLSLQ PPP\PGS
10738	24639	A	10822	168	1	PLRGLSDSSLGIMKMATDLSSLQPLPP G\SSDSPASASRVAGITDSHHAWVIF
10739	24640	A	10823	97	405	LCVNICFNFWLGVLEWLNHIIGVGLTFF FEMESCSVARLECSGAISAHCNLL/LPP SFGSSDSPASVT
10740	24641	A	10824	186	2	EPGTISLVALKLQKWPRR/SDHLRLAVR DQPGQHDETPSLLKNTKISWAQWQAPVI PALEPV
10741	24642	A	10825	199	1	KKTQIGGAPGGALFFFFFETGFPPFVA\ RLQCSGTNQAQCSLNLSSSNPSFPALQ VTGTPSACP
10742	24643	A	10826	252	381	GQQEFFFFPCSVPOAGGQWCNLSLQAPP PG\SHHSPASASRVAG
10743	24644	A	10827	77	427	IPQVHCPSPPVPMACIPRVSSFTSWVF HNLLPSECPGLPLVPASSHPRPCVCCR PCTWS\CPLWPRPPCSNSPV/TCVPCL PCLCISEIPSCVPWP/WTYSSLCPSMV PDSPCPLP
10744	24645	A	10829	20	518	SFAFSLLOHLTETSFAINCSSEATLLFL SVFL/RAQTLTAPCQTRGPRRGKDRGSG SSSPSGPKATKESSEVERKSFDSWGHFRF AA\QRLMDNQAERESEAGVGLQRDEDDA PLCBDVELQDGLSPEEKIFLREFPRLK EDLKGNIDKLALADDIDKTHKKFTKAV
10745	24646	A	10830	351	3	LHFSFPLQHRONIKVWLMRASMQRHSRT HGAFPLHQDEIQTRELRSAASSGPSLL SDHILSTLPFTCANLSSRFCSPPCSC SCLRA/CCTCHFDLSTLIHAHTRTHHT HTHTMY
10746	24647	A	10831	8	376	GMLPAHLADVLRHNSVGRPKHMRVMAGA LEGDLFIGPKAE\EHRG
10747	24648	A	10832	336	38	GVATEGVGEAAQGGEPQPEQ/PPPQPY PPPPQQQHEEEMAEARQA/AGAPMDG FLSLDSPSYVLYSDRAEWADIDLVLQNV GPNPVVQIIYSKYTLWK
10748	24649	A	10833	206	1	TYFFFFPPGLFFIAGIFFFFLETGSH/ SSLRLCSGIITASCNLNLPDNDPPAS ASQVAETTCATMY
10749	24650	A	10834	226	376	RISQAIISFYFYFLFETESRSVAQAGAQ WSDLSSLQPPSPGV\SDSPALPS
10750	24651	A	10835	213	1	DRVLLSPRLGCSGMITAHCNLHLPWFK RFSCCLPPE/SSWDYRCPLP/PPRLTSV FLVETGFHHVGOAGLR
10751	24652	A	10836	351	447	RENWLTPVIPALREAKAGI\LEPRSSR PAWAT
10752	24653	A	10837	71	472	SASTAPMAPVKLVVKGK/K/KKQVLK FTLDCIHPIDGIMDAA/NSTNYEQFLQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						ERIKVNRKAVNLGGVVTIERSKSKLTVT PEVPFSRRYLKYLTKKYLKNNLCDWLC IVANSKESYELRYFQITQDKKEEK
10753	24654	A	10838	37	382	SRCIMAFYLYGIRSFPELWKSPLYLGVP GHSYVSLFVAGRCGVRNQRLCSVKTMS PQNTKATNVIAKARYLRKDEGSNRQVYS VPHFLIAGAGKERSQMNSQSEDHK/LA/ PVRNAV
10754	24655	A	10839	313	617	AFFLIVFQYVARERERSRS/VNCGLYQ HCYFRTL
10755	24656	A	10840	309	511	WEQGSWEHVLQAPCSLIAPRITHAYTHT HTHTHRYTHLYPH/APTSIL
10756	24657	A	10841	269	450	TPWPLKKEFFFLKWSLALVAQAGVQWR DLGSSDSP\LQPSRFKQFSCISLPSSW DYR/PC
10757	24658	A	10842	420	1	LERGENGTDRDRKGLSHCHQPMDSVLP PLCHPPPLVMTMEEIITMLFIDIGSSMY KAGFAG/DDASRAMFPISIVRCPWHRGVM VGMSQKDSYVGDEAQTKHSILTLYPIK HDIITNE\WDMKEIWHHTFYNNKLHVAP CI
10758	24659	A	10843	431	1	GEHSWASDLAEDVTKVTRGPLGLFWGL CSGNLSFSGCVPLPAGAVPPWVPVFPQ GGA/SWVWKGPSPTLHLLRTWGLAGG VGGRSLGRWRAPGNPGSQGQAPPAHQ ATGTPRSRTGSTGGIETVILEGSHVSG MGIR
10759	24660	A	10844	55	297	QRWPGTLLGVQPG/APPDSTSASGSGGA RGGVPVPTLEGNTGSRKWEDPCWGSQNS PSSDGSKPPPGPLTSKVCDDSRLE
10760	24661	A	10845	109	427	QTGPSAAGLLEFARGPLQLFANVPAV AAEQQIFVNRECCCLIVPLBFCLRGVPC CVRCQSA\LLGGASQLG\SRGSGVRDPL EGGSCPFSDLQLHAARTALFTA
10761	24662	A	10846	17	416	SFLWKFCLEVPGRARCLSA\LLGGASQ LGYSQVRDPLEEAVCPFSDLQLRAGRTT TLFKAVRQHLSQLRILLPVWQCPAPI GGVYRDRQASLSCSGLHPIRA/SRAAVP TQASAMAGAPPDLSPPCSLSSN
10762	24663	A	10847	265	429	LSGASCCLFSLPIVLFALLLSVLSFSF CAWCVPWSLSPTLFLTFLVHLF*RFIS CF*VNSNPKNLTFMVNFQGGKMKIGLAL ERICICGCSLVFPEAILETSCQNLFCY ACAGVLSSVYDYLALLAVSFLFL*FFSL FFFFLYLFLFALGASLPGLYLLLYFL LCCISYSLF
10763	24664	A	10848	12	462	QTLGTMNEGLFATFIAPTILGLPDALL IILEPPLIPTS*YLINNRLIITQH*LV KLTSKQMITIHNKGR*SLILISLI IVTNNLLGLLPYSFTPTQLSINLAMAI PL*AGAEVIGFRSKIKNALHFLPQGT TPLIPILVII
10764	24665	A	10849	2	462	TTLHAFGTMKREAFITLLCLFSAANSRG VYARDAHKSEAAHRIKDLEKDFLALV IAYAQLQQCFBDHVKL*NEVTEFART CVADESAETCDKSLHTLFGDSLCTVATL RETYGEMVDCAKHEPVRYECFLQHWDD CPNLP*VVRPEVD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
10765	24666	A	10850	164	1	RGFQVRGE*NSGRETER*RE*KLARE RAIGQEREREKSREAGRERERERKE
10766	24667	A	10851	417	100	MMLVVGNLRLWSQAQTIPCTKQRSSL FFPVLNAIFRSKSKVLNLCLEYFLGNTL FSWDLIPEILFPLSHYHHYHHHHNHQY *KS*QWSASNTRFQGILDKNY
10767	24668	A	10852	339	3	ETTHSEARRGRSAAASCRGSALRRGRFP ESRRGREAAFPVCPRHVLL*GAQSKQAAY AGKRSGTRHASRWPKSLFPRRRRISLK RALHFWQQSADPSPSVSRIPPHGVGSS
10768	24669	A	10853	1	373	LQQGMRKRAGQSEMAPAGVSLRATILC LLAWAGLAARDMYLHPHLVIHNEST* EQLTKANAGKPKDPTFIPAPIQAMTSPV DEEALQDQLVLVAAKLDTVDKLMAAMVT MLAIFLGFRYIG
10769	24670	A	10854	1	423	VSCSFLKLLTKMKHGLLLLCGFLLLKSQ VNYTEGGFRARGHRPLDKKREAPSLR PAPPPITGGYRARPAAATQKKVER* APDAGGCLHADPDLWV*SPTGCQLQEAL LQLERPITNTVDELNNNVADSQTSSSF L
10770	24671	A	10855	343	3	RGCEAHPLPRSEGPAGSALAQPVMYCTI FAGTLITAISSH*FFT*VGLEINMLAFI PVLTKKINPRSTAAIKYFLTQATASII LVIAILFNNILSGQ*TLTNTNQ*SSSI I
10771	24672	A	10856	147	1	TRTPTGQCVPKSMFLGAVAHSCNPITL GG*GRRIT*GPEFDPPLANMV
10772	24673	A	10859	189	422	NHTMDDFERRRELIRHKREEMRLEAERI AYQRNDDDEEEAAR*RRRRARQERLRQK QEEESLGQVTDQVEVNAHNSVP
10773	24674	A	10860	90	273	SHQIEQNSAMAPRKRGGRGISFMFYCL RNNDQRYMT*RL*SGIGWMLLSSGRMGY ALPG
10774	24675	A	10861	25	411	APCAKPCGDWRSRGS LVWAMSGCNARKG DCCSRRRCGSHL*N*IPDWPLN*FFLT AKVKECFPKKES IYSQTVY*SPG*KM*T *DKEHPRYLIP*LCIQFYHLCWVTGTGG GIILKHGDEIYIAPSGV
10775	24676	A	10862	33	302	SRRTLIYVDMENGEPTGRVVAKDGLKL GSGPSMLALNGRSQVSAPRFGRTFNAPP SLPIATIRALGTVNRATEKFVKTNGPLR Q*QPRS
10776	24677	A	10863	1075	1521	YCHTGKGEQLGERFCEGVSRRGPAERGS DSQTPWPWPLCAAAGTSAGTSHSGSSSG AFSSWPCWTAEPAAARKRGRPAGSWSSP ATGAPGRCRHRILSRGAGGSAGFVCSGL AESGL*ESSSPGRSQ*PQGQRHPQPNG LPAPPSTSV
10777	24678	A	10864	245	418	TSKLAFPISTIPVIYANKVCP*FSKKKKK KKKKKKKKKKKKKKKKKKKKKKKKV FFEGPGFFF
10778	24679	A	10865	132	398	LNMGKGDPPKPRGMASYAFFVQT*REE HKKKHPDASVNFSEFSKCS*RWKMSA KEGKFEDMAKADKARYEREMKTYIPPK GETF
10779	24680	A	10866	115	455	LLTRNMDRLLILAGGMPGLGQGPPTDAP AVDTARHVYISYLALLKMLKHGRAGVPM

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						EVMGLMLGEFDDDYTVRVIVDVIAMPQS* TGVSAEAVDPVIAQKMSDMLKQTGKPEM D
10780	24681	A	10867	64	483	QGERPAAAMRI*SLTLLSFLLLAAHVLL VEGKKKVKKGLYIKVDSB*KDTLGNTHI KQKSRPGNKGKFTVKDHTNCTNAVTBQE EGISLKVECTQLDHEFSWAYAGNPTLCL KLTDETVYWKPVARNLRLQNDIMYSPQ
10781	24682	A	10869	229	1	DTTILKLGRLIILQWLLSEGKSHMSFTL NQK*EIIKLSKBCMSKAELSQKLGCFQ VGSQVMHAKEMLLKEIKSAT
10782	24683	A	10870	934	515	KKVLECLPGLGCGGVILAHGSLALPGSS SLHLSLQSSWGLTGM*YDARLIFVYFFR EMGSCHICQAGLNSYNSSIPPTLVSONV GTTGVSHRAQLAPVFCFCFVTLVDVKAL HFGKQENRIFFFFILFPGGSRDEDRVA
10783	24684	A	10871	373	424	EFKTNLANMG*CLKSQHLGRPRCANHMR LGVQNLQGOHGEIPFLK
10784	24685	A	10872	1	469	RSRSGDSLPAHDRPSGASALATCETIFS AISCFWDLPAFSLRLTPSCQPTMSSQIR QNYSTDTEAAVNSLDNWYLQASYTYLCL GFYFDRDDVALBGVSQFFRELAENREG YDRFLKMQNQRGGRALFQDINTPAEDD* GKTHNMTAAMGLETK
10785	24686	A	10873	244	2	NIYSCKETFSVPLLAHVHFLVGRGGS QGTEMLWHRVDLRYREQAGHSGSHL*SQ HFGSPRQVDQLRYGVSDQRQOHGE
10786	24687	A	10874	83	427	ISLNMIRIAALNASSTIDDHE*SFTRH NTQTKEAQEAKAFALYH*ALDLQKHDI EESAKAYHELLEASLLREAVSSGDENEG LKHPLGLIKYSTYKNLAQLASQREDLET AME
10787	24688	A	10875	94	1	KSQKACNPSTLGG*GGWIT*AQEFTTSL ANT
10788	24689	A	10876	2	413	GVTRGFNMRIEKCYPFCSGPIYPGHGMF VRNDCKVFRFCKSKCHKNFKMKRNPCKV RWTAKAFKAAGKELTVDNSFEFEKRRNE PIKYQLELWNTIDAMNRVBEIKQKROA KFIMNRL*KT*ELPKVQDIQEVQLN
10789	24690	A	10877	65	417	RFAGAGAIPEARAWPTDVHAAEEEEKEMD LPDLASRVFCGRILSMVNTDDVNAILV QKNMLDRFEKTLBMLLNFNNLASARLEQ MSERLLRHTRTL*DMKPDLSLFRPIRT LEWKL
10790	24691	A	10878	4	442	APTPDAMGHFTEEDKVTITGLWGKVNVE NAGRETLGRLLDVYPWTHRFDSFGNLT SGSVIMGNPKVKAHGKNVLTSLGDAIKH LDDLKGTFA*LTBLHCDKLDVDPENFKL LGNELETDMATHFGQDFTPEVYAYLQNM VTVVAN
10791	24692	A	10880	1	419	GKHTRQYHEEKETGQRINIHEYVLGNML AKNLLFEKEREABEKEKSYEIPTKNIQG QMTPIYPVGMGNGTPCS*KQNRPRSSTV MYICHPEKHEILSVAEVTTCYEAVIL TPLLCSHPKYRFRASAVNDIFCQSLPG
10792	24693	A	10881	54	335	REIFTMSGALDVLQMNEDVLKNLAVIT HLCCTKTDSPMEQIYGS*TEYIYSIKL NRT*QNLMLAVP*NYDI*NHDEVTVMTF

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						NNTLQMFEP
10793	24694	A	10882	216	3	MSIKSMSICCLRKKKGHFQIRGK*NSG RETERERERERKRARERARGQERERQKT SEGGREERERERKKE
10794	24695	A	10883	3	390	GELKCSKEKCSMSAKSRTIWIIGAPFL KGQPRGGVEEGPTVLIKAGLLEKLKEHE CDVNDYGDLPFADIPNDSAFRIVKNPRS VGKASEQLAGKVAEVKRS*ISLVLCVN LGGGLECLCGHAKVYSR
10795	24696	A	10884	3	375	STMRAWIFFLLCRAGRALAVPQQESLPD ETEVVEETVAEVTDVSVGANPVQGEVGE FDDGA*ETE*DVVAENPCQNHCKHGKV CELDENNITLMVCVQDPTSCPALIGEVEK VCSYDTLTFYSS
10796	24697	A	10885	95	2	KCTQGPSAFAHACNPNTRGGRGWIT*G QEF
10797	24698	A	10886	1	114	MGFHHVSQDGLDLVTL*GACFSLPKCWD YRREPTHLAH
10798	24699	A	10887	1	368	EPTMELTTAEKTNKGAAMKRVGAHAGEY GAELERMFLTPTT*TYFPHFDLSHGS AHVKGHCCKVADALTNVAHVDDMPNAL SALNYLHAHKLRLDPVNFKLLSH*LLWT LSAHLHVEFT
10799	24700	A	10888	336	9	FRGQVIPAIFFPFQTTSLSYFQTGQPN* TPFFQKILKLTTRGGGKLLDFQTPGRLRQ KREDPLPGV*NCN*P*SHPWGKTQNP VSKKKKKLKTSSI FVHRVSMSP I
10800	24701	A	10889	3	362	GFLAPLEMQELGTPMNRILQTLAEQE TFLTPALLLPIPHQTYSTASAVPLAKPD T*PKDVGILALQVHFPAQYEDQTDLENY NNVKALKYTEDLGQTLMGFCVQEDINS LCLTVEQP
10801	24702	A	10890	66	333	TLFNGIGISFVERVMEVLRPQLIRIDGR NYRKNPVQEQTQHEED**DFYQGSMEC ADEPCDAY*VEHTPQGFRITLRAPS*LY TPIVG
10802	24703	A	10891	405	49	IPWMGTERTRASAQRDVAGPARNPACPL PEQCFFPGPAEWGTGLTPPGSC*LPGER ERHGPCCWGPFRERLSSGQTHPPSPQGA NTCPCHKHQQLLAGGVAVFYKLFYRYG NSPKWDL
10803	24704	A	10892	2	197	PQPLRLVWTAHLAAMAPSSRTSLLLAPA LICLEWLQKAGAVQTVPLCTLFYHAMLQ THRAHQLVIDTYQELEETYPKDHKYSF LHDSQTCL*FSDSIPTPSNMEETQOTSN L*LPDIPAPGFCPDLPALASKGWCRPNR SAMHAFLPRYAPNASRAPTGH
10804	24705	A	10893	3	334	DQLPEPLKVLWTAHLAAMAPGSRTSLLP PYALL*LPWLQEGAGAVQTLPSVRLPDHA MLQAHRAHQLAIDTYHEFDETYIP*DHK *SFLHDSQTSFCLPDSIPTPSNMEET
10805	24706	A	10894	3	341	LLTPGVSDAICYILDSGYIIMSDTFTAY VIG*RFEVNG*HATVRFPAVVPVALPW LGV*WDNPERGTYDGTHEWTVYFKCRHS TGGFFIRSNKVNLTGTFVTADKNLYVLD Y
10806	24707	A	10895	25	351	AMIQTRDLQGGRAFGLLKAQQD*RLDEI CTQLLDDLKYSNDEDLPSRLEGFKKYM

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						EFDLIGNGHIDIMYLKLMYKLAVPQTD LQLPRSIGEVYSGSGETISYPDFLM
10807	24708	A	10896	364	38	FSQFKIAQFLKKIPFPFGSFFPQNGGNF LKFSKFFPNKRGFFPHPPF*KRGFFFCP KWGPQGHIGAHGPPAPQGGKIPFPQVFK KMGIKGPTPPPGFFFFFFFFFFFSW
10808	24709	A	10897	136	3	STLKHR*RPGMVAHACNPSTLGRSGRI T*GQQFKTSLTNMVKP
10809	24710	A	10898	193	269	GNKYCLTILLLLLLLSFKRQSLTLPTL ECSG*TRTPGPKGSSLLNPS*VAGHGGV CL*SQLIRRLRWEDHLSGV*GHSDPRL HHCILTWATE*DSVS*KTTTTTTTK
10810	24711	A	10899	316	374	CCCCCCCC*CCCCCCCCCYKETNFB QQ
10811	24712	A	10900	38	206	VVCVLVFTICTLLCNTSLGLFHPPEFFF ETESCCVAQAGLQWHHC*SLRLLPHRII
10812	24713	A	10901	364	2	DYQHISPEKHCRPEGSGMVYLMCRKKK RKKNLSTKILNPQPSFIL*KPRNSARK S*QKEITKIGADSLIENRKRRIEKIYIN ETMSWFIENKIDQPLARLTMIERKDS TKFRNERG
10813	24714	A	10902	132	3	ATSSPWGYSAYRVAILLFLYFSNKLAPT VLYGFV*NYFLQEI
10814	24715	A	10903	234	352	NFCFFETGSCSVT*AGVIMAHCSLDLPG SSNSLTSVSEE
10815	24716	A	10904	250	356	TMEMMLDKQI*AIFLF*FKTGDKAET TLNINNAL
10816	24717	A	10905	280	322	QT*SLILVSLIICIATTNLLGLLPYSFT PTTQLSINLAMAIP*AGAVVIGFRSKI KNALVLCTSTPLPTSTMLPVHMDTSSD IHPKI*SIR*QTCIQHRLLLWLKC
10817	24718	A	10906	271	365	KWRPGVVAHTYNPSILSGRGWIT*GQE FKT
10818	24719	A	10907	135	358	LRYKLTNPKLTLTLCGLIFLKGNIIVNIG QCNGVHM*YQHFRPGQDCLSPGIQGH GQHKESLSL*KSLKISWS
10819	24720	A	10908	107	212	IKNEGMCQVRWLMVPVIPALWEA*VGCTP EVSHSWL
10820	24721	A	10909	165	383	PKNRPIIPLKRSSISNPGDFQKSLRPGL TPMGPHFKRGNYSYDENLENLCPVGGNK GPGSH*GLLTCETCRGF
10821	24722	A	10910	119	291	GGYRFYVKDTF*K*GFNPLTLFIILKPL AGHGGACLSWRLRLK*EDHLSLGGRG CSELWLCTLA*ATE*DPVS*KVRLALN FVYNTKTFSRWWCMPVVLATHEAEVGG SLESGRSRLQ
10822	24723	A	10911	283	2	SDNTTDTFLFFIYKYIFPITWEQGETWK KNPRNSRLKKTILRSETIAQIPLKCNLWP GMVAHACNPYTLGD*GGWVT*GQEFETS LANMARPSC
10823	24724	A	10912	1	360	PHAFGTMKWVTFMSLLPFLSWANSRGGF RONAPKSEVAHRLKDWGKKNPKAWG*MA LAQNLKQGFENHGKLGKEVPFAKPGV ADDAEAGDKWLNLTLLGNLAPVAAVRE TYGERAEC
10824	24725	A	10913	270	361	SKTWPGTVAQTCNPRTLGSQGGWIT*GQ EF
10825	24726	A	10914	157	1	VFPQLSRLAWKGFSRFFVFETESHVA

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						*AAVQWRDLGSLQAPPPGFTFFSS
10826	24727	A	10915	1	357	LEEWGPEREFAEEKEKNTKKKKIKNS TPPKKPARKGEEKPGPFKRAITTFVAR IPLFCLKGFLWPSC*IIGRSSPTPGSKG HTGAPNCPPLAFAFKDVPNPNPKMVE AVKNPIL
10827	24728	A	10916	102	471	PSTPIILTSSYPHYVKSSVTSTFIISLF PTTIFMCLYQEFIIISN*HLPTTQTTHLS LSFKLDYFLIIFILLTFLVTWSIIEFSL *YINSNPINQFFKYLLIFLITILILLT ANNLFQLFIG
10828	24729	A	10917	2	138	REPTMVLSPADKTNVKAIVGKVGAGAG* YGAVVLFVTLNVLNVID
10829	24730	A	10918	178	393	LVLCTVLLMWRFFHDSLSILKAQDVTE NLSNPTVLRGETGPSAVAHTSNPSTLGG *GKWITQGQEFETSLA
10830	24731	A	10919	278	124	TAWADWGSNETPFLKLKPKKLT*GGGVC LEFQVLGRVPRKPNFNLGNQGFN*PKFR PWTSTWGAQNFV*KKKKKNKNKPK*NS RHTPPP
10831	24732	A	10920	221	243	IIIGSPLIDIKISKCFKIVAFGQAOQP VIPALWEAEAGRSPEVGSPPA*PGSLK VHVDNNWESIN
10832	24733	A	10921	33	292	GTMWLEIRHAVEVQCVLVSELVIPTSGD KPEQC*DHYLIT*YLILGKWI**ISGA LEKKKKKKKKKKKKKKKKKNKIKTGG FI
10833	24734	A	10922	108	3	KLAVYGSVCL*SQLLGRRL*EDHLNLGH GGCSEP
10834	24735	A	10923	106	2	KLAVYGSVCL*SQLLGRRL*EDHLNLGH GGCSEP
10835	24736	A	10924	195	2	ASLFKSQLNRAFIYLFYVFIFETGSL* PMLVCSGVITAHCNLHVLGSGDPPTSAS QVAETMVL
10836	24737	A	10925	127	2	YVCILKNLGRPGMVAYACNPSTLGGQG GWIT*GQEFKTSL
10837	24738	A	10926	639	282	PFLSIKGVVQFMPIIPTPWGLKQBDHL RPGLRDQPVQNSKTPSLLLKI*KLARRGG ACL*SQLFRKPR*ENCLSTGELKPKGGI FIRLVQNKIPTTRGEKRRQSHTSYQCP KIKKKG
10838	24739	A	10927	1	363	ALLTQALTCRQAGAEAPHAGATPSLMPP SLPQGFRCSPSDAAYTMENTIDKKQONQ VIILFKFMGKAAQTTRNINNAFGPEI ANKGTVQWRFNFCRDESREDDE*YAO PSKVATDQL
10839	24740	A	10928	53	379	TEABELLTLYLLPNALLNHFTSPPLMFAD RRLPCTNHIDIGTLYLLFGA*AVVLGTA LSLLIRAELOCQPGNLLCNHINVIYTA HAFVIIFFIGLPIIIGGFN*LFPL
10840	24741	A	10929	180	350	EPMAKGTESPGPKRCGP*I*WVISORG TLRFRGAGLFFMGFELRLGENLLEIPRG A
10841	24742	A	10930	361	379	RRYWWLG*VQWLMFPVLPALWEAKGRSP KARNL
10842	24743	A	10931	121	543	HRNTGSTHASAHAYHIVHTNP*PLTGAL SALLMTSSLAMGIHFHSITLLILGLLTN TLTIYH*WRDVTRESTYQGHHTPPVQKG

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						LOYGIIILYIT*VFFAGFF*AFYHSIL SPTPQLGGHWSPTGITPINPLKDLLNT S
10843	24744	A	10932	227	339	VGGVKSQVQLLLNCHFSR*MKMKKKKKKK KKKKKKKKKKKK
10844	24745	A	10933	64	409	DQRNKAHLRAHLKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKRGE*KKIN WAFFLPLLRKFVGENFLKKNFVGGNI GGQISSKKYRGGGK
10845	24746	A	10934	2	362	NKLSGPYPPEKVGTYTLPLMPLAQLVIY STIFAGTLITALLSSH*FFT*VGLBIDML AFIPVLTKKINPRSTEAAIKYFLTQATA SIILLTAILFNILSGQ*TITSTTSQYS SLIILRAM
10846	24747	A	10935	154	3	GCPLSPLLFNIVVKULVRAVMQEKIKS IQIGLEVK*SLLTDMILYLGN
10847	24748	A	10936	250	363	TAWPGYLYSFSFLY*ETTKIWLGAHA CDPSTLGGRG
10848	24749	A	10937	199	339	NVLGILLVPRIIIVBIYKCGRLWLGTVAH TCNPSTLGCQGRQT*GRE
10849	24750	A	10938	130	240	KNEQDPRDL*DNDKWFNIHVIGUPEEDK DNGTERVFD
10850	24751	A	10939	35	235	FILVENTKKMCICPLLNMIYAILYLFVP SVFL*EENKQ*GITEKKKKKKKKKKKK KKKKKKKKIKPGGL
10851	24752	A	10940	179	12	DQPGQHNKTLSLQENKNKSSWVQCCV*P QLLGLRLRWEDCLSPGGRSCPEPCSHSG
10852	24753	A	10941	297	278	INQDNELTLNQSSQIKHKNINQTLRT KMENELFA*IAATILGLSATVQIILFP PILIPTSKYLINNRLITTQQ*LIKLTSK QMITIHNTKGR*SLGGD
10853	24754	A	10942	3	318	FGGGRGVNYPDAFVLSVLLPSRLLP LFPFLPPLPPLGLAPYCPFL*YF*K* *LYYSQSIIFFFYREMKNLVFWAINL FFLYYYNYMEMWTLCYWRN
10854	24755	A	10943	190	3	KLSHKQSVYFKTPFI*KNHVLFX*KNLW VYPNDKFFFFFPESLALSPRLQCNGTIL AHCNLR
10855	24756	A	10944	281	1	KKWLFSSVSSLYGNGLFLIPPFLRVSGF GKGFWKKFFFLRARGALFWGSPKGFPL GFPWVFFFF*DGVSLLLPRLECNGIISA HCNLRFPGS
10856	24757	A	10945	169	319	NGVEDAFKNMVLGWAQWTSVIPALNEV KVGGSPFVRSFRPTPI*YGFRLGTVG YICNPSTLGGQGRIT*GQEFQTNPANM VKPC
10857	24758	A	10946	312	1	FARPGLKSWDFQP*PLDPVWGFFFKRF PENWLEFEIIFPLIIMAKRKLKSLFP FPFLG*FKD*GQKTPFFFTVSLLLPK LECNGAISAHCNLCPLPGSSD
10858	24759	A	10947	208	329	IFTGDRSRNNRIG*ARWLTPVIPSLWEA EAGGSLEPKSLR
10859	24760	A	10948	116	374	FYPGYLLFFCFPEMAPCSRG*SWSARG QSFCNLIFPGSSDYVSAFRVARITGAR DHACIIIVFVVDGGCVDITITSGLAGWLR RG
10860	24761	A	10949	264	434	QLAFCTDTLTSVREQEQL*KCVKARKR IELCDEQ*SCRSHTD*DCDELDFDLHA

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10861	24762	A	10950	226	429	NFGFRLDKTVFFSKIRINAWAQWMPVM PELWEAKAGGIT*AQELETSLSNIVRPW LYKKFKN*VWWC
10862	24763	A	10951	188	433	YSAEWKIDLGIEVFWVGKMTYKQ*FPWF VFKFLFF*RQRTLSSKLEWMSVITGHC NLDLLGSRETFASAFQVWTIGSCHS
10863	24764	A	10952	298	445	LFSKCSSKSIKEEGPGVVAHACKPGTLG GRGGWIT*GSEFESSLANMVK
10864	24765	A	10953	244	1	KTPQGLVVFCFLFKKSPKLGKGVSMGVL ICFPLKSRINLFPNPRGLQQRKNFPPFF ETDSYVAQTGVQ*HNLGSLQPPSC
10865	24766	A	10954	199	3	QETKKEQNKENKQIK*RSTRKKHRQGTN KTKRGERQTPPVGNRQPTLGIHARPR RRATTSPRA
10866	24767	A	10955	157	3	YSYTFSTFIITTSILIIQTLSGHGGACL* SOLLQRLRQDNHLNLEHGGCTRA
10867	24768	A	10956	263	357	GLSLKVLITQWLGAVAHACNPSTLGGRGG *IT
10868	24769	A	10957	333	2	KWKADMLIPLVIKSFFLGIFFKMFINSK RYIFLLQLLAQHSSEFFSFIRCMEL*WPY PIPLCYGQSNQPSV*LAYCRDLFNELIF FFFFETEFHSCCPGGISAYCNLCLSC
10869	24770	A	10958	130	228	GSSFLGGSPSVAQAGVHLDPDHGSLQ*DK SPSVQKMSKWIGCSGACL*SOLLRLRC QGRISP*GQACSEP*SGRCTPAWATEGD PPKKLLPYTTDS
10870	24771	A	10959	250	3	VQACSITGALYQRRNAEDEPQTARPISG FTTSIAMRLMLLTCSGHIWVPADLAFSG IMP*GLFFPSRQNLALSPRLCSARA
10871	24772	A	10960	199	326	VLGRMWSNQKNYTLARM*KIK*NNTR CWGGCGATRRIIHC*QECRI*KCQPQSL WRTV*QFLNTLNIR
10872	24773	A	10961	323	3	LLFFHLPDNQWQ*YVFCYHNSFLQFYI N*IIQLVVFCVWLLSMSIILKSHPCFHS K*LSTVTFFFRQSRVSRLWEGAI SAH CNLCLPDSSDSCASAS*VAGSC
10873	24774	A	10963	120	3	PPFFFFF*EMRSCFVAQARVQ*CDQSSL *PSTPGLKQSSC
10874	24775	A	10964	168	441	LTPVIPALWEAEAGRSPEVRSSR*SPP
10875	24776	A	10965	19	207	APLKLNVAMELSLGQWDVSRSLNWEIPL KKGDTGRVQWLTVPVIPALWEAEVDRTPE VTSVTRC*PLKLNVAEMLSLGQWDVSR NLWEIPLKKGDTGRVQWLTVPVIPALWEA EVDRTPEVTSVTRC
10876	24777	A	10966	209	1	TKSALSNMVVTTHIGLCKNFCIVL*DRV SVTQIGVQWHDLSLSLQSLPRLKDPPTS ASRVAGITGMHLV
10877	24778	A	10967	109	1	DYLRSGV*DQPGQHGKTSLLKIQKLAR LVGPIISC
10878	24779	A	10968	141	2	GLAMLPRLENIIFRPGTVAHACNPNTLG GRGGQIT*QGEFKTSLSC
10879	24780	A	10969	175	348	LVYECKHILCVFNTSLFFPH*TCYK*RG VLWLGEVAHACSPGTLGGRGGWIMASGD RD
10880	24781	A	10970	108	2	KTKKLHMRSGVVVAHTCNPSTLGG*GGWI T*GQDSC
10881	24782	A	10971	184	2	SFLWKHLHRLGVPGRVRCQAPTRGASQL

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						GYLGVDRDPLEEAV*LFSDLKLCAGKTTT LFLV
10882	24783	A	10972	245	339	SQISGPGTVAHACNP SILGGRGEWIT*G QEF
10883	24784	A	10973	295	340	KRVFF*ARKKNPFLSPLWGLTLENPLGF RLFLNPFLGLKISQFFPRQI*PLAFFF WGTLPRLNLKFGPFFFFFFFFFFFF*DG VSFCCPGWSQARRYIEINISLSTCPRA
10884	24785	A	10974	186	340	RPYLTRFRKGHPNPPIQ*SFFVLFCYC FDTESRSVTRLECSGSNSAHCNL
10885	24786	A	10975	253	491	FLECTSLLKRQRVHPGQHSKAPPTKBLQ TTGRGALLQSHLLRLRQEHCLGPGVG SYSEP*LHHCTPAWVIEGDSKK
10886	24787	A	10976	141	1	SFSFFKFSPTGDMIGFF*HFFFLRRSH SVAQAGVQWCHLSLKPRA
10887	24788	A	10977	3	138	HEETGFHLVSQDGLNLLTS*STHLGLPE CWDYRREPPPGREGDF
10888	24789	A	10978	186	323	YESRSATQAGVQWCELGSL*PSTSRFQ* FFCLNLSSTWDYSGLAPS
10889	24790	A	10979	183	3	IKILFFFFLRLSLALLPRLECSGTFS AHCNLCLLGSSDSAS*VAGITGTTTSPM QLV
10890	24791	A	10980	309	55	KNFGPNWVKFLGGKGGEMAF LGKFPFPP FFFFEKESWVFQ*MQWGDFRSLQGP PGVTQISRLGKIGGPLFPKKKKRERGN M
10891	24792	A	10981	637	838	SOHLGRPMRVDQLRPGV*DQPGQHGEMP SLLRIQR*AGHGGTHL*SQVLRVRQDN CLNSGGGGCSE
10892	24793	A	10982	275	2	RNRTLKMEFLSWFNGFWNLLNMIRPKN VKDSTSKSMENDTSPWHELFKELGKINA FDTPDLLVRGKFSDSIHNTFDHM*RTK EYNEARA
10893	24794	A	10983	98	346	GHGHATLRGLCVLTFSFHITALSVSGTN DAEDCCLCETQKPICGYIERNLLYLLIK DVCRVPAVV*VVERVYSLISRYSLWRD
10894	24795	A	10984	30	410	LPEFTGRPKRTRTRGFSTNHTDIGTLYL LFGA*AGVVGTAVALLIRAE LGQPGNLL GNDHMYNAIVTAHAFEIIFFIVLPPIIG GFGN*LVPLIIGAPDMAFFRINNICF*L LPPSLLLLLASAIAE
10895	24796	A	10985	141	360	QTLRTKMENLFAFPIAPTILGLPAAVL IILFPPLLIPTSKYLINNRLITTOQ*LI KLTSKQMITIHNTKGRT
10896	24797	A	10986	3	347	HELRTKVNEHLIASFMGPTSLGLPAALL IIL*PPLLIPTSKYLISNRLITTOQ*LI KLTSNQMITIHNTKGRT*SLILESIIII IATNLLGLLPYSFTPTTQLSINLAMAI PL
10897	24798	A	10987	46	317	KSMTPIRKINPLIKLINHSLIDLPTPSN ISA*NFPSLLGACLILQITTTGLFLAMH YSPDA*TAFSSIAHITRDVNYG*IIRYL HANGAS
10898	24799	A	10988	245	1	VSCLEGLKLTNRKDIHTKNPSVHHHQ PKVDKTTKMGKKQNRKTGNSKKQTASPP PKK*SSSPATEQSWMENDFDELRRE
10899	24800	A	10989	255	1	SCLPWANWISVQNHKKTFIVRTFFPY GSFHVT*LLGPPLILISPPRIFFFFETG

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						SFTVARAGVHSGAISARCNRLRLGSSNSA
10900	24801	A	10990	166	307	GEKPWGPLIWGGLVGRSSWASQVLELL *EMVFRHVQAQGLKLLSSSNPPASASQS AGITGVSH
10901	24802	A	10991	109	330	TNQFKTKKEREAGKKVKELERERERBK KRKEQRKNEKERR*P*NMD*RRIRERNH SFDVYEFLICGLLNLHV
10902	24803	A	10992	244	326	GRYLGWLDGPA*AVVLGTALSLLIRPE LGHPAILLGIDLISSVIVTAHAWGILLV RVIPIIAGFGN*LVPLIIGAPDMAFPR INSISF*LLPPSLLLLPPPI*QMRAGV GEREVRVR
10903	24804	A	10993	101	2	KTFWARFVGTC*SQLRRRPRQEDHLRL GGRGC
10904	24805	A	10994	177	1	TPSLLFFVNIICFCLNPGGGGYSEQKLC LCTPAWVTE*NSISRPSQNNRSQRQVN HLF
10905	24806	A	10995	214	326	KEERKNPRAIRVV*PWGFFFLFKEISL FLFVFRFWHGYFPFGAFFSTQKWLVF*T MVLFFFFFF*VSLLEPRLECSGVISAHCN TFLPGSSDC
10906	24807	A	10996	184	379	LCGMVYHFPISILLYL*CKLFFSPKLEF SSCCPLECNGTVLAHRSRLRPASGDSPT SASRVAGHGGTCL
10907	24808	A	10997	136	3	GRVDGQHIMTHQSHAYHIVKPS*PLTG ALSALLMTSGLAM*FH
10908	24809	A	10998	274	363	PWAYAEPLTLHDATYSC*SLIRASFTL FIA*TRLRLLP*SFTPTTQLCMNLAMA IPL*AVAPDIGYSSMITNALSHLLPQCT PTPLISILGIETVSLLIQIPITLGVRR ANIT*CHLLMHLIGSATLSISTI
10909	24810	A	10999	305	1	NLHTPSQIPLT*PLPNINIHNLHLTTT Q*IKYLILIPSNLPHNKNPLKTAYSVPP SPNLHLPPSSSNPASASQVAGNAGARHY AWLIFVFLVETGYLLV
10910	24811	A	11000	154	2	IVVGILQSRRCGR*SQHFRPRQADC FTPGVPDQBYFTLLPEVVFFLV
10911	24812	A	11001	142	367	GVCLYQRISYIKTKKLSQGLFYFLLL LLLF*EGGSHSVTKLECSGGVSAHCNLC LLASSHPPTSSSQVAGTTG
10912	24813	A	11002	60	385	GNTLLSHTLRAHLIENLHAEFIDRTILG LPAA*LIILFPPLIPTF*YLINIRLMA NRH*LIKLTSEMITIRNSIGRT*SIIL VSLIITATANLLGLLPYSITRTT
10913	24814	A	11003	214	83	SKKSASPLTFNIVFQVLDSVREERIRY TEMEKEEIKLS*FVD
10914	24815	A	11004	241	368	SYLL*PSP*PLTGALSALLMTSGLPMRF HFHSITLLILGLLTNTLTIQ*WRDVTR ESTYQGHHTPPVQKGLRYGIILFITLEV FFARFF*AFYHYSIAPTQ*GHWPLT GINPLNA
10915	24816	A	11005	3	396	HEPHALGMPLTADLPSMASCQSOTSLLLL LHLLHLPWI*EARAYQAAGCSKLPDHAM LQAHRAHQLTIDTYQEVEETIIPEDHKY SFLHDFQTSFCFSDSIPTPSNTEETYQK SNLELLRISLLLESWLEP
10916	24817	A	11006	156	335	FGCCCCFLFF*LVYCCYVMMLYIYVLI

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						SFGFYF*YWIM*YFYRLVYNIYLVLFYL LYMS
10917	24818	A	11007	107	2	KCSSSKHFTKEDSQITNKHIEKCSS*LL VREMQUII
10918	24819	A	11008	129	412	KTRSGFKKTPGQKGKTPLLKKTPTKITGP GGGALKPPFSGGFRPENPLNLRDKSSG PKTPTFPSPWGKK*NFFQKKKNLLYPG KIPFFWMKNI
10919	24820	A	11009	63	268	CTFKFNKHCSTIQSTT*LDRSEKKKKKK KKKKKKKKKKKKGGPL*KNFSLKGG
10920	24821	A	11010	154	422	NEFSFFFFFWKPKPPFFAQVGGQVRNWG *LKPRDPWLKNFSGFASGEAGITGGVPH PG*ILVP*VKAGFHIEIENLVNSETGNQP ACASQ
10921	24822	A	11011	23	375	TRYLTAKKKKKKKKKKKKKRGAPFLK TPWGAPFFPGSAIFIFFFFGGFF*TPLG FFWETLFFWGKILGHLSPKILPFWGKK NFFVWKGKKNLLNSPFLKIFFLGVFFKK FFPPG
10922	24823	A	11012	151	361	ACTTTPSSFFSNIDTVSLCCPG*VEGHN NSSLINPSPFLRSWYRHPHPAHFFP ILIRSYVAQAGLEFLALRDTPISDCPC TVHYPPSLAN*SVFFFLTQSFVSLPRL KRK
10923	24824	A	11013	146	378	NFVVSFIEFLHICY*YVSFICLIKVPL* *KKKKKKKKKKKKKKKKKKGENLKAG GGKKFLGGGKNNSFFRNGCF
10924	24825	A	11014	82	264	TEFLYITICNWSAILYILC*RNKVLSP INTEKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKIKIRKI
10925	24826	A	11015	381	2	GRTALFTLLKGPPIHRPQMFFTPLRVFPG SYTGISIRQSGFFFIKRVIFPRL**KAL FLLPFLFPFFSFFFLKIGTYSVAQECNGM IIDN*NFELLGRNPSTSAQIAGNTSA Y*HTQLVFLCEDGI
10926	24827	A	11016	1	251	PNCIVHSLRTGTNLNFIILLLLCFTFE*F LNKNLI*FESQKKKKKKKKKKKKKKKKR GAPLKKTPGGPKFYPAASKKKISPOKGG
10927	24828	A	11017	234	1	DNIKGSWVGIPKPSVLSLQLFCNSKI FPN*KLKKKNPNPEGMVHVHCNPNSTSG GRNGQMA*QGBFKASLANMAKP
10928	24829	A	11018	107	342	FQLCIGATVHCFLFMKQHSYKSTDHRA SSKCHTVQSSSLSTSAFKQK*THKKKK KKKKKKKKKKKKKK*KKKGGASF
10929	24830	A	11019	264	1	CFKPLLEFKYPGI*IKAVNLVPSTASATFH CK*YVTFSS*KKFLCVGKGTGSHSITQ AECSGTIKAHCSLELPGPGDTPPTPSRV AARA
10930	24831	A	11020	1	288	RTRGTSSRSRAATLFFFFPFKKGGFFNG NLPTTFGLGNKKFPLNLFPGGPPLPHG GLKKGPGAPQVPPPLFKKPQTSPP*GLR EGPPPLKKFYLF
10931	24832	A	11021	115	287	STCEISFGCSRGCCWDYLMVWEFSHFYF *FLETECCSVA*AGVQWSNLSSLSLHP E
10932	24833	A	11022	186	1	RPKVDKTKAMGRDQSRKA*NFKNQKASS PPKEYNSSLAREQNWMENEFELTEVGR KSVITN

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10933	24834	A	11023	180	353	IFCFCIFSRDGVSVCP*PGWSQSPELMIH *NTKIS*AWQRPKIPATQEAEGESLE PG
10934	24835	A	11024	155	1	PQARRGGTCLQS*LLRRLRLRQEDRLSP GV*GYSEL*SCPCTPAWETERLV
10935	24836	A	11025	22	325	KLILLYDPQLTFIFLNTRAVVAHCAFC WPIHFVFGNYGFVFSCLFTFIFVYSGKA DLFFKPKKKKKKKKKKKKKKK*KKGG RGLKNSWGGPIFWGFPK
10936	24837	A	11027	127	259	GQVQWLTPTVIPTLWEAMVGGSTKLRSR PFFSTP*PCIVMILYG
10937	24838	A	11028	37	408	IASGALFFFFKAAGKRGDFKTEGAYQRQ RTIFKNKKRARRREKTGRENLRGNYKNMG RGLKTPRGALGGPYLDKKGPLRGKGPFO GGTLLGGGPKIKIQGTL*IRRNYWPIYR RYNRFKKRQKNM
10938	24839	A	11029	146	3	LLVLKDLPRIMVRSAPTYIYIYTYLYIY IYIYTHTHTHTFIT*VLFC
10939	24840	A	11030	268	435	LMCLRNEN*F*KVE*WLGAGARTCNPK TLGG*GGRIA*GQEFETRLRNIVRP
10940	24841	A	11031	322	2	KLPHLQQQCVKVCYKPPFLKNGKIGHGG VCL*SQPLRRLRQENHSNPQCTSAWVT QRDSVSKNKKRMEKYFSSVRQNKPVK HTKRMSPTKADTKSTHCGGGRV
10941	24842	A	11032	251	380	HKRLHTIYFVPLKKMGPGLVGHTYNP STLGGQGGQIT*GRE
10942	24843	A	11033	64	324	FWFFFFFFFFFFLNPFGGKKKKKPPPL GKKKKRKGKGEKFFSPPPRGGGGGPKK ISLKRVLKFF*NPPGGTKKGGPFLIPP GSP
10943	24844	A	11034	420	534	CPGVVAHAYNPSTLGS*GRQITIDREIB TILANMAKPH
10944	24845	A	11035	196	1	KNHSLPPGPQKGTFFPKKKKTPKINLS ELGKSKAYSWPGTVVHACNPSTLGG*GG WIN*GQEFE
10945	24846	A	11036	10	248	PSDR*LFSTNHKDITLYLLFGA*AGVL GTALSLLIRAEIQPGNLLGNHINVI VTAHAFVIF
10946	24847	A	11037	32	405	DYVSKRKEKREKRNIVLETSSSHLVE WMLCSRYHPLIKKRSSVRILIALCPQK VRDMS*GIGSKKCWDSWLSIWIKMESD PFLIPYPKINA*RLKDLCEINLKIIK REYLHDYRVKKV
10947	24848	A	11038	337	448	KNPRGFFGKNPFFWGGPFGGPPPKMG FGEKKKF*FKRSKKKKKKKKKKKKKK KKKTG
10948	24849	A	11039	307	415	RFVCSITIKVLRDLSSDRSNPGRVLSTN SSLK*KKK
10949	24850	A	11040	213	403	VHRGIKYFLNKLPDFPQRTFRK*G*RL GAVAHACDPSTLGG*GGWITLQTFETS LTRMGKS
10950	24851	A	11041	104	2	SAFFF*ETESCSVAQAGVQWCDLSSLQL PPPGFK
10951	24852	A	11042	177	3	AYTAYICVGIHYLYK*MYICINHVHCK ITYLYIYKYLKYNAILYHIGFPSFLHTI S
10952	24853	A	11043	314	395	TVYILNLSINSVQSVLLSVFHLRHQPR GRVQWLTPIPALWEAQAGGSP*VRISQ

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10953	24854	A	11044	310	403	IKTPA RGKGGKKPRNPGGGKS*ALTKKKKKKKK KKKKKKKKPGGALKKKPRGGQKKTGGGK KKFLPKRGAKKKPPGDFGKKNIQGGGEK RGKTPPKKKKP*GKKNLKGGGKKTTPK SGGGKKFPFRVV*KKKLPPGG
10954	24855	A	11046	181	3	EGPLSLSLFFFF*QISSLRLRLKYS GTIIAHCSFKFPSSRNPPTSASQAAS TGVH
10955	24856	A	11047	392	41	KESRSLSQGGREKGPFFLAPPAPKFKR IFRPHPLKKLGPKGPPSPS*ILSLKKK GGPILARWFNNSCPQGPPPPGPKRLG FKGGPPPPPLF*KKKPPFLGGENQKVK NFFFF
10956	24857	A	11048	147	307	TVIVFVFLRLKGLTLLPRLES GMIMAHLS*PPGLKQSSCHSLSSW DYRRRRG
10957	24858	A	11049	118	1	HGKIPSLQ*HK*IAGYGSACLQ SQLLRLRWESRSISI
10958	24859	A	11050	54	284	RKIRRGGLHLSNLLGRRLWED LLGRRLWEDRLSPRRGGCSE PRLCHCPPANATE*DPVSKKKK KSLFVEKPQGGG
10959	24860	A	11051	130	340	HNMHFAAHGSRINFDFFFFF FERGFPCPPVGRAGTHFGLLE PPSRV*KQYYWLGTVAHVCNP STLGGHVGS*GQEFKIS LANIVK
10960	24861	A	11052	140	337	NIIMFFFFFETVSLLLGLE GKGTIWN*NLCLPG*GDSPLGCS
10961	24862	A	11053	197	428	IRSNINPTVASQYSEWKSHI PLILNQNLDMIKFSEEGMLKAKI GILLRQTVGQVNAKEKFLKKN QSATPLSI*IRK
10962	24863	A	11055	180	1	AITALLYSLGDIARRFHLRR KKEQWQGMVTHVYNPSTLGGQ GGRTA*TQEFKSSLG NIA
10963	24864	A	11056	158	426	FFPLPLPLPTVSLFPRSPS DAEPKLDCTAAISAHCNLPA* FSCSLSPSACNCRRAPRLTAS ASRGAGIADGVSTQCSMV PRL ECGSV
10964	24865	A	11057	220	421	YALHLNMKNNSYF*MRKKK KKKKKKKKKKKKKKKKKKKK KKKKKKKKQNKDPGGAVYKKIP
10965	24866	A	11058	162	464	SCSVGLKLFMTSLALSYV CLLLLLLTHYYYYYYYYY* SLVFM
10966	24867	A	11059	1	134	APENRVDPRVRKTLVPLI PIITTLANPCKKD*YPIYV KISIA
10967	24868	A	11060	382	273	SSCL*PQLRLRLQEDYLS* GA*GCNEL**CHCSPA WVTEQDPVSKNIHTYIHSQS INYGSMIGYIHEQKGIAD HKPIIAEPE DSTYPRDHT
10968	24869	A	11061	298	378	SCSASPCSSRHGWS PCG*QTCLLLAIALRCLP WLREAGALHTGPGCRL FDHAMLQAHKAHQV IDTYQEIGENYIPDQKNS FLLESHTSFCFSDSIT TPSNMEETQOKSNL KLLRISILLIETWLEP VRFLTRIVANN
10969	24870	A	11062	39	486	RPTRPDAYHIVKPS* PLTGALSALLMT SGLGMRFFHFSITLLIL GLLTNTLTIIQ* WRDVTRESTYQGHHT PPGQKGLQYRIM LFITSEVFFAGFF* AFYHSSLAPT PQLGGHWPPTGIT PLNPLEVPL LNTFGILAI GGSIT*AHH

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10970	24871	A	11063	269	429	ATWQKLPLQIQKNYPGLGLVAHACNPST LGGQGGRIIT*GQEFINQPMNVNTH
10971	24872	A	11064	248	65	IIIEGQAQWLMFVLPALWKAEGGSPEVG SSKPA*PCDEPPASASQSAGITGVSHRTQ LILNS
10972	24873	A	11065	176	1	LFPPPKKVPFPGNTQFKSICLYTTNFFF FETESRSVARLECRGTISPCHKF*LPGS RE
10973	24874	A	11066	2	397	MVLWTAHLRAMAPGSRTWGLLTFFALLCL PWLQKAGAVQTVPI SRLCDHAMLQAHRA HQLAIDTYQEFKETYIPKDHKYSLLNDS QTSFCDSDSIPTPYNMEETQOKTNLEVL RMSLLEIDS*LRPAQSNKR
10974	24875	A	11067	172	399	QILYL*KYAYTVTMOHLSPIL*KKKKK KKKKKKKKKKKKKKKKKKKTGG
10975	24876	A	11068	192	3	PKLTFMLKLIVPHIILLPLT*LSKKHII *INTTTHSIIISIIPLLPFNQITSNLF CSPTFC
10976	24877	A	11069	204	345	DKSGEHSKTSSIQNLRLGAVTHTCNPR TLGGQGRWIT*SQEFQTSF
10977	24878	A	11070	3	416	HELPPQLRVLWTAHLGATAAGSRTSLLL DFALLCLPWVQEDGAGQTV*SRFLDHA MLQAHRSRLGIDTYQEVVETIYPEDRK LSFDDCHTYFCF*HSIPTPSHLGETLL TSNLELLRICLVLIDSWLEPARILTS
10978	24879	A	11071	108	2	PSPPFFETESCSVT*AGVLWRDLCSLQA PLPGSSC
10979	24880	A	11072	400	278	KVK*LRQENQWNSRGRDCSEPRSRHGT L PWTTEQDSIPKNKTKPKYKIS
10980	24881	A	11073	139	3	KLACGGRHLSPQLRLRLREDHLSPPG *GYSEPWSRYCTPASRA
10981	24882	A	11074	17	421	DHVGQPRWLMFVILALWEAEPGLLEP KVQDQPGQNCSSLSLLTIKKKRNFP GGTQLCSQLRLRLRVGCCIDPKLHNC L PAWMTERDPTFKRE*KKNDVLEAKNFT ILTFMNTTKEKMVAQRIGSLFHG
10982	24883	A	11075	412	1	QFFFLGVCCPTQIFGVGKKGEKKKKRG FPPRVFFFNPQIFSPFFPGPFFFLGK FPPFFGERFLFFSKSKFFPGVFKRGFP FPPKNFFFF*RI*KFWSPPKPPFFFF FFF*DRASLCHPGWSTVAQS*LTSC
10983	24884	A	11076	279	410	VFCVAGRDGAPGVKAHFFAAQKPDGG FPGP*SAGVGPPP IPR
10984	24885	A	11077	12	386	IAHLLLSFYHKDTGTLYLLFGAGAGVL STALSLLIRAEQGPGILVGNHDIYNVI VTAHAFGIIFFIIPILIGCYGN*LATL IIGAPDMAFPRINNISFGLLPTSLLLL AYAIVDAGARTGW
10985	24886	A	11078	412	3	LAILSLSLSLGFPYSLRYKNIKIRPINN PTMASKCSSKRTKRTSFTLNQNLMLKL IEKSTAKAKRLKVRPLVPVSQVNAEEK FLKEIKSAIPLNIQMIR*QTSIADMEK VSVL*IKDPTSYNIPLSQS*IHSK
10986	24887	A	11079	78	443	RHRLPSDTCLTAAPV*PCGSKKKKKKK KKKKKKKKKKKKKKKKGGGFKKNS GGQNFAAGGKKIFFFFGGGVFNPLWIF WKKTFWGGKISGQLSQKLSLWGEKKI FWCGGETSF

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10987	24888	A	11080	395	2	KRVPKKKPKKNSPPGGRKGSGPP*SPFFGGPDQPIF*VGGFDPEWLTPEPNFFFFKKNN*PGKGMPLILKSLGGWGKKIFTPGGGLPKN*KETPPPPPGGKKIPFPKKKKKKKKRAAADLELVPTRP
10988	24889	A	11081	24	182	TVSTTKCFSLLIPYYGRKDME*KI*IIQKKKKKKKKKKKKKKKKKKKKKKKKRGGPP
10989	24890	A	11082	173	3	NNVICYILYIPSVPKYKTTLNMGRSAFFF FFFFFFF*DGVS LCHLGWSAVARSWLTA
10990	24891	A	11083	284	391	SVAHACNPGTLGG*GEQITRGWEFETSLTNMEKARL
10991	24892	A	11084	257	3	IKKLREVNMLGWLYYMRBEARPDVYVHWRGPEYSSSLTKTIRNVIVKGHQHY*KASARGGGSRL*SQHFGPRPRADYLKSGVDRDQ
10992	24893	A	11085	42	171	ARRMRAGIHRVSYQEGLDLLTS*SAHLGLPKCWEDRREPLRLA
10993	24894	A	11086	176	325	FKRSKKKKKKKKKKKKKKKKKKKKRGGALLKKF*FKRSKKKKKKKKKKKKKKKKKKRGGALLKKFLGGPQISGGGRFFFFF
10994	24895	A	11087	67	379	KKKKKKKKPKTKKRTGFPVRQNVWRGRLSPGRAPAEQPGGSGTESPPLLVGRCILILGLREPGVPPAAYGRFLRDYMNISIQGKLEKORPQ*GLPSLTGAELIKH
10995	24896	A	11088	128	326	KKKSGGGVFFFTIGGGGHFPGGGRFFFFFFLGGGFFFKLFFFF*EKFFFLGGNLVKHSSKKSSWVGW
10996	24897	A	11089	109	2	KTHSRPGTVAHTCNLSTLGGQGEWIT*GQEFETSL
10997	24898	A	11090	52	347	DHSLLELQMKLYASAQAAITKCHRMGGNLNTHFLFLFLSLFFFFLKKQSLALPRLKGRGPILVN*KLPLRGKRDSPASPPQCVGITGLAHPRLILFF
10998	24899	A	11091	386	48	IHLQPPLOICTLKFFTINKNPHLFLTGCPKYALIFLCFGALVKTGPHHVGGAGLQLVPLCPDRLGLPKCSD*RRPPEHPAKKQFFIDRVMLCYPGWCPALGINPSSPVGLPKR
10999	24900	A	11092	164	3	VYSLLLRCPPFS*ALTAKFINRCTYIHVCMYMCEPYAYTCLYTSTHIVCMYIY
11000	24901	A	11093	148	325	CLKLQPPGLGVVAHACNPSTYFISYQ*LSPVIPALWEAKTGGSPSEVRSSRPARP
11001	24902	A	11094	162	3	LGGLKRPFIFFPWGGKFFPPFFFFFBIESPSVAQAGVQ*CNLGS LQPASGRV
11002	24903	A	11095	259	358	LRPGTVADTCN*GQARWLPVIPALWEAKAGGSLEVGSRLAWP
11003	24904	A	11096	254	2	SWGFIPEERERENRYWDRQQGHAIYSNIVINAFLYRYTEREKPGVLSLSPRVCSGMIVAHCNLSLVGSSHSPPAAS*VAGTTG
11004	24905	A	11097	132	3	KKKKRQPRVVAHACNPSTLGGCGGWIT*GQKFRSLVMNVKP
11005	24906	A	11098	2	455	LNLEQLIEPLEVLWTAHLEALDPSSRTFVLLAFALL*LPWLQAGAVQTVPLSRLFDHAMLQAHRAHQLAIDTYQBEETYIP*DQKYSFLHDSQTYFCFSDSITTPYSMBE TOQKSNLELLRIYLLIESWLEPVQFLMSMFGNNLEYDT
11006	24907	A	11099	2	375	QLPEPLMDLWTGDLVAMAPGSRSTSLLLAFULLWLP*LEAGAGQTVPSRLFDHAM

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						LQAHRAHHLAIDTYQEFETYIPKDQKY SLLHDSQTSF*FSDYIPTPCSMEEETQQK SNVELLRICLLV
11007	24908	A	11100	1	359	LQLPKPLTVLGTALHPAMCLAYATALIL GCALLCLA*VE*ARAAQTVQSNF*DHA MLQAHRAHQLAIDTYHEFBETYIPQDQK YSFLHDYQTSFCLSYIATPSNMEEETQQ KSNLELL
11008	24909	A	11101	1	370	LPEPLTDLWTAHLVPMAPGSRTSILLAF ALLCLPWLQAGADQTV*SWLFDRAHL QAHRAHQLAIRTYQEFETYIPKDQKDS FLHDSQTSFCF*DSIATPSNMGETPQKS NLELLPISLLL
11009	24910	A	11102	2	361	AHLAMAPGYRTYLLAFALLCLPWLQE AGAVQTV*SRFLDHAMLQAHRAHQLAI DTYQEFETYIPKDQKYSFLHDSQTSFC FSDSITTPCNMEETQQKSNL*LIRICLL LINESWMEP
11010	24911	A	11103	8	366	PLRALWTAHLAARAPGSRTSLLLAIAL CLPWLQEAGA*QTV*ISRLLDHAMLQAH RAHQLPIDTYHEFEKTYIPKDHKHSFLH DSQTSFCF*DSIATPSNMDETQQKSNLE LLRIFLL
11011	24912	A	11104	3	341	EPLDLRTAHLVAMAPGSRTYMLLAFAL LCLPWL*EAGAAQTAPLFLFDHAMLQA HRAHQLYIDTYQEFETYIPQDQKYSFL HDSQTSFCFSDSISTPCNMEETHQRSNL E
11012	24913	A	11105	240	329	RNWPGAEAHYYPSTLGGGRGRQIT*GRG FE
11013	24914	A	11106	2	316	HEERERERERERESAIYRQIHTQEGELT ELVFFYRRPAPSGLKFTFVYVQEHILGV GGNGLSPLQIGVILRDGRGLAHIRGTR NKILRILKSQGRAPDLS*DLV
11014	24915	A	11107	169	1	EDGHSGSLHKSQQKQPAWPSMVTHTCNP NTLGGRGGWIT*GQEFETSLTNMEKPCCL
11015	24916	A	11108	192	355	GMSLTGHSNYIILNLFNFWPCVVAHTCN PMTLGGQGGRFT*GQEFENNLAYRGK
11016	24917	A	11109	145	383	EVNKDKGYHVSQGIQSFSYVAVYVPRK LIYTMMTIVNSALLYTELVICQGRRLV FDEGF*FWFFETESCSVIQAGBQ*CDLG
11017	24918	A	11110	199	400	TRAGFFPPFKKFLKGGPGGAPPFNLFN GGRGGGFF*IPKKKIYPLLLPFLKVQKT PSKPPFFFFFLRQVLLCCPGWSAMAR SRLTRA
11018	24919	A	11111	373	177	QFETSLGTMSGSPFYLN*KSARCGHTC MRFQLLQQRSDHLSGGVHRCSNP*LH RCTITWVTK
11019	24920	A	11112	204	399	NHFWDVVYHFSSPFFFFFEKNLCSVPR AEDQGMNLS*LNPLPPGLKQFFA*PSQE AGIIGPGHH
11020	24921	A	11113	192	16	KKTENNKR*RGYGETETPAHCGRACKLG *PLWKPV*QFLKKLKMCLPYDPTIPLPA IFS
11021	24922	A	11114	113	369	AGGGQPNLFLQKPGPPGLKGPPLPLEG GGNYGGGPPSRGIF*FFEKKGPGGVPKV GPNLRG*RDLPAPPKGAHPLNGFFSR N

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11022	24923	A	11115	250	387	ILCDVEHSLWPGVEVHAYNPSTLGGQDGR IA*AEFETSLNNIARL
11023	24924	A	11116	192	1	VCDLFWKPSPHALTRRRTSVFHLKR*FS WLGAVAHTCNPSTLGG*GFWRT*AEF ETSLGNMV
11024	24925	A	11117	289	202	VFYQ*KFIRKKKKKKKKKKKKKKKKKK KKLSKKIKKMDQQKLRSPTIK
11025	24926	A	11118	412	421	RA*PTEQVTLGITQSVSRGHINNRVHD LDVGS*HPDGAAIKGSFVQRLKGY
11026	24927	A	11119	16	472	DRLKPSATHAFADAYHIGKANP*PLTGA LLTLMLTSLTM*VHLHSITLLILGLLT NTLTIYQRWREVTRESTYQGQHTPPVQK GLRYGIILFITSEALFFAGFF*AFYHSS LAPTPQLGHWPPPTGITPLNPLEDPLLN TSVLLASRVSI
11027	24928	A	11120	304	346	GLWHATGITP*PLTGSF*LLMLTSSLAM *FHYHSITLLILSLSSLTIT*WREV TRESTYQGHHTPPVQKGLRYGIILFIT EAVFLARFC*AFYHSSLAPTPQL*GLWH ATGITPLNPL
11028	24929	A	11121	174	420	FISALLKSAIQNNAMFSTYYALTCTVG TAVSWSSVS*PQRNMMS*VHAPAMAGR LVCHYIRVYRRFEHVCKRAVHGQYP
11029	24930	A	11122	299	466	IFILHEICITFFPETRHFC*AEVHWCS LGLLKPPPPGLRCDPSTSPSRVAGTRPS
11030	24931	A	11123	138	1	NPFNEKNPPKPGPKNAFFFFFPEMES CSVAQARVQ*HDLGSLQP
11031	24932	A	11124	241	499	NQRERS*HLYLLYNTVCLTHGLPILITY SAYQLAYDLLLRDALRLQADLADRR RGLQPKKRFAPKTRRKDAASSTKVDAAP GI
11032	24933	A	11125	252	391	PLSLDLQSNASLSHFTSPPLMPADR*LP STNHKNI*TLYLLFGAWA
11033	24934	A	11126	45	459	AFLKNHPLET*SNHSFIDLPTLSNISA* GNFG*LLGACLILQITGLFLAMHYS PDASTAFSSIAHITRDVNYG*IRYLHANG ASIFFICLFLHSGRGLSYGAFLYSQT*N IGIILLATIATAFIGVLP*GQISF
11034	24935	A	11127	109	301	QDSLMRKSKNRSPSHER*RSKCLERKR SGDKKKKKGGPPKKKIGGPPGGQME LKPFSILGGF
11035	24936	A	11128	322	2	SCHHVSSLGDRARPCLQKEKKKKRKKVG DFNTPLSIMDGYQHWYQARKIIIMDGT TK*KITRK*KIRNQ*DLTDVYRTLHPRVK YTLSCAYGTFSRTHRIRGOAI
11036	24937	A	11129	182	2	FLPRGFQPPPVVPGPLGFLFPSSRD PGFSPMPFFFFFFFETESCSVS*AGEQW RNLG
11037	24938	A	11130	138	1	GWVFFLVVFSFSLFFFLR*GLSLSPTL ECSGAITAHCSLKLPGLS
11038	24939	A	11131	304	83	WKKTDFPRKGRNSASRLPSDSNCNSSL LQGLSLLYRFWTYHVTGKGSQSRPQEQ VLGYHARKNSR*VHRVK
11039	24940	A	11132	247	225	KNFWGGPPLRGCKKNFFFFFGGYYK*L LLCLVMYI*CV*YI*HKRIISDPKKK KKKKKKKKKKKKKKKKKKKKKKKKKK K
11040	24941	A	11133	242	3	KKKKIFFPPRYFWAPPYFFFLGPPPPFF

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						FFFFFFFFFFFFFFFFFVF*TFHLS PRLECSGTISAHYNLHLPSPDC
11041	24942	A	11134	361	2	ASQSAGITGVSHRTRPTHGFKDT*RKPA EPEVTIH*I*ITLMSCNIBSPEKVCADL IRGAKEKNLKVCRPAGTPIKASRITTRK TPCEGSNTRDRFQMRIHKWLTDLHSPFD GRVGGRV
11042	24943	A	11135	1	370	IRQTFQKREIVGIILCYWNVGYYSQHLH *SSRMLWIFHYRVVISVILVILVPH EKKKKKKKKKKKKKKKKKKD
11043	24944	A	11136	273	2	GGRAGQQILFCRGIWLGPPRSCQCTFRS PPGLAL*PWECSLEPPALKIRFSPFLPF FFEMEF SRLSPRLCNGVTVAHCNLRLP GSSNFP
11044	24945	A	11137	130	354	GQLNKLSGPYPENVGTYLPLVNLPLAQP VIYSTIFAGTLITALSSH*FFT*VGLLEI NMLAFIPVLTKKKKKGGPL
11045	24946	A	11138	366	2	LVEMGFLRVQRNGLYLLTS*SARGLSK CWDYRREPPCPASDWVFILTSPLIHLD GKEHTHTHTHTHTHTGLGICQSSLGKQS GGWGLSANRGQFSPFAVCLVVSFLPEV PVVTSALFT
11046	24947	A	11139	228	1	CRAGRGLPAVLIILFPPLIPTSKYLI NNRLITQQ*LIKLT SKQMIAPNTKGR T*SLILVSLIFKATTNLLG
11047	24948	A	11140	157	337	HIPTPPHTTCPERPSIRHNSIYLLKRYC LLRIILSLLPLQTS*PLTGALSLLLMT SGLSM*SHLHSITLLALRLTYTLTIYQ *WRDVSRRHSTYQRHHTPPVQKGLRYGII VFTTSKDIVFSGLF*AFYHSRLAPTTQL *CHWPPSGITPLN
11048	24949	A	11141	188	3	IPTPGGPPPLPPQKVLFPKGNPRAPPGV FFFFFFETDSRSVVRLECSGVI*AH*NLH FRGSR
11049	24950	A	11142	224	3	SVSSPCISNTHKVDVRSSALLQESTSSR EVMTHGFHYLIYET*LRSLAQ SARLAC SGTISAHCNLRPLPGSSN
11050	24951	A	11143	262	371	SYCGPGVVAHAYNPSTLGGRRIT*GQ EFETSLTN
11051	24952	A	11144	244	379	TIGKQRCHAGIBEVSDSSQAPWLKPVIP AL*EAEAGGSLEPRSLR
11052	24953	A	11145	1397	1565	DRLESILEMHIPGVYPNQWNTNFYLFYI FEABSHSVAQTGLQ*RHLGSLQLPPQV
11053	24954	A	11146	284	1	GRGRQGGDSSGKGEGRAMDITGGLVGK QGAGAEAFVEVWEKELRGFKVEGEDMD KERVVD*GL*GGRERERERERERERE RERERERESLV
11054	24955	A	11147	64	286	THALAWTRNQRIGSGHGAMCLYSHLLRK LRQNDHLTPGV*KCLEL*LHH*TPTWTT KPTAKAIFFNKKKDSWD
11055	24956	A	11148	230	358	VSVSLIIFATTNLLGLLPYSFTPTTQL SINLSMAIPL*AGAV
11056	24957	A	11149	81	367	QTLRTKMKNVVASLIDPTILGLPAAEL IILFPPLIPSKCDVINRLMTTQQ*LI ELTWEQMITHNTKGR*CLILECLIMV IATTKLGLLP
11057	24958	A	11150	257	2	SVCAVITKYLRLGCFADAADTQRPLPPA TVKLTMPFNIAHGEPLGCI*LFVDKV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PKTAENFHALSTGEK*FSYKGSCTPHRILP
11058	24959	A	11151	257	1	WRCGEKETLIRCWWECKLVQSLGRTVWR FVRELKLELFPNPAIPLLGIHPKEKK*L DPCTCMFIVALVTIAKMWNQPKCPSMDLV
11059	24960	A	11152	17	367	NHKDGKKTEKKQSTSPPOKDCSSSPAM EQSWTENDFDELREEGFRRSNYELQEEI QTKGKEVKNFEN*DECITRITNTENCL KELMELKAKARBLCEECRLSSRCQLE ERVSA
11060	24961	A	11153	213	2	TFCHFFFFETESGSVAQPGVRWCDLGS LQAPLPGFTPFWSWRQLQ*AEIVPLHSR LKLHFKKKAGVFSC
11061	24962	A	11154	1	347	GTSNHFFPLYTYQVHNSTDYPRNRCCLN PSLRHTSSKPLPARPHIMTHQSHAYHI VKPSP*PLTGALLALLMTSGLAM*FHFH SITLLILCLLTNTLSIQ*WRDVTREST YQG
11062	24963	A	11155	223	3	YSTNLKILRNHFILFF*DRVLLCLPGWS AVASSRLTANSASCLSLPSSWDYRRAPP HPANFCTDRFHHVQGV
11063	24964	A	11156	143	1	RGFLNQCPSONFFFFFETESCSVTOAG MKWYDLS*MQPPPPRFKLIV
11064	24965	A	11157	149	355	LQPLPPGFKRFSCRLRLTSWDYRKDVDS ALLSNYVT*KYISKTLCRHQSPDIVREF LTAMKSHKLTQVG
11065	24966	A	11158	156	370	RSDGCQKIPRNMLGGWSVLHHTVDEQ*G PNRYIKKCSASLIIREMHIINTVRRCLT PATMATVRRKTTSVG
11066	24967	A	11159	298	4	HFQVVMWRQLVKGRLOAQKNAAFTDSH THLCYLKCVYFCVCMCICVFCV*SR AL**SLYLFLCIKAVKAGHSVSGLESQH YGLRQADHLRSGV
11067	24968	A	11160	364	285	NSNGKIKILKGK*PPPPKKIFFPKYPQS FFLSPP*KKTNFPHPRKYLSPPGIFLK APPPLIFFFFFFFFFFFFFFFFFFFWG
11068	24969	A	11161	198	406	KSVYMTLKKRGSFHERGDVPAICNFFF *IHIMCVYIHICVYIYIYTHIYIYTH QIYIYIYIYIYIY
11069	24970	A	11162	95	376	KIITKHNIARTNPYTFICIMN*LEITLQG EPKLRLPPKPKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKRGGGFKKKPGGGP KIRGGEKIFFFFLGGD
11070	24971	A	11163	343	391	WR*LSSTNHNDILTLYLLFRARAGVLRS AVSLILAEQQQPGNLLGDDHIYSAIDP AHAFAIMFFIVIPMIIGGFN*LLAVRN GAPEMAIPHINNISC*RLPPSLLLLLAS AIVEAGAGTG*TAYPPLE
11071	24972	A	11164	1	158	QPMTPNRGFLSP*PLTGALSALLKTSGL AM*FHFHSITLLILGLLTNTLIYQ*WR DVTRES
11072	24973	A	11165	265	466	KLLTSLSFNLLRETNQVGLLELSQARY KKTPLRGTVAVHCNPSTLGGQGWIT*A QEFETSLANMA
11073	24974	A	11166	204	458	KRCLLPLPDSNTQSSQCRREQIGRAIR KILTFETQNIKRLKTEKQLLKLE*SK ITACNLDLPSSSPPTSASQSAGITAG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth ^{od}	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						S
11074	24975	A	11167	256	3	KILFFKPGVLSPPWGGVNFQLMPPFQGG PPKKKRGPLSPPKKGPPPPPPPPPP*ESR SLLPRLECSGAISTHCNLCRLGSSRTRG
11075	24976	A	11168	1	457	HRTPSVRTPNCRGDPRVRSSTNHKDIGTL YLLFGA*AGVLSTALTLLIRAELEGQPGN LLGNDHIYNVIGTAHAFVIFFFIVIPPI IGGFGN*LVPLIIGAPDMAFPRINNISC *LLPPSLLLLRASAIVEAGAGTG*TVYP PLAGNYSHPGAS
11076	24977	A	11169	343	428	GR*LFSTNHKDIGLLYLLFGA*AGGLST ALSLLIRAELEGQPGNLLGNDHIYNVIGT GHAFVIFFFIEPIIIGGFGN*LVPLIIGAPDMAFPRINNISF*LLPTSLLLLLAS GIGEAGAGTG*TVYPPLAGNYSHPGAYV DLT
11077	24978	A	11170	91	2	PRQDEPFFFFFF*TESGSVAQAGVQWCD L
11078	24979	A	11171	219	1	IFKSKILCLEPPEPNNNNNNNNNNNNNN FFMRHGGACCSPSYLG*GERMT*ASRV AGTTGVCHYAWLIFVFL
11079	24980	A	11172	292	365	RI*SLGQAQWLTPVIFTLWEAKVG
11080	24981	A	11173	251	1	ICDLQILTHGITTCKMGLTTLFVSGIT FLIHHSLAIKFGV*KNPS*LGTVVHTCN LSS*GGRGGRIA*AREFETCLGNIVRP
11081	24982	A	11174	200	407	KIFETDVYKCSNLCWASISFSNYPFG GPFYLN*FLSYFSFLETESHIVAPLE CSGMLAHCNLC
11082	24983	A	11175	11	155	STNFFLFSETGSGSVLQAGVQWPGDLLL ASSHSPASAS*VSGTTVDAA
11083	24984	A	11176	140	1	PSTFFDVVAMRRVSCSLSGDKGQV*WLT PVIPAIWEAKAGGSPESI
11084	24985	A	11177	210	1	TDELLLLMDEQRK*FIEMESTPDEDAVN IVEMPMKDLEYIINVVD*VVAGLKRTDC SFERSSTVGKMLSN
11085	24986	A	11178	133	148	STSTR*LFSTSRKDIGALHLLFGA*AGV LGTAVSLLIRAWLAQLGSNKEA
11086	24987	A	11179	236	1	KFWKKDPLTKGGCPLKKKGGGGIFSKKK KNVFFPKKKFKGGKKKNFFPKKKKKKK KKKKKKKNKE*LFISFAHIAVHL
11087	24988	A	11180	210	1	QSLGQENLQVFFFLFGP*PNYLDKGEKW IRVGKIWGHLLLLFFETESRSVAQSPRL CSGALAAHCNLC
11088	24989	A	11181	292	348	KKGALFFSPGG*KNFPPGGKKKGPLFS KKKNPP*KKPGEKEKTRFPPFLGGLGG GFPLAPGGKPPRNRVLAPPNPGGKKKK KTPFSQKKKKKKKKP
11089	24990	A	11182	168	3	KPEASMLRMDFFFF*EAGSHSVAHAGVQ WYCSSLQPTPELSDPLAPSSKVGGIT
11090	24991	A	11183	87	351	KGIKWSLNIQRGVQPHLSYNYSFFSFF S*DWVLLRLRLECSGTTTAHRSNLPGSSD PPTSASQAAGTTGMHCHTRLIF*ETGFH HAVQ
11091	24992	A	11184	55	344	TSLNLCFFFFFWGEEKSPFLPPGGDEGGL FGQLDTRPWGIEKIFFAPPP*KGKRGVP PGGEEFKNPPAPKGEPPPLS*KK*NQPGQ GAPPCYPPFLGGGAKKIFSIPOGRVSN* PKRGPSSPPGGKKGDFSPQKKKKQKQFR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EV*PNSPSGAP
11092	24993	A	11185	344	190	LVETRFHRVSQDGLNHLTL*STRGLP KCWDYRCEPPRPANTANSLNPFM
11093	24994	A	11186	135	3	IFPKVFGGPPFFFF*ETESRSVAQVG VQWCNLGSLQAPP PGFT
11094	24995	A	11187	305	14	IMLITSIRSRSLSTAEKGLSRLRYCG RVAKYLINRLITRE*LIKLTSKQMIT ILNTKGR*SLILVSLSVVGYHLP*G* FD*SLLLY
11095	24996	A	11188	198	1	LEQTFNMFPNPKSIISIPSGFLFKIS FPFLFF*DEVFLLSRLECNGTILAH CNLCPLGSSD
11096	24997	A	11189	352	3	QLCNTPLPKTNHMLTSSNANTLIYRRS AIAAASSPPILPPASKILLNSRLITPHQ *LIKASKQMIAPNTKGR*SLILVSL IICFEVSLISHCWVISRLLMRYLEVGI NRGG
11097	24998	A	11190	270	137	CIINRLVVCVYIYIYIYI*YFYMYV YNILCILGHRRESGVI
11098	24999	A	11191	18	342	ACRKRKMSKFAIRATGNCYISCTPCS ISFPHPK*MPCYQKKKKKKKKKKKKK KITV*K*SKTKNIKGLGAR*ELSLA*L LGEPIPAKGHPMLKWEICKRP
11099	25000	A	11192	169	3	ERSGIIRVYQD*NOCLAWSLA*KIHPW LAAVAHTCNPSPSGGRHGWT*GQEFK
11100	25001	A	11193	407	1	KRACFRWLTLLISTLWEAKQENCLNAGV HDQPGQHGETPSPQIKKSAWHGGPRL* EVRWED*LSQGG*GYSEPCSHCTPAMA TERDPV*KQKRSIPWELASERKDSGR RWLVREMPSCQASVIQVRRISF
11101	25002	A	11194	110	412	VCGFRLHSPAILMPLMPSYFRRHSNT EIKPISNPTVASKRASKTSLSLTNLQ KLEMIKLSBEAT*KAHVQKLGLLHQKV SQVVNAKEEFLKEIESA
11102	25003	A	11195	34	155	AWHEGMHVSQDGLNLLT*DACGLPK SWDYRRKPPCPA
11103	25004	A	11196	289	453	NQPGKSTFMISSTFHFMFEFTLVHAGV*W LDLGLLQPPPPRFKGFSCHLHPSGWDR
11104	25005	A	11197	177	432	KWEKQATLGGGNFPKGPTRVGRNFBK LKGNPPFLCL*KRGKGDTPWKKPAPS GERGIPGKKGKTPPGFKGPMKIKRG K
11105	25006	A	11198	139	3	AMVSLSPRLECSSMIAHCSLGLSSD PPTSAP*VARITGMHHP
11106	25007	A	11199	150	492	GDPLPGHHPV*EVRREFARQLPRLRSE PLRPVATPSGK*GASLSGSHPIQEGGG GOPLPGHLPHPGWRSGVKPPGQSARPG GEGHLLPATPTGK*GGPQSQPHLSGGR RE
11107	25008	A	11200	239	64	YQKYYYYYFF*ETESRSVARVKSSGLIS AHCNLHLPGRSLQLCLFPTSAVFGQESH IT
11108	25009	A	11201	31	396	ILTMREIVHIQAGQCGNQIGAKFWEVIT DEHGMPTGTYHGDSDLQLDRISVYNE ATGGKYVPRAILVDL*PGTMDSVRSRGP GQIFRPDNPVFGQSGAGNNWAKCHYTKG AELGDSVLDV
11109	25010	A	11202	85	407	VLLPHSEALEGADTMPHSYPALSAEQKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
						ELSDIALQIVSPGKGI LADECVGSMAR RLNQIGVENTQENRRLYRQVLFNADDRA KKRIGGVIFFHETL*QKDDDGVT
11110	25011	A	11203	302	115	THLDHVAIYLSIYLSIYLSIYHLSIYHL SIYLCRF*LID*DRVSLYFSGWLQMPGL KPSSCF
11111	25012	A	11204	130	348	GNAVGGPCSVLVQRT**IPALTFFSTCL DSKFQRDVLTRTDFSNFTSNTVAEIQAL LTSQGESGLDGALGWQ
11112	25013	A	11205	232	62	ISARNEGFTLN*RTFFFFFSSHCLSR LECGMILAHCNLQPGESLEPGRQSLQ
11113	25014	A	11206	161	2	KKKGFLPLIEPFCTQEIQLRLGVAHT YNPSTLGGRGGWIT*GQEFKTSAN
11114	25015	A	11207	251	3	PNHLPKAPSPNTTLRIRFQHLNFRGAQQ TFGLQHKLTSKQMITIHNTKGR*SLIL VSLIIFATNLLGLLPHSFTPTTQL
11115	25016	A	11208	145	287	GFRLL*INQKYSFLKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKK
11116	25017	A	11209	436	110	ISGRGEQKFYFSPAPFFRGINPPPLGG E*NQNLKPP*KKIFLGSPKVPKKKGPGQ KILKKGPGGGPPLFPPPLGGQGGFPF SQGFKTPPGKKKKPPPKKKKKKK
11117	25018	A	11210	217	2	DKWSVLHINYNLSSSLVHVLFKYLEN* K*KKNLWPGMVAHACNTNLGGQGGRIV *AQEFETSMGNTVKC
11118	25019	A	11211	146	3	QKVSHAQYRCLSWGYFFFIPLFLETRSRS IAQAGVQWRDLGSL*PPPA
11119	25020	A	11212	187	384	GLICFYLTCFYFIFFYFILFYFSLLCYVM LCYVLCYVMLCYVMVCYVMLCYVI*DRV SFCHPDWSAA
11120	25021	A	11213	373	482	MIKLRLRLGTVAHTCNPSTLGGRGQWIA *GQBYKTS
11121	25022	A	11214	64	362	ITGVSHFTQPLPFIGGLALSPKLECRGM IIAYCNFELPGSGDSCHLSLPSSWNYRY MPCMP*SKKNF**RQGLTVLSRLEKDY LL*DFSALRSFPWGR
11122	25023	A	11215	181	368	CDSAVPLLDIYPTFEKADLKKIRIPMFI IALFAVAKR*KQPTYPSIDKWKILWAG CGGSRL
11123	25024	A	11216	268	369	TTRPDMVVHTYNSSTSGGQGGTIT*AQQ FKTSLT
11124	25025	A	11217	90	3	IGQAQ*LTPIIPALWEPKSGGSPEVRSL
11125	25026	A	11219	277	272	SLTAPGL*SQLRLRLRWEDHLSLGQSSF SEP*SCPCTPAWVTQ*DSVSKKKEKKKE KKRKEKEKVNQTPKATESPGQALIGSHS LQVQKRVYAHPIIL
11126	25027	A	11220	19	343	LELEVEPEDVSELLQSLDKNYLSCFLEKR FLEMKYTPGEDVVNTIKMTEDLKYNNTD LVDKAAAGLERINFNFEQSSSVGKMLSN SIWYSEIFYEROSQFMWQT*LLA
11127	25028	A	11221	266	356	FFEMESHTVA*AGVQWCDLGLLQSLPPG FK
11128	25029	A	11222	105	2	RFVCSTIKVLRDLSSARSNPGRFI*TSN SRPRKS
11129	25030	A	11223	145	350	RKGRQLLD*DLGWV*WLTPIIPILWEAB LGGSLEARSSRPAAW
11130	25031	A	11225	155	348	PLFFFCFHNTFY*KSVCRFPPKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKKKKKKKKKKKKMEGGGGCANTKELY GENRKPPPLFFFF
11131	25032	A	11226	271	3	NFLSVFNFTTRICLGMCFLLIFGGS LKYQLFLAQGFFFLHYFFTSSTHSSLL Y*MLDFLDLFFLYLFFCNFNFSVFLFCI LSKFF
11132	25033	A	11227	3	413	SPAEPHRSYTMWNVKGVNGFGRIERLV TRAAFNSSGKVDIVAINDPFDLNYMVYM FQYDSTHGKFHGTVKAENAKLVINGNPI TIFHERDSCIKRGDAGAEVYV*STGVF TTMDNAGAHLG*ATRGIIISAPSAD
11133	25034	A	11228	48	413	VEVLVSCGFFFFFWWEKKICFFWPQKK RGKIGGTGTGFGPKGKGNFRGPPPKNKEK GGPPPPNNFGLKKKKFYQGGQGG*KT RNFGKPPAPNPPKGGDLGGGPPTQGGNG FLKKKKKQKK
11134	25035	A	11229	172	404	EFENSCSPGWQRRGVMIPGVTVEDMNOQ EFIRALVALLKKSRLKVPEWVDITKLA KKKELT*DEKWFT*AASTT
11135	25036	A	11230	247	2	QPKKKSVSKKKKELPCDPAIFLPGIYP KEKKSVMKDNHLRVYCRVFTIAKIW NQPKC*SGDK*IKKI*YIYTVDLRR
11136	25037	A	11231	1	372	TETTVEVANCELDRLTKSERORFKEE AEMLKGLQHPNIVRPYDSWESTVKGKKC IVLVTELMSTGLTKT*VHQYYS*PRSM REFDFLNFRSTSFTLVVQPKGTVLPTV TVLAYFLAHKVL
11137	25038	A	11232	311	464	KKATPRNLCKWPGTVAHACNPSTLEGRD GWIT*QGEFETSLTNMVP
11138	25039	A	11233	64	418	VPVASSRRRRRCGRVGGGKAMADLDKINI DSIIQRLLEA*GAKPGKKVQLHENEITG LCLEPREIFLRQPIIL*LVAPLKICGDI HGPYYDLRLFEYRGLPPKSNYLFLEDY VDRROH
11139	25040	A	11234	233	421	PTTSMRSRLRGASS*KKTAGPQQRNL EPALPRRWGGRSADNPPSGSLRKSGKNM QKTPGTA
11140	25041	A	11235	343	1	NNTHGLSHSSVGRNPGAVSGSCMSGIK LSEGLRSLLEAVCISRAAVIKCHSWVAS NNRHFFSPSSGG*KSEAKVWAGPCSL*R RVPSLELPASGGSRLCLVCGCVTPPSAF TW
11141	25042	A	11236	122	419	RTPRGPKPNPGLQRTFFLIGGRITKYL GIFGKDLFWGGKNWDTLLEKI*RSREN KNF*REKWNLPYPGCLKNARQQHFA HLLILRDTTKTYMLAF
11142	25043	A	11237	1	379	AFNHLHAGHGLSGAAMKSLVLLCLAOQ WGCHSPHGPWLIYRQPCDDP*TEBAS LEAIDYINQNLPGYKHTLNHIDEVKVW PQ*PSGELFDIEIDTLETTCHVLDPTPV A*CNVRQLNEHAVQ
11143	25044	A	11238	1	397	QMTENRGLPLCPKSLDRSSHVISLPLHS ATHTRPTNQHTNHPMMARRSTRKHRR APHTTCPKRPSIRDNPIYYLRNFFLRRI FLSLLPLQSPSPYPIRRALAPNRHHPAK SPRRPTP*PLTGALSALLKTSGLAM*FH FHSIALLLGLLTNTLTIYQ*WRDVALE STYEGHHTPPVQKGLRYGIIILFITSEIF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFAGFF*AFYHSSLAPTQLGGHWPPTG ITPLNPLEDPLLNLSVLLASGVST
11144	25045	A	11239	267	3	FVSVRITPIYASAAATWLSYVWVWASSPN VCPDGRVALSPRVECSGTISAVRNRL PGSSDYPA*PADGWAPPQYRCPPRL ANF
11145	25046	A	11240	391	31	VFFFFFFFFFFFFFFFFFFFFFFFFFFFF LKNPFPPPPNFFFCPKF*ILFLN*I*F *IKF*I*KLPGFFLNPPFFPPFFFP GALFFFFFF*EGVLPSPGWSAMSHLLS EKRLTPRMSYN
11146	25047	A	11241	371	491	KIFLCWARHDAHACNPSIFRGQGGHIT* GQEFKTSANMV
11147	25048	A	11242	1	221	HRIDPLCRNSARAFFFLSTGCHRVSQDG LDLLTS*SAHLGLPKCWDYRCKPRLPAL NCFERTISQLNLNLCKID
11148	25049	A	11243	382	333	TYKIDFKTF*RWFHPNISRVEAEKFL SRGQRGDFLARPSSESPGGFTLSVR
11149	25050	A	11244	169	477	TQKDEKSTTTTKNAENSKGQSAVSSPS DCNTSLARAQN*EEAEMDELTEVGFRRR VIMNFVKLGHILTQCREABNDKTLQK LLTSITSLAWNINDLMELK
11150	25051	A	11245	200	462	SLIYNELCTIHILYQYVVA*QRS*CFQ LMSFY*RTLKNLKESLCKVALLYPSFLK WKRGLGTVADT*KPSTLGGQGGRIA*A QEF
11151	25052	A	11246	484	301	IFCEKKGL*FQLLRVRWEGPFNPGNQ CS*LLSSPCPPGWITE*DPVSQKKKERK RNQVMELVSAQENKNKPRSVGLQACARS MLAFSTTPR
11152	25053	A	11247	226	458	NTVAVDWGPCFFSLLLSHAENCDMWFT KIELFIFTNHLKQDLEMLW*GQAHAC NPSTLGGRGGWIT*GQEFETS
11153	25054	A	11248	304	436	SPSRCK*KIG*AQWLTVPVISTLWEAKV GRSLDPNRSRSATWMT
11154	25055	A	11249	216	451	THKLYFYLYGYNPMYIERETGSCSIA* AGVQWYSHGLLHP*PSGLKRSSQVAGVI CLANFFFLKKWSLVVLPRLG
11155	25056	A	11250	260	474	DKYFLLYPLKALNVVLGAHINI*KVSKI MC*K*DKNMYNFFFSF*DGVSLLLPRLE CNGTILAHCNLCCLPC
11156	25057	A	11252	193	496	MTSCYSFYL*IKDASMVKKKKKKKKKK KKKKKKKKKKKKKKKKKASSSQKAQDYS KADYK
11157	25058	A	11253	348	478	DLGWLKLGTVAHNTYNSSTSGGQGRIT* GQKFKTSANVVKPC
11158	25059	A	11254	174	475	MHHWVLIQDIDNT*NCNLHFSLCSQL KSIQKRRKKKKKKKKKKKKKKKKST
11159	25060	A	11255	292	48	LPLTCHRAVSHTHLAFSNPTAGITIF* TRSSWNAGTFIIFKIVTFLLFFFF*ER VSLKLTRLERSGAIPAHCNLHLPEF
11160	25061	A	11256	347	16	TQADWCINPPARHKSSPSPHPTQ*PS WLHLVDPAPGPWVELPTSPAPSACTPOQ LGSRWDPQPSKGCPCPSGRLGPGSPPO VGLGKAGWRSQALPVGLTRSIESHWW
11161	25062	A	11257	238	590	APGAYIFPQQHNPDSQVIFSLTASHLL ICSPLCISVLHFNMGNNIDENRNAHVHA RACAHATHHTHTHTHTLYLMNYRETL

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IV*MTTKELQYYINLVEKVLARPE
11182	25083	A	11279	334	488	PLNTCGY*NLN*NFQPGSVAPACNPST LGGQDRWIT*GQEFETSLANMVK
11183	25084	A	11280	527	356	FFVFLVETAFHHVAQDSLDTLS*SSRL NLPKCWDYRHEPQRQAKNVGEFSETRSI Q
11184	25085	A	11281	486	248	VRQLFSLLLPRLCNGVISAHCNLRLP SCDSSASAS*VARITGASGSQAVVLQVQ CLQPVQPGELLRVDLPQLVVLQR
11185	25086	A	11282	38	157	STGLHHVSDGVDLLTS*STLPKCWDYR HDPLRPASQRL
11186	25087	A	11283	474	339	FVFLVQMGFHHVQGAGLELLTS*SACLG LPKCWD*RHEPTDPAK
11187	25088	A	11284	2	462	LETTTRTARWNSVIALRHHNSCPYKMANL IDKVCVSDYSKDWPFPFLPLLRPPYCL RHNNMETRSINNPPWPSKCSSEKTNEEG MLKVEIG*KLCLLCQTFSKDMNAEKFL KEIKSATPMNTSMIRKQNRLIHDMKVL VIRIEYQASHNIL
11188	25089	A	11285	65	280	SRAVEFNLLTT*SACGLPKCWDYRCEP PHPASP*FSKLLSSNLKTYLSSL*DSHS GFYSFVCSLGLILI
11189	25090	A	11286	244	488	MRLGRVPSVLFYVVRMQREGIILEAENK PSPDIESVGALILDPTASRTIRNKILLF IIFPG*GILDSPNPV
11190	25091	A	11287	345	445	KRPGTVAHACNPHTLGG*GRWIT*GQEF WTILA
11191	25092	A	11288	223	500	SPGTRPKVLEQSTLGRQATILLGEGWL WGQSHRLGVQSQLCLCVLWDLTCSLSCS FQIIKLR*RPGVMVHTCNPTLGGCGGR IAQQGEFK
11192	25093	A	11289	157	22	LSCQEVKEIGEAEICWAQWLPPITPAL WGAKVG*SPEVRSSKPA
11193	25094	A	11290	305	497	KLVCNICYFKGVSFMVRELYCNKIV*WLG TVAHINYNSALGGACGWIT*GQEFETSL TNMAKPR
11194	25095	A	11291	478	1145	QHVOACPERPQMMGTLSRAVASKIGH SYSLDSQPARAVGKWPQQAQTRVTELT EATGKLIRTSIHGKPHQSFQPAATQK LRPASQGGVQMKTOGGASNPALQIGSHP MCKSSQFKSDQSNPSTVKHSQPKPFHSV PSQPKSSQTKSCQSQSPQTKPSCKSTQ PKPSQPWPQSKPSQPRPPQPKSSSTNP SQAKAHHSKAGQKRGKH*RANSRDL
11195	25096	A	11292	352	468	TFFGQHGKIPSLKIQKLAGHGDACL*S RLSPR
11196	25097	A	11293	295	24	ENIQGSKKNERQHMHNVGVTWNSNPGFV STWVYRNCLACLDISFSFIKWVKSHKDT SMGMFTAALFTIAKT*NQSTCPMSVDWN STTRTS
11197	25098	A	11294	274	429	ECEPVQTLWKIRKFLKLLKIELPSDPAI PLKGINLKEVKSVP*SDTYTPMCI
11198	25099	A	11295	168	469	PSLGNKSETSPKKKKNLFLGFPYFREK LVGILLKTVLQKGAGGVFFGPKNPPEKN PDPPLDSPPKTFRRLGAFVKTFFPKGLKA AVVFPALV*POGQMG
11199	25100	A	11296	37	348	IKIFNKTLYFKKKKTIKKKKKKGGGGL KRPRGGPRIYDPGARKNLPHIGTAKKH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GGYWEKNPHGGGGNTGPTPPQKTRPLGG KNNLKRVOGEKPRPRLGGGKTRSQLFSC HA*P*VQGEKPRPRLGGGK
11200	25101	A	11297	93	388	DEYASDNCCYPPGSSHDSQVKQIGSQFT TQIQAHNLAKPRRAL*NHS*PMEMRSK CLLLAYKKKKKKKKKKKKKKKKKKKK PKYLSRSGKDH
11201	25102	A	11298	61	243	YYIHRTTVFMCNM*GLKDNVDK*TIDLC LCKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKPQGGGA
11202	25103	A	11299	250	341	IYMSLTGLQNL*EHLTHKDSHKLQVK GWKNIFHANVNQKQTGVALLISDNIDIK ATTVKKKKKRENPTILNIYVPNTGAPKF MKHLLNLKNERDGTIVLG
11203	25104	A	11300	3	285	DAWERKKRSQMNQKTTNKVAGVSPYLSI MAWNVNELNFKIKRHRVA*CIKTKSMI CYLQETNFIKDTHERLKIRGWKKIFHPNR N*KLAGVVY
11204	25105	A	11301	175	407	AENNPDLVLQKA*TSRGTFMP*ILLRVK RGSNSRNNRCWQGWRTGMLLHC*QECK LVQPLWKTVWRILPDLESEIL
11205	25106	A	11302	75	280	YHLNLVLYPHPPKNRVC*KKKKKKKKKK KKKKKKKKKKKKKKRGGPLKKNLLGGP FFPGGKKKNFFF
11206	25107	A	11303	299	3	IHASFLFRGCITLAFTVRCSHRSITSSE TSDLTHYYYYYYYY*LASQSVALAGVQ WDQLGSNHPPTSAS*VAETAGASHHARL IFNFFVMEVSLYC
11207	25108	A	11304	137	323	FFTUNGRHRKEKSKNDQNLGLHDFLD NPLLLF*KYLGREKKKKKKKKKKKKKK KQKKKK
11208	25109	A	11305	64	481	RPTRPHVYHVKPI*PLTGALSALLMT CGLSM*FHFHSITLLILGLLNTLTIIYQ *WRDETRESTYQGHHTPPVQKGLRYGII LFITSEDLEFFAGFF*AFYHSSLTPTPOL GGHWPTGITPLNPLEVLLNTSVLLA
11209	25110	A	11306	142	330	FFTUNGRHRKEKSKNDQNLGLHDFLD NPLLLF*KYLGREKKKKKKKKKKKKKK KKKKKK
11210	25111	A	11307	259	440	RPWIRDNPYYLKSCLRTIFLSLLPLQ PRPYPTTRALSPNRHHPAKSPRSP*PL TGALSALLMTSDLTMLHFIYITLLILG LLTNTLTIIYQ*WRDATRESTYQGHHTPP VHKGLGYGIIIFITSKVFFARFF*AFY HSSLDPTPOLGGHWPTGITPLNPLEV LLNTVRL
11211	25112	A	11308	433	3	FPPDIRHSRSLGFPSPFGRAGFLNFAF SKGQEPALPGGFYYPSPKKNLAFCSPP LFYWGKFGSKFSLGVGPLFFP**SPKSF CQLENKGFPEKSFFFKFFPPAGGCVF FSEGGFPFCLFFFDVWLCHPGWISV ARS
11212	25113	A	11309	2	423	GRVGDR*LFYTNHMDIGTLYLLFGA*SG VLGTALSLLIRAEGLQPGNLLGNDHIYN GIVTDHAFDIIFFIAPIIIGGFGN*LV PLIIGAPMAVARINNISV*LLPPSLLL LLAYAIVEAGAGTG*TVYPALAGNYSHP
11213	25114	A	11310	234	1	TFFGKFPFCLKFKPAQRGGENTFGPFPF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						LVFFFFEMESRSVAQTGVQWRDLGSSN SPTSAS*VAGTTGACHHARLIF
11214	25115	A	11311	406	211	LSLFLHSLISTHGARTDPVGLVPTQDG LDLLTS*SAHIGLPKCWDYRRAPPCPAC GFDLHLPND
11215	25116	A	11312	379	398	KT*NPTVRGSIPLLNIPMASMTFSKKK KKKKKKKRGGLKKNPGGAKFNGGRKRK IFSLKGGEKKNPGGILEKKPFPGGKKKG ENPPKKNKGLREKKKF*RGKGKKKQKG GGKMGSSSAKTPTWG
11216	25117	A	11313	390	489	RYRLGVVAHACNPSTLGSRRWIT*QGE FETSV
11217	25118	A	11314	286	434	ILWYMYISIKLLKIIYKLGAVHTCN PSTLGGRGGWIP*GWEFETSL
11218	25119	A	11315	322	3	FTFYGCRQFQVF*IVTKNDRIIFSSTYK NLLKIYLGly*FYVPLLRKSLKKTGS FESNLSFK*VFLWSGTVAHTCNPSTLGG RRGWIA*QGELETSLTNMERPR
11219	25120	A	11316	251	389	TFFFFEREFHFVPQVGQGSLSLQAP PPGSHSLA*ASPRCWDGG
11220	25121	A	11317	313	80	EYICPRCLSPGFRD*PGQHGETPSLQKL QKSAGCGGAHLRSQLLRRLGDRVRHCLK KRIYLSLFLNSLVLNNRPFQII
11221	25122	A	11318	145	410	APKTLKVALTSAAAARESCQLGVDEL VIFLELNRTDORPGAVAHTCNPRTLGG HGGWIT*AQEFKTNLANMVKTC
11222	25123	A	11319	393	3	NFFKIIPTLSPPLPLIFTPPPFFFFKFI PPKPLFFGVFHSQTCQISFFKNFYFPL FWFNNPFFLLFSPSRKGPFFSRFFFFK VGNPLFFLFFFFFFFFFG*EGVSLLLPR LECNGTISAHYYLRPV
11223	25124	A	11320	135	1	HRDVKLEYAIRKMEVRPGVAAHACNPST LGSRRGWIT*QGEFETS
11224	25125	A	11321	282	2	NSESVLIKEKGDREKVLFSLLPSKRKV LESKTFPTLHSGCKRSYFLKITTSFL *PRVBCSGVIDHCKLKLGSGBPPTSA FPVARTTGM
11225	25126	A	11322	149	30	WGGGQVRWLTPITPALWKAEGGSPEV RSS*PVWPCLY
11226	25127	A	11323	316	399	STLGGRGAQIT*GREFETSLANMPNPIS
11227	25128	A	11324	223	397	IIKAYQ*DVNREQIKTIIYFQNKLCI KKMIWPGAVVHVNPSTLGG*GGWIT*G QE
11228	25129	A	11325	3	396	NYSTAALFLRGHIWGRNGTLYYGSSPI YCRGLNSTLGLYPLNASSNPHPRKLC KIYTHIAKCPIGHKIIYPYANTPIH*HH THTHTHHTL*DSLLWPGVVAHTCNHNT LGSWGRQIT*VQEFKTSLA
11229	25130	A	11326	113	442	KRYIQIRAHSEVLGHELGWTLHNPVQT IQTWEPFPLPLCSRVTSKSHRFVPL LFHL*NRNNSHHHHHHHHHHHRNPC* ECCRAHSDSYAVWSDKVSQEPVAAAM
11230	25131	A	11327	145	3	ELDIKPPNFFCHTGVC*CDLGSPLLP PGFK*FCLSPSSWDYRCA
11231	25132	A	11328	189	1	KTNLLLIHSLRLHLQSSVFQC*SKSEK SNVCT*CAFSCLPKLFWLGKVAHACNPS TLGRRGG
11232	25133	A	11329	193	405	ID*QTLTKKKKKKKKKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AYTSKKT
11233	25134	A	11330	209	11	GGKRGTPPTINNIFNFFF*EKGSCSS RAC*CNGEI*AHCPRLPGSSNSPAAAS RVQETATTPS
11234	25135	A	11331	38	390	VDQSTVCKMGQSAGCGWSDKGIGAGCL K*QRQKKKKKKKKKKKKKKKKGGG LKKKFLGPGGEEKFFFFWGPFPPFGGR FLKRGGGKPGYKKNKISGHPPLGGG KKKKR
11235	25136	A	11332	38	326	VDQSTVCKMGQSAGCGWSDKGIGAGCL K*QRPKKKKKKKKKKKKKKKNNRGGG FIKKLIFGPGGEKIFFFWGPFPPFGG FKKRGGEEKNL
11236	25137	A	11333	1	234	RTRGKNWMAFIKEGWVPTGRMGGSFIKH SFLESKNITWLGKKKKKKKKKKKKKKK PHDKIKDLFDPV*NKKQNISIP
11237	25138	A	11334	244	398	INHLYSNKNDLIFLLVFFLFFFP*RRPG EPPLIKGWLPLYGGVNLNRKDPL
11238	25139	A	11335	174	1	HQVYPYVKQEHYKQDSCQCYIKYMNWVP DAVAHGCNPGTLGAQGGWII*GQKFBRT RG
11239	25140	A	11336	148	411	LLLLPHCYLLNAPSILYLNPKVYNLH LCVSAVCLLVPVHSPHRTCLY*KKKKK KKKKKKKKKKKKKKKKKKGGAFFK KLIF
11240	25141	A	11337	237	453	GQRPLLSFREKGSFFFLLETEFCFAPQA EGQGHNLG*LQLPLWG*SNLVSSEV GITGAGHHPLFFVF
11241	25142	A	11338	65	347	VCRVDDFVPEARTREFFKSI*EAWNKNKI KPLLSTFSQVPGSENEKKCTLDQAFIGI LEEEIINHSSCENVLAIIISLAIGVTEG KYGSVLFCLK
11242	25143	A	11339	158	393	VPCTHSEGRKGRKCLPKTRENAREERD KKIPPGLC*AGKLFQEKSSWPGKVH AWNPTLEGRGGWIT*GLEFKTT
11243	25144	A	11340	117	3	GIRPGAVAHVCNPSPLGG*GRWISRDWE L*TSANIR
11244	25145	A	11341	292	60	SGQGLRLRGAFRGKVAKEWMPPIKLG LVKDMKIKSLEBIYFFSPPIK*FEIIDF FLGASFKDEVFFLVCLFVCF
11245	25146	A	11342	149	30	TQIFPPPPPPGKKKKFFFPKKKKKKKK ERKKDRKNKQK*KGPGVGVSPPLFPPLG GQGGGFPQGLGFKTPLAPKGKWPFP*KT QKFPRRGGGPPKIPLFGGGGEKKFPSPG GQGSNPKKFFPPPPRGKKKNFFSPKKK KKKKRKKERKTEKTNKK
11246	25147	A	11343	120	504	GVHDLCLWDMTRRPPAAATACPAGRP PPRREEHSQLLLISQGFGRWD*DDQVN TPNLDHLAREGVKAYLMPPLVMTSPS HFTAITGKRHSAHFRCPSPNQRSPFPV IRSKSSVSSREVEVA
11247	25148	A	11344	213	399	ALVIHCLTTTIQVSGLSGSKYLMRQGMV AHGCHPNTLGGRGWIT*SQSEETSLAN TVKPC
11248	25149	A	11345	308	3	NPTPRSGDLWVEEGSPGAGNWCGLSEQT LRAIKATTSYFYCYFFETGSHSVAWA RVQWYNPGCSICGSSHLPTSAS*GAGTI GMHHHAWLIFLFFVENE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11249	25150	A	11346	189	433	GHCRAGTSLTLTHLGGSAEMLTTHLGLCLGRMKFIHTTCIILFLFSLSATQAGGQGGDLS*LQPPPLGFGKQFSCFSLPRSWD
11250	25151	A	11347	257	3	KWGEELCFLTIKEERMGFPLAKKRKIKGVF*FGLFFFFETESHVPAQAHCNLSLDS SYSPASAS*VAGITGACHNQLIFIFYE
11251	25152	A	11348	159	434	LSPSCRDVGTYTSARAHPPHTHTRVRAHTHACTHVRANTHTTTHAGSHLTKEQPGLCTLPGSSW*PGLGGRAIATAQAWVHCAG IITAAHPP
11252	25153	A	11349	240	406	AFKKLAKNNSMGVNRSLSRPGVVAHAWN PSTLGGGRGQIT*GQEFETSLANMVKP
11253	25154	A	11350	163	360	PQLQLMKFLQN*LLELRFPONGNLLEG LACESRSRPCAPVWRTERDSVSSPQPR PGAGGRPSFF
11254	25155	A	11351	145	406	PLNSGAKPTLPPWSPRRPELNAPPPPPG EKEFFFFLGRGFLFAPQEEAGGENIV*G KPPPPG*REFFAPPPGGDGNKAPPPPP LFL
11255	25156	A	11352	122	337	ILWVLLLVRESLKFFFLLLFFLFFET DVA*AAVQ*SDHSSRQP*PPGLRGSYTS AFRIAGAIGICHLY
11256	25157	A	11353	325	416	KCVYIMGWA*WLTPVIPALWEAGAGRSLEV
11257	25158	A	11354	260	415	LEELQNTACQKLEPFLSRTETKQCLLS PRLFNIVLEVLA*AVRQEKIKGI
11258	25159	A	11355	160	2	ISEISTKRNNYFLKNWLGVAHACNPST *RG*GGQTTRGQDFQTSANMVKP
11259	25160	A	11356	160	3	ENLKLYNGSPFLKI IWLGMVHTCNPST LGGQGRIP*AQEFKTSIGNVRRP
11260	25161	A	11357	235	408	GQPLFAALFFYQWHLHFKELLAHPWGKT VWRFL*PLKKEGPHDPAIPLLDIYPKNK KW
11261	25162	A	11358	11	393	QTERTPTPKPHLYVSFPNNSQDPOLQGG KLINRKNTHTKTPSVCHHHQRPKVDKTT KIGKKQSRKTGNSKNQASPPPKCCSS PATEQSWTENDFDELREBGR*SNYTL KEEVRTHGKEVKNLE
11262	25163	A	11359	283	475	FMVSVSIKVYFFIFIFLFFEMESCSVTQ AGVQWHDCLSLC*VLASSPGNSSPVR
11263	25164	A	11360	266	407	LEIHHSKTL*FWLGIVARACNPSTLGG* GRWIT*GQEAIIILANIVK
11264	25165	A	11361	93	1	DVLSILLPRLECNGAISAH*NFRPLPGSS NSS
11265	25166	A	11362	131	377	MEEMIKGRGLSKPPALSSYLTKSS*LK RVRARRRLFLKSRFSLDLQVAGPFVCLF VFWDRVSLCHPGWSVVVQSRLTAALT
11266	25167	A	11363	212	392	QAEECAPLFIGVKEPPKNLTHWLGTVAH TSNPSTLGG*GGQITWQGFETSLANMA KPCV
11267	25168	A	11364	141	3	NELWLNHQNVLWLGTVAYTCNPSTVGR WIT*V*EFETSLGNMVK
11268	25169	A	11365	215	384	ANFNIRPEISLASKCPSEKRSRTLLPLN QKLEMI*LSEATS KAKTG*KLGLLHQI
11269	25170	A	11366	48	373	EPWTRKEVLKISSSLKIHCYLSILCLIL MPTLECTAAIMAYSNLELPGTSCPTCA S*VAGTTGACHRAPTVLKIPLDRIFFF FFTNVITYPWCHTPADPAIFKANAR

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11270	25171	A	11367	310	2	GLICLNRENAYFFVIRQISMSCLEKEKP ARYSSPYAKSVTRGEKRRQRFFLSRAPP IPFLFFI*IV*AESRSVAQAGGQWLHFS SLQTPP*RRTS DSPASAS
11271	25172	A	11368	303	50	MFALTNRGVQGSPIVPLGVFLISKMOFT CFKGFSRFKVLVFFLGVFPSPFFFLRAR VLLCCPGWSPTLGIK*SSCLGLPQCULT
11272	25173	A	11369	109	419	QSNASLSHFTSPPLSVADR*LFSTDHDKD IGALYLLFGA*AAVLCTAISLFILDWLQ QPCNLLRNDHIYYIVTAHAFARIFFIG IPIIIGGFGN*LVPLIIGA
11273	25174	A	11370	112	258	GGRFKGNSFTSAGMQRNIFFMGPBK*NS RAGV*ORGEKNPGVTKLNRL
11274	25175	A	11371	823	1078	SQHFGMPRWADHLRSQVQDQPGQHGTEL SLLKIQKLAGRGGCL*SQILRLRLQBN CLSLGGRGCSEPRSHHCTPAWATQ*DSV S
11275	25176	A	11372	184	420	IKQOKNLFLLVKELVQLLWKTIVWQFLK KLNIELLCDPAILLGIYPRELKMVYHT KTCT*MFIVELFIKSKK*KQPTC
11276	25177	A	11373	234	44	LATITDRLLALSDSAIPPLGIYAKEKKS VYQKDNCTYIFVAALFTVAQI*NOQKCP STRTRGS
11277	25178	A	11374	73	456	PPIGSPLVPYIPSPALSSPQAPRMGSH CLIPSASCHPPLETDFLSLLPTHFLAV FTKERFSPPPSPYPRF*KFLRS*KFSF FLPPFLFFGGTVLLCLSGWSAVAQSWLT AASTSLGSSDPPTSTS
11278	25179	A	11375	43	456	EFFHHVQDGLDLT*SAHLGLLKCDW YRREPPRPASDGHY*TDATGSLPSSGTT *IRTKPSQAPASWGLWNLAAHPPRSHPS CPMANLICSTLSSFDGSGPTGPGWC LGLSGSPARAVFKDSSCSLHPLATGI
11279	25180	A	11376	288	484	EWVLSAVGGSQYGVCLPFLHCFIFETE SRSVAQDGVQ*CDLGGSSLPFG
11280	25181	A	11377	129	1	NFNALNLRAGAVAHAYNP SHLGGEDGR IA*GQEFETSLSNTA
11281	25182	A	11378	307	1	DSEIPLGLAKFWNHRREPPCLALFTL NQKLEMIKLSEEGISKAKTR*KAGFLCQ RVSQDVNAKEKFLKEIKRATLVKTQMMR HQNSFIADAEKVWMAWMK
11282	25183	A	11379	200	397	CISLFSHYKDLPETGSFIKRGILGSH WLGAVAHACNP SILGGQGRIT*GQEFE TSLASMVKPC
11283	25184	A	11380	167	1	SNGLYSREARMVQHTHIRPGVVAHTCNP STLGGHGGRI*AQELKTS LGNIVRPC
11284	25185	A	11382	12	395	AHSSFLSLDLSVFATCPHPRAETQTGHR FSTLLPLSALYPK*DYFKKKKKKKKKK KKKKKKKKKKKSGGA
11285	25186	A	11383	160	2	TMEMLDIK*I*EIFLFEFKMGLKAAET TONINNTFGPGTANEQTAQRWFK
11286	25187	A	11384	274	389	GQAQWLTPVIPALWETKAGGSLE*GQAQ WLTPVIPALWETKAGGSLELKNRPSLG NMVKFP
11287	25188	A	11385	389	37	WSYESSWSFIFKSLFSFMISAYDM*YA SQILFTPKLYRTHPYFLVLFLILSILV ILETGSRFVSRLECGGGSAYGSPK*LG SGNPFAAASLSSRIPIYVHSCWSDLA FN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PEFEM
11288	25189	A	11386	214	374	KGGGRFKGSKFTSPGGGEKNFFIGAPK* NSRAGV*KRREGKNPGVTQLKKGVG
11289	25190	A	11387	142	410	RFVCSITIKVLRDLSSDRNPGFRFLSTSN *KKIKKKKRGAPPKKKNFFYRGGGGKY FFFGAPKINFLGRVFPQGGGENPGRSPF KGAWG
11290	25191	A	11388	144	1	CLSNEDSIKTPKGLGTVARTCNPSTWGG RNGWIT*GQEFKTSILANTVK
11291	25192	A	11389	167	2	RNISSHLLNMAITKQTNNNCW*GYREI ITHIC*WEPKMMQLQKLVPOKVKHT
11292	25193	A	11390	2	412	SDOVQDAGRLISSEASLLGLPTATPILLC LPTGFALCTRVPGVFLLLRTSVILREGP TLVTSFYLNLYLLKDLVSIQSHWGLQLQP MNFGETQFSL*QKL*KEKESMPGMVAH ACNPRNLGGQGLIT*GQEFKTLA
11293	25194	A	11391	1	206	TGRLAGHRVSSLPIRGGRAPLTSRTG RLNQDGLNLLTS*SARLGLPKCWEYRRO PLRLAVISGFLT
11294	25195	A	11392	262	388	VSK*KKKKKKKKKKKKKKKKKQ
11295	25196	A	11393	78	414	ICFFLRAPPPPPPPFF*TKIFFFPAL NSMANFFFWTPPPLGGIFLPPPPFLEG GGPGLASPPGGAFFF
11296	25197	A	11394	238	11	IKWETAGRSSACL*S*LFERLRRENPLN PGVHG*DEI**HCTPAWVTVRPLSKY INKNKK*ARLAARCGSRL
11297	25198	A	11395	340	1	KHILVPPFINVSEIQRYSLV*HLLFVGV *NLFFLFLSFKKPVLCM*IICHEIISP PSKPKCKASHLSFV*KKNSNLWLGAVAH ACNPGTLGARGGRIT*GWEIETSLTME K
11298	25199	A	11396	363	245	QMDLNRHLSKDDK*MANQCMNRCLTSLA IRQMQIKTIMI
11299	25200	A	11397	292	2	DPKKEAGRGGAQL*FQLLRFPKHETHLN PGG*GCSESRSHSSPPAGATK*NGVSKK K*Y*APKEERHPRPVLVEPRVPQVPSPG SQTYRQDHSPRV
11300	25201	A	11398	121	321	KKLYTHKSKSDVMIFLKIETVSWLYCPG WRVMAHCDLKLGGSSKPPTSAS*VAETS GTCHHARLIFL
11301	25202	A	11399	118	394	QALPQPIPVILLQFFFFF*GTGFCFV AQIGGQGGHYG*LEPPIRGLKPSRRRL RGGWD*GGHNAQLILGFTEKTGSCFVV QAGLKALA
11302	25203	A	11400	273	379	AEPGVVAHSYNPGTLGCRGGGIT*AOEF YTSIGNM
11303	25204	A	11401	360	38	KIFGQARWLTPVIAFWETVDGSPVEG RSRPA*PS
11304	25205	A	11402	254	404	GPAGHDFHMITPSKSTETGLGAVAHVCN PSTLGGRGWII*RDLETSLA
11305	25206	A	11403	161	3	ILTPTLQYIKINLRQANWFTHVIPALW KAK*SGGLELRSLRPAWVIEGDL
11306	25207	A	11404	1	170	MGVSLSPRLCNGVISAHNCNLL*FT FK*FSCLSLSPSSWYRCVPPCLATFLIY
11307	25208	A	11405	249	3	NAKSRIQVISIWVFTVKFPHLYLNCNFS Q*NEMAGGQSIFRKHLDFSLEHSGMMT THCSLDLPSSDPPNSASSVGGTRH
11308	25209	A	11406	70	401	CGKHGVNLIHSFLNHLKYLILLQMANL

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						FISQFLITCVSEPLLF*YCHQIIKVGRL HEVKQMRGTTKKQEKMFYWNNDKNVCPG VPAHACNPITVGG*GGWIT*GQEFNT
11309	25210	A	11407	257	389	GGSLQKYLRLPLVAFLFSFFFFSFETES *SVVRLECNMGMSAHC
11310	25211	A	11408	364	420	SQPFGRPRQADCLSSG*AQWLTPVVPAL WEAKAGRLLELRSLR
11311	25212	A	11409	312	413	TSGMGPGVVAHACNPITLGGQGGWIT*G REFETS
11312	25213	A	11410	283	425	HGHKDYVHWLGAVARACGPSILGGRGMW IS*GQEFETSLANMVKPCL
11313	25214	A	11411	389	3	CRIDGLFFNLVFLRLVVMKF*VIFFLSY FSFLVILQLFTYMLNCTFF*QILNLF ILVLLTKILNTLLSTENYCHFSLLYCLE FWFHPILKHMYNLFIL*FILIFILRQS LARSPLKYSGTISIH
11314	25215	A	11412	267	3	QEFQQEDTSELDLEIRSLCKRKGGLKQG DTKDNLSKRVVVEDTKGKAAWPGAVTH ACNPSTLGGQGGWIT*GQEFETTLNRC PRV
11315	25216	A	11413	3	281	GAWSCRIPGEGSLASQATQPPSLYPVN PQ*ISLSARKKKKKKKKKKKKKKKKKKK KKKGGGVLKRIYPPRGEKKKFFFWGP PKKTGGGGF
11316	25217	A	11414	275	2	KTAFQLFNSDFKFPGRNPGQSWSPRA KQSFCTQALLKYFLK*MNEMKLNKSRSG AVARTCNPSTLGGQGGWIT*GQEFETSL ANMAKPR
11317	25218	A	11415	319	1	RNLGVQVYEVVVLVYKCSVSSNNKMK KRDLLVI*VPGIVIHLYRLIKENPELY ISLFIYSMSRLKLTYPGAVAHACNP TLGGRGGWIVCSQEFETSLGNM
11318	25219	A	11416	121	428	LSCDKWGNRDMTKMLSKELKKKKKKKK KKKKKKKKKKKKKLGDDEEDKE*QSSW GGGALIKNILFPSSRAASGFLLSLLKYK KLGAAYYIILGKRTILWL
11319	25220	A	11417	79	253	KIFNFQFSNMLENNSHTTRINNYFPGRE RWLTPVIPPLWEAKAGRSLEVR*RPSC P
11320	25221	A	11418	180	4	EVGFMPKPGLCGVFLEAGSHSVALTIVQW CDLGSPQHPPLGSRDPPP*ALQIVGNTR RVP
11321	25222	A	11419	154	3	STLKDKENQKLSIQPDTMAHVCNPSLIG GRGGWIT*VQEFETSLNNMVKP
11322	25223	A	11420	436	478	AIPLEH*KKILHAALFFFLKGSFVLS PRLECSTKIWAHCSLPPNISNPASSS QEGGTT
11323	25224	A	11421	143	398	AAFGFWFVLIRFLRQLALSPLRDCFFA KSACQPRPP*FKRVCWLSLPKSWDYRF DLLCAAGLVVVYLSVSRHLHINEKNQPPP P
11324	25225	A	11422	1	138	MVFRVQDGLDLTTS*SAHLGLPKCWD YRHEPPRPAHSYFLHKK
11325	25226	A	11423	2	390	LELPILLNTLILFLFLILYIYLVFSPN AFRILFITIVLESFSLVPSKPKWYS LILSNAPVLCMMISSPPFLFSLSTTRI NKKLDFWLGAHAHAYNPSTLGSQGGWII *GQEFETSLTNMAKPHL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11326	25227	A	11424	267	414	VFQITFCIKNFPGVVAHACSPSTLGG* GGRIT*AQEFETSLGNMVKPC
11327	25228	A	11425	189	73	HQDGLDLLTS*STRGLPKCWDYRHKPP RSARPNWVAP
11328	25229	A	11426	318	33	KKTISSHARGRKLGSFKTAAPFFFFF*T GSCSLAQAGVKWCSSMQPRPPGLK*F SASGSAGIIGMSHHTRIAGFLAKLKK KSNSTGYGGAHV
11329	25230	A	11427	291	393	DRVSLCLPGWSAVLPS*LTAAQISWAQV IFLPQP
11330	25231	A	11428	51	399	KRVARQNPPNGQGFQWCSGSPILYQSR AQGENIYKLLGSGEWPGQLIIDVEREQL EDWRQGDLLGRGMWMTKARVHKGPLVAG TCNPSTLGGGRWIT*GQEFENSLANMV KPCF
11331	25232	A	11429	242	420	VKKKRRGGRFKGSKFTSACLOGISFPKG APKLNSRAGF*QRWEGKNLGVPOFNRP AHP
11332	25233	A	11430	77	405	TKRGDSSFCLYRIWIIDSVMKNQSKAA AAAAFFFLRGITLLFLFLKKGKVGASVI *NFCRLRGWGGSPASPSKEVMEGACHNS GLFFVFLEKRRPPLVGQBFKTRAN
11333	25234	A	11431	121	439	LPLPTSGPEDPLALSFKPTFPSTLGM IYTGHPSPHTSHLMPAPPVNNKACRF FKT*KKKKKKKKKKKKKKKKKKKKGPL KKKKIFAPPGGRIFFFFWGPKK
11334	25235	A	11432	109	283	LTPWNLDNRCEIKGNGKQENHLNLGGG GCSEPKSHHCTPAREKQNSVSKK*INK IK
11335	25236	A	11433	296	1	FLKKPSKGFSLPHLPQNLNLFPPPK*K CPRAKKDIPPPSF*KISSLFEGG*GFTG SRPPSLNLENPPKRIFFFFFLDRVSHC RPGWSAMASSCPRV
11336	25237	A	11434	385	418	QSETLSQKQTK*E*SWLGAVAHACNPS TSGRGGWIT*GWEFENSLTNMVKPCL
11337	25238	A	11435	3	405	LLHQGRMLGQWNGRKTLLMRENVGK FPAEPSCSALGVWLQALACYPGLVRRQ* ANHWEKKKKKKKKKKKKKKKKKSGG G
11338	25239	A	11436	221	3	KHEFQTIQESMK*NTSIKICIYAS*IQ DCLRYQWRPAVAQAITEHFORPROAD HLRSGVSDQPGQHGET
11339	25240	A	11437	288	366	KMFFSWA*WLMPIIPELWEAKAGGSL
11340	25241	A	11438	160	370	LWYHYFPVRDGLTILVTYQLKAIIRLLT LKSRSGAVAHTCNLTGLGGRGGWIT*GR EFETSLANMEKPHL
11341	25242	A	11439	230	404	MQHGQVGIYSQGGGWRPVDKKNSQLGTV AHTCNLTGLGGRGGWIT*GOBFKTSLTN MV
11342	25243	A	11440	302	54	LSGVWFLTPPPKGGGFTP*NGGAPGFF PPPPFKNPPPEGLGGPKKKKNFPPPGG EKLVLKGAAPPPPPPPPPPPPPPPFL
11343	25244	A	11441	271	416	KRTLSTELQYMCCLLIKSKSIFK*KKKK KKKKKKKKKKKKKKKKKNPPSLP
11344	25245	A	11442	254	392	SVTGMTIMTSSCCYKIQKCTRIQKLARH GGTCL*SQLLRRLRQENS
11345	25246	A	11443	390	150	LLKNQKTLGGPARNPPPLGGPNGGVPKA GNWGPFGPPGGTFFFPKNQKITPGGGGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						P*FPLRGGGPGNPLYPGGQGC
11346	25247	A	11444	122	1	PAPLFFFFFFETQSCSVA*AGVQWRNLGSLQPPDDGTRL
11347	25248	A	11445	272	403	RPKVDKTTKMGNRQSRKAENSRKQSSASSPPKDHNSSPAME*SWM
11348	25249	A	11446	70	397	LCHCAPAWATERDPVLGEKKRTMMSYCHPPMRMVEKKIVGDIKC**GYGETGFLTHC*WECKMVQIL*NIV*QCLKNLVHSPYELAI VLLGIYPREMKTYIFTKKTSM
11349	25250	A	11447	3	401	HASAHASAHASAYRLCAYPKSSFLYPSFLLVVSNNFPLNILDTTIGPKATETLFIKHMHDVISMQLKSKTFYNYFFLLSLNVFYFVLSCCCKRRKRSLQGMVSHICNPSTLGGGRWIT*QBFETSLANMA
11350	25251	A	11448	333	1	KSGCIPPKGQVVLFPQLKTAKIGSPKPVSPPRGKQGFPPQGLRGFY*FLPPPQGVPEIFFFFFF*DSSHVTLSPRLEYSGMTAHCSLHLPSSNPASDSHIAGSTGTCHH
11351	25252	A	11449	104	402	VVCRPLLGGVSQLGYMGVMDPFKEAVCLFSELKHCAGRTTALFRAVRQGCCLSLKNFLLPFFQLCPAHRGGVL*RQ*ALLSCGGLHPVRASRPLCLPTQA
11352	25253	A	11450	198	2	KYKFAGLGGSC*SHHFARPRQDGLSPGV*NQPGQHGGETPSLQKQVSWANWHASVEAEAGEQP
11353	25254	A	11451	171	3	TTPPRATSLFFFF*TESHSVSQECNGTISAHCNLCPLGSSDSPASASRVAGITGA
11354	25255	A	11452	177	461	PMTGGKYISNSTCSKPNLSPLHLPLKTQTKNMEHFGRLTRGDCLSPGV*DQPGQRGKTLQLQKISQALWDVTAHAWVVPGLPTRERRRSLSPFTG
11355	25256	A	11453	247	3	EGECCGIESR*ILHLKGRICWHINYLKITKIKN*VILKMYKQLRPGAVAHAYNP SALGG*GGRIARAQELTRLGNIVR
11356	25257	A	11454	328	57	EVHSNICATLSTHQMILTKGTRHQHIS*GFF*EGEVLTLSTKLECSGVIMAHCNLNLGGSSDPLALVSQVAETRGASYLLLAICPKVNK
11357	25258	A	11455	70	435	ATRAKLHLKKKBEGRKKEFFPHWQGOPTPALVFPQPRTHFIFKVSIFSLKKNREQLPYTVQTQSLPLNSHWGQVA*AGVQWRNLRFSCLSLPSSWDY
11358	25259	A	11456	112	401	KCWDYRRERPCPAPNICIF*LTFFFLGKLKLNQSFPPFFFLKGSVLVLPRLKGGGAF LFN*NLTLQKNNSPASPS*RAETLGLGPHAKLWFVFLKK
11359	25260	A	11457	198	3	EKTSVKQSGSDSNKKAWLEMKTNKSLKR*GVVAHACNPSTLGGRGGWIS*GREFETSWTNMEKP
11360	25261	A	11458	179	1	FFHMYNHIVCEYTTLSVNNINSQGPGR AHAYNPSTSEDRWIP*AQEFKTSANMV KPH
11361	25262	A	11459	210	5	RLIHFFKNNLPSGGGSTA*QGEFEIRLDNTVRPHFLKK*KISQVWCMVVVSATQ EVEVGNGLSPGV
11362	25263	A	11460	139	2	RILALSKLFFFFFKQESHFFLPMLECSGVISAHCNL*LLGSSDLS
11363	25264	A	11461	388	272	S*KKKKRGGRFKGSMFLSPAGQGNPFPM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						GPLKSI SLAVV*QRREGKNLGAPHITRL GAHPLFAGWHKTQGAEP
11364	25265	A	11462	2	387	CVWKSNNKKAPPVCAALRFWRKODMDEM APGKHWGGLTSKVQSGGLMGRYTGPLTK TENSILLKNPYFEAGHSGSRL*HQHLGR PRWEDYLRPGGQGCSEL*SSHCTPT*VT EGDPVSKKLKRTIFGG
11365	25266	A	11463	325	398	SLPTWAVCAPRPSG*GSGIPELKTMLAG VILEDYLDIKNFGAKVVGLSCTLATGST LFLGKVGPPVHLSVMIAAYLGRVRTTTI GEPENKSKQNE
11366	25267	A	11464	174	2	YLEILFFETGSRSTOAGVQWSHPGSL QTPPPCPSNSPASA*VAHASADAWADA W
11367	25268	A	11465	105	411	TDVELLLMDE*RKWFLELETTPEGDDVN IVKMTTKDPGYSINLVDKAVSEFKRIHS YFERGSAVGKVLSSHIVC*GEIFHERKS PLMQQISLLTFILFYFSE
11368	25269	A	11466	291	404	SOEGVKIKRQGTVAHTCDPSTLGG*GGR IT*GOEFKTS
11369	25270	A	11467	64	236	THASGLDLLTS*SSCLGLPKCWDYRHEP PRPARFSSFYSGSLNLNYLAKIKRDAFC I
11370	25271	A	11468	278	416	NPQISCLKQHVWGAHAHCNPSTSGG*G GRIT*GOELKTLVNMVK
11371	25272	A	11469	178	325	RPEVKDQGASCRDQPHRVGGLLPVCSDE RVPOKKKKKKKKKKKKKKKKKKKKKK KKASSGGARF*KKKKKKKKKKKKKKKK
11372	25273	A	11470	264	60	DINHQSWSLGRWTPLSWVSISQREDRR GFSASIYIYIYIYIYIYIYIYIYIYIHT YT*SYHFNQNT
11373	25274	A	11471	95	399	DFPHLLFLPLSQFCTACCPVPENRCFM YFFLIFSALCWEMNSRISHSNTARVBQC CKVFKILQMKSVLQVQWLTPVIPALWE AEAS*LPEIRSRNQPGQ
11374	25275	A	11472	139	2	NHVSTKLSLHTMAHTCNPSTAGGQGGQ IT*GOEFKTSLATMAKP
11375	25276	A	11473	179	3	RARWNPQVFC*GFLPVFPKILPIWPLRK GVFPFPNFFFFFLRVSLCHPHWSAVARS RL
11376	25277	A	11474	282	12	KYIRNE*IVLFVIYFCRNRIWCCPGWS *TPBLKRSSCLCLPSCWDYRHEPLCPAE MNKLDRLNKMDDTKWIIQKKKNHRTQRQ DNKII
11377	25278	A	11475	145	3	VCMQLRTDFQPGAVAHACNPSTLRC*GG WIT*GREFTGLNNMEQPC
11378	25279	A	11476	61	397	PQTPRLKQSYHVSPLSSWDYSWIYHERL VNPGRETDWATCYSGGNIQLQENKLNTP TDSTLWVSLCCPRLECSAIPADCSLNL PG*SDPPTSTSHVAETTGAACHYAQLIFG
11379	25280	A	11477	156	3	FIFLKSSQNSYI*KCWPGAVAHACNLDT LGG*GGWIT*GHRFKPTRRPRV
11380	25281	A	11478	224	383	CWVCLIHRAFLAPRPVLGCQ*QKKKKKK KNKKKKKKKKKDSRGGG
11381	25282	A	11479	339	58	NFKNKLFCASGYLDSKDSQHYIIFIR WSLALLPRLRWEDCLNPGGGGCSEPRSY HRTPAWVIE*DPVSKK*IK*NKIK*KQQ DWLRLHDKIF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11382	25283	A	11480	244	407	SFGKKIGFLFGPKKFNNGSGSYGNYKINR RFFFPILGEGFSPHVYF*NLETRTTGGG LLET*TKTTFNLLGRKLGSLGPRSLTAA PTGTTIKLTGGFFQFQWGVFFPRMYIFW KDEWKGGF
11383	25284	A	11482	308	30	SPQKNPPTYSGFKKNLSASPGQKAKPRF FLKNQFLPGIMGGGRQFPLLRRVRPPNC FNFGGKRCN*QKLGPCPPGGPKETVSKK KKKERQQ
11384	25285	A	11483	226	407	NHWNKK*FWPKVAHTYNLSALGGQGGRI T*GQEFETSPSNMRPHAS
11385	25286	A	11484	10	411	QPPIYFLSLRISLFWVPHINGIIQYVAI CVWLVSCHNFSRPI CVAACDQDFIVFLW LNNIPLCGYNILCIHSICPNWRTTGLFP LLAII IKL*TFVKKKKKKKKKKKKKKKK KR
11386	25287	A	11485	184	1	TDELLPMDEQRKWFLEKKPTSGEDAVN IFBMRKDIECYVH*VDKAAAMYERIDS NFLSN
11387	25288	A	11486	435	222	AKNLNRHFSKKVI*MASRHIKRCISILT IRET*IKSIIR*HVIPGQMTFIQKTGDM FGSVSPLKSHHLKL
11388	25289	A	11487	317	408	FRPGTVAHACNPSTLGGQGGWIT*GKEF KT
11389	25290	A	11488	340	469	GKGDTKCHLWLGTVVHACDPNTLGGQGR RIA*GQEFKTSLSNM
11390	25291	A	11489	38	389	KRPTSLKKSNFCSLQGGFFFGLSQKPGK SNRSPGKKKNPFFSGGKAP*KGFF*KIFL SPGLGGSPQKPHLLGGLGEKNYLTLEKG GCRDPK*CPCFPWAGEGNPFSKKKKQK FFPFG
11391	25292	A	11490	235	2	FVLMWLMPKLHIPVTEFRRLFAFPEFL* FLFCFVLSYFVLLLETGSHYVITYAECSGA ISVHCSSLNLPSSDPPTSVLV
11392	25293	A	11491	25	417	GTLCRLRIGFINISHHCMLKENSLEFFF WETKFFAFAPQADGRGPNLG*WNPPSPG* RSGPGPTSRKRGNGGGGPPGPVIFGFLR KNGVPPGGLKGPKS LAPGIGPPGPPKDR GLRGPPAPGLLKKNPKVW
11393	25294	A	11492	234	438	MVVIIAQQCDCTECHY*LKMAKMINFML FIFVHTHTHTHTHTHTHTREGRPSYI YGVVSFKLTHL
11394	25295	A	11493	344	477	CFTMFIS*IKT*KFNISQLVAHTCNPSI LGGQGGRI*GQEFKT
11395	25296	A	11494	35	482	GIPGFHHVGQNGLDLLTS*SIHLGLPKC WHYRPGPPRPAISITPST*AYLLGNQKI GVTHFLAILALFFSGTKAMISPKYVCII FYLLVEEHLGCFYFLAINTATCVVYKL FDYMYQVESHATHEFISYFFPKILCSL SIRLYAVLL
11396	25297	A	11495	307	484	LSPSERHELKCVLWPGAVAHAYNQSTVG GRGRQIT*GPEF
11397	25298	A	11496	487	349	FLIKTEFHPIGQEGFDFLT*FARLGLP KGWDYKGEPLRLAFWHPF
11398	25299	A	11497	224	417	ASGASALKVELCSFSRYKIYPRHKRRYA RTDGKVF*FLSAKCEGITFFLSFFFFFL EVLFCSPG
11399	25300	A	11498	17	411	KRLVFGGRGRTDRFISQYV*AEYVSINL

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						LI FLTKKKKKKKKKKKKKRGGALKKKKP WGGQNKTEGKKKNFFFLRGKKKPWGDF KKKNFFWGGENWGKPPPKKTPWGKKKI FKGKGKTPPYFCFLKKMG
11400	25301	A	11499	117	370	VSESADLAWSLGICFFIEPPSDADVAGL ETAFFLGGWTGSCSVVQPGV*WCNHSSL QPRPSGPRQSSCLSLPSSWDYKYMPPCL
11401	25302	A	11500	244	1	EELFECYSCSPTFFSSDPLTTPLLILTT* LLPLTIMASQRHLSSEPLSRKKLYLSIL ISLQISLIITFTATELIIFYIFFET
11402	25303	A	11501	130	55	RFVCSTIKVLRDLSSDRSNPGRPLSTSN SSLKKKKKKGRPF*RDNSAILF
11403	25304	A	11502	186	421	SFRKTIAGTIGVHCTWLVLILNLVLL K*ITFALKIMMFSKYSYSDIGQAQGLMPVI PALWEADAGGSLQPRSLSLGNK
11404	25305	A	11503	1	213	GELLEFLYIFA*WFLFLPKLLKFVIVCLC ELQFNERFIMVLCIIILGVGGFFLFCF LL*PCDFDFFFWRG
11405	25306	A	11504	82	6	AGVQWPRSWLRLP*LFFTQVLMIFPPPF YHQNFFFP*KGFFFLGGLSHFFPPPNKG FFFNYPQGFFFSPLKKKFFFSPIFL APPGIFL*GPPRFFFFFFFFFF*BGVSL CHLWSAVAAILAPPAGFTPSSCLSLPS S
11406	25307	A	11505	245	440	WAPCIG*QLLKDPQVLFAGYKVPHPLEH KIIIRVQTPDYSPOEAFPTNAITDLISE LSLLEERFR
11407	25308	A	11506	256	370	GKLM*GHHVQAGLKLTTSSDPPALASR SAGITGVNRHAPPRLNVTLYTKQGTIIL YHNQYNQ
11408	25309	A	11507	1	149	GCMWPRTVLFAPQHKFVNFLKTLGDFGQ VQWLMRVIPALWEARAGKLPEARRWRPP *PRTVLFAPQHKFVNFLKTLGDFGQVQW LMRVIPALWEARAGKLPE
11409	25310	A	11508	316	420	YTYIYEPG*VQWLTVPVIALWEAKAGGS LEVRSLR
11410	25311	A	11509	136	2	LDNRLWPGAVAHACNSRTLGDQSGWIT* GQEFETSLANMMKPHL
11411	25312	A	11510	167	420	PTPRSGNTALQPPHHTHTHTHTHTHR HTHTHTHTHTTRACI*KVRVRALFSPKKK PLFCLSVSQIYVGRCLLKRLLFIFLYRH
11412	25313	A	11511	124	415	IYISVANTIILIFIAIHVLAISFFFFFK EVLFLPPRREGGAF*VN*NLFCWG*GN FPA*PSLKKGITGALYTPGLFFVFLKKT GFRHVQAWLDL
11413	25314	A	11512	121	1	PPVKFWAPFFFF*IGSPSVAQAGVQWN NLSSLQSPPSCL
11414	25315	A	11513	245	13	VLFLSGFFGPINYPTSEPPQLPFPASG NHPSTLYLHEFNCFYFYFLFIYFF*DRV SLCRPGWSAVARSQLLVPSDS
11415	25316	A	11514	434	2	RPPFFPVWGSPPPPFFFGEGIWQEER KGASSPPVVSRLRGGGPFGGPGAPPT PLKKPPLFFFLAPPFLGVPPRFFSFPTV FFLEFFVCPKKREALLGVPGPRPFFFR SFLFFFSGD*VSLCRPGWSAVARSQLTZ SLAS
11416	25317	A	11515	247	390	QGLRIYSQDFFFFLETCSRFAQAGEQG GNLG*LEPPPPPS*SDFMASP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11417	25318	A	11516	269	368	FFFFRESCSVTRAGVQWHRLSSL*PLPPAFRRF
11418	25319	A	11517	256	404	NILKIFYLRI*KKKNQLGVVAHACNLRTLGGRGGWITRQ*FKTSKEKMKV
11419	25320	A	11518	211	404	YLCFTRCSVHSHLK*VFLHKCVI*MYRPHHT*TGL*CMQVHTHTHTHTHAHTHTHTP LSQGGDCI
11420	25321	A	11519	41	232	ESVEPRRRRVPPRAQITPLHCSLGDRA CL*SQLKRLRHENLLNPGGAGCREPRS HHCTAANATEQDPV*KKKSLNFKTVRA INLKMGLALISFHLFLWGIWF
11421	25322	A	11520	146	2	LIDQQGVNQLPRMECSGAIHAHCCLELP GSSDELTAS*VAGRPPTRP
11422	25323	A	11521	297	437	TDHFWNRILSSCGDTFRDTWLGVPVHAY NPSTLGGRARRIT*AQEFE
11423	25324	A	11522	244	460	NCATITTSRIPLQLQKKHCTKWLST SWQSLISF**ICFVFFFTNLAVSLRLE CSGAILAHCNLCLLSS
11424	25325	A	11523	222	1	ESKDLDFRCQLAPRNSSCFVLPFCVFP LEIGSCSVAQAGAQWNCNHSGLQPPPIA SAS*VAGTINVRHYVQLF
11425	25326	A	11524	308	424	ITFLTMTFKIYLQFDPALPLGIYPKDY* SCCYKDTCTRM
11426	25327	A	11525	98	2	NIGGRPGAVAHAYNPSTLGGRGGQIT*G QEFE
11427	25328	A	11526	113	399	LDRFLTLLPRLRREDCLSPGGQCSEF* SHRCVPAWATE*DLSSKKKKGVLEKPF LPPPSVGKPPPSPPERLFFPILRPPLGG VFPSPSKKIIIS
11428	25329	A	11527	280	3	PKYCQI*VLQCIAQLFKLSIYNTYTH THSLSLSLSLPPPKVNKWLMSSEFTLTF KMYTFGPGRVTHTCNPSTLGG*GGWIT* GQEFETNL
11429	25330	A	11528	284	2	FWGPKKNFSFPPPGKIGSFKRAPPFF FFFFETKSCSVTQAGVRWCDLGSLOPLA WATERD*LNK*IKGMSKKLHT*VCMFRT RGRTRGRTRG
11430	25331	A	11529	134	2	DTLLPRLECNGTITAHCSLKLPGSGDPP ASAS*IAGTTGMCSHA
11431	25332	A	11530	104	1	GRGFFFFFFFFFF*EVESCSVAQAGVQWL NLGSIQ
11432	25333	A	11531	157	373	CVFYTYSTSOLRCYIFIGNTRSVFRCH IYT*KNRFWASTVAHTCNFTLSSRGKW II*G*EFMTSLANVVR
11433	25334	A	11532	237	389	ICKCSKTGFG*DFQEFETSLGNIVRCP YRKIKASQV*WHAPIVLATWEAE
11434	25335	A	11533	259	122	HISPSVQRHFFLFYF*TKPHLVAQAGVQ WCNLSLQSPPPGFKRF
11435	25336	A	11534	164	1	SSVVSQALILLFLKKTCFWPGAVAHACN PCTLGGRGERIT*GQKFETSLASINL
11436	25337	A	11535	106	310	GGDKGTVDTLHFFDGGQKRLDHNKDHWM TIHAELPHELSA*CYAFKKECISGIGSI *AEKEYKIQFDG
11437	25338	A	11536	167	378	ASFSGTTITYKTLVYVYMFERFIYIYH MYTF*RQGLVLSKLECSNVIIGHCNLKH LGSSNLPTSASRVA
11438	25339	A	11537	101	396	VNNLKQRIGLSKRGEKKLLVLISGFGGG FPGAGWIKKGKPPPGFPOGLGP*KRGGP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GKKGNFNKMGFNPKTLVFNQNFPGGGA KPGTPGVRGPLGDL
11439	25340	A	11538	18	361	QIGPRLY*DONGETPSLLKIQKKIPGF GGGPLKSQLLGGGLGWENH*NPGGGGCRD PK*PQGLPPWGTNQNPFVKKKEGREKKG EGRKEGGGEKKKTLPGIGALNLGGLLT SP
11440	25341	A	11539	134	365	PGFQNKKTGGGGPFRPKTKTNFKVF*KY LKICFGFWPKRPPPPGGFIEITRSLFFI FFLGFFF*ETKSRSVTRLECSGVILAH NPRLVGSSSHYP
11441	25342	A	11540	2	318	TTERFIYRITPGPKETEVDLPGAPSEP VAALRLREARSFILKL*SFSLVDFDFFLP F*KTGSCLSPLRECRGEIITVHCSRRLP S*SHPPTSASQSSSGSGGFHLG
11442	25343	A	11541	294	409	GTISFFRTCRIGMVAHTWNPSTLGGQGG *II*GOEFQT
11443	25344	A	11542	1	123	GKQRQEPALSYDHATVLLTS*SAHLGLP KCWDYRSDPPCLA
11444	25345	A	11543	69	350	VGAKHWIHMDTKIEADPGNYYSGERGK RPRAEKLPVCYYALYLGNGIICNPKPPC CWKGHDFIYIYVCGHIYIHIYICTHIYI YFF*DGGLLC
11445	25346	A	11544	103	340	LFCAFFLSPSKLDIFYHLSFYV*TLFLKD LISLAFFFLFWEAGSCSVTQAGVQGPNS THCNLCPLPGSNNPSTASQAAGT
11446	25347	A	11545	256	354	PYPFGPKPRGDHWGLGV*NQPGQGETP SLLKI
11447	25348	A	11546	196	335	EIVARLKRSFVGRAQWLMFVIPALWKAK ESGSPSEVRSS*VKKITCRPGTVAHACNP STLEGQGWIT*GOEFKTSLANMVK
11448	25349	A	11547	202	377	TIHTKGVVMGNFILVVFYQNFKTF* D KILGWARWPMPLIPAFWESEMGLLLEPK SL
11449	25350	A	11548	396	26	PPRIKKEKRSFNGAFYFPFCWNF*KKN LSLAKRFPDRDSVFFVSW*GSYLPTTFL QLLRWYVLTSHIAVSFKHLCEPHKNFTL QHSIPYLYIIEIEVYSYFINRNTIYKIN MDFSIVGFVFL
11450	25351	A	11549	232	371	REVFFENIKIGQVQWLTIIIPALWEVKA GGSLREARSL*KYQNWPGAVAHAYNPSTL GGQGGRIA*GQKFEISPANMAKP
11451	25352	A	11550	174	381	NRDEGFRYADRAEVQRLTGITILEHCG L QRPL*RSSCFTLPCGWDRH*SPSHVA GTTGISHTRLIKKAFFSQTGVSSC
11452	25353	A	11551	262	359	DYSNLGLVWVLTTPVLPALWEAKAGRSSE VRSS*PALWEAKAGRSSEVRSS
11453	25354	A	11552	70	380	LHKCSFIYINHCNNPIYGLISLYPKQLF SYENFKDFCNKI*P*IPNFELKSTP*L EKL*NWAMARHGGSR*SOHFRPRRAD HMRSGVPQPGQGESPT
11454	25355	A	11553	319	56	TFFLGPPGFF*KIFFSVGPPLIFFFLPKK FIGEQKNAPGKNFFPGFLPSLFFPFL TLSSALECSGAMSAHDNLCLPGSSNSPA SAF
11455	25356	A	11554	230	399	MMGEIINQANIISVCQIIRRLRHESHLI PGRGYSELRSYHCTSTWVB*DSLKK
11456	25357	A	11555	376	396	F*IFWRDGVSPCCPGWSQILRLQSTCL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GLPKCWDYRPPHPATAASCPYFVHYLL KIWRYSFDLSCLWNLVWGLAFG
11457	25358	A	11556	176	384	KAWPNVRNNYR*NFFFQCCLNFRKRLK CFRCGADKFGKTGFSCLQYALKPTNWGR EQWLTVPNTNFGK
11458	25359	A	11557	295	391	PYKLLITHTHTHTHSRHTTI*HTTLLS LYTF
11459	25360	A	11558	1210	1753	NTWCMERLAVAFGSFNRSPLRGWALWL TPILALWEAEAGGPLEQEFETCLGNM VKHCLYKNLKNVSGV*DLPGQHGETLSL QKFKKCVRRGGTCL*SQRLRRLSWEDCL SQGGQGCSEP*SHQCVPAWVTELDPSK KTKTKKFFGLPSPPLFVCLTHIYVKE YAFVLAEEASGKTSKLTMTSRNGLGK TKKFFGL
11460	25361	A	11559	172	3	KQKFFPPPPSHQIKIFGGGAPEMPFFFF FFBKESRFA*AGVQWRNLSLLHPPHP
11461	25362	A	11560	143	1	GQAQWFMPVIPVLWEAKAG*SLEARSSR PVCATATPPQLIPK*YBGL
11462	25363	A	11561	84	2	KPLDTLGGQGGCIT*GQEFETSLANMV
11463	25364	A	11562	12	387	QGILLPCFMSSEERGIYSNTFSFFFF FGKGGQINPQGGGQATEPRLREPSGL TLQPGNGGPPPPPGQNFFFKKKGGYPG GAGGVLPNGPKGNTPPGPPKARKKRGGP PGPGQKFL*NPKG
11464	25365	A	11563	230	375	RAKGLLSESLLSIQSFKKPSVHTCNPS TLGG*GRWIT*GLEFTTSLA
11465	25366	A	11564	287	55	PPDGRVQWLTVPVPLWEAKEGGSLKSR SS*SQINPVGSVPYSLRVLR
11466	25367	A	11565	115	411	FFFFFPLGENSEFSSFRGGPRGGGHIFW NFPFPG*GVFPPPPPGGNGKGAAPPG FFFFFP*KTGFPLPGGPPPLFGPPP FPPPKGYNFRDPPP
11467	25368	A	11566	139	356	CLLIGWYNTGCITQGSTRTKIGTFFLRQ SSSVAQAGVKCSGMILCYRNRLPGSSN LPDSAS*VAGTTATYP
11468	25369	A	11567	101	410	FLPFFFFFLKKIFFPPRGGGGGN*K KQTPPLGGKKNFPPPPKRGGGGTTPPP PLLPLVF*GEGGFPAGGKKTPKGPNP PPPPKGGEMGRGPPPRGG
11469	25370	A	11568	417	56	EDCLRTGVRDLLPNHPNLQIAGRDCAR L*SQLQEHHLSPGFRGYSEL*SCHCSA WATE*AYRKQNKTKQNYRSSALLHLYTP MATAWIKIAFLRAGDIFLSVLSFLPNYSY PLFSHPQS
11470	25371	A	11569	301	443	EDTTFVCFEVESCSVAQATDSPASAS*I AGIIGVCHHARLIFVFLVE
11471	25372	A	11570	44	408	RGRGHGPHSPWRRRRRLRVVEGRKATES KRRAYKYPLPALCASHQWKPNWLDQSI KIPTGL**LK*PSFIFIFIYLFWKQGLS LAPMLECRGAVLAH*HLRLPRSSLSHAS ASQVAVTTG
11472	25373	A	11571	201	1	AERPVTGPPVYAEPLQGRQG*KNMFKN MQHPRWADHLRSVQDQPGQYGETPVST KNTKITQAQCI
11473	25374	A	11572	343	1	FGLLFAFTLEYKLYESINHFAHCCVCRF SSGTLHVVCNRRHPNKLDEWNSGGGGRQ DLTLTPRLGCSGVI MAHCNLVLLGLSNP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VSAS*VAGTIGAHSHAWIDKLFVKTGPLY
11474	25375	A	11573	209	3	VGPPPKSLPGGFFFFCPCFPRLLKKKKKKPGLVAYTCNLNTSGVRGKKIT*AOBFKKSPSNIVKFWY
11475	25376	A	11574	312	430	QRYARPGPVVHCYNSSTVGGRSRGIV*AQEFATSLCNMT
11476	25377	A	11575	125	3	NSLGPVVHACNPRSLGG*GGRITSAQBFETSLGKIRRLPY
11477	25378	A	11576	190	362	CVNNYID*EKKKKKKRERKKKKKKKKKKKKKK*GGGAPKKKKFTPGGGRNFFFL
11478	25379	A	11577	231	340	KRITRVNQDGLDLLTS*SAPLGLPECWDYTMKPLY
11479	25380	A	11578	60	3	RMQSV*IFTPMSLQAYLIYSSSVAAGAQSGIECKYQFAWRWNCPERALQ
11480	25381	A	11579	285	406	KKGNWPGAMAHTCNPSTLRGRGGWIA*GQEFETNVGDMAK
11481	25382	A	11580	121	1	NLNCPGVAHASNPNTIGG*CRPTV*GQEFYTRIANTVKP
11482	25383	A	11581	199	384	KKTPPGGIFFCPEAGPAPPL*TPFC*TPLFSPAPFKPKRALKFFLKPKRGFFQIPFFFF*DGVS LCHPGWSTVARSCPRV
11483	25384	A	11582	677	934	YGSRHICICFLOAISEILFLKNPARHGGSQVQDQPGQSKTLTLRKKSK*ARHNGSLSSQNFGRRLRQEGHLSPGG*GCSEL*PRHC
11484	25385	A	11583	104	2	KKIGGGPPLFFFFETESCSVARLE*SGAISAHCN
11485	25386	A	11584	349	9	GGRLGPRKTRVQWGIPEFPPLHLGGKAKPCFPKKKKKKVGLNKHYSKEDIQMVNRYMKKCSLSPREKIKTIMRYHFPPIRMAIRKIKDPKQ*GCIEKGSVVRPMYL
11486	25387	A	11585	163	1	TAVRIKHNSYTLTPCLRHSRYLINVTCWPGPVAHACNPSTLGGGRWIT*QQEF
11487	25388	A	11586	192	41	SKSKYHIYGDALQKSTVYKWIHFHKKG*DDVKDKAHSTRLSMSICEKE
11488	25389	A	11587	30	374	GWSPEDLFPGLPALKGFSGEGG*PFLPFQKKRGGGGSSPPFVLKRVPRNRLYPGGGGFR*PKQGPCSAWABPDLSLKKKGFQKQKKKKVLEKT
11489	25390	A	11588	66	245	SLCFFVFFVFF*TESCSVTQGV*WYNLGS LQPPPPKKKKNIKKQKKINWGRGFKRRL
11490	25391	A	11589	243	402	FLHLKKKKKKKKKKKKKKKN*KDAG
11491	25392	A	11590	205	3	IRLLGIKNPTPAHCQ*K*KTGEPLW*VVM*FFRRLHTELSYDPAIPLLCINSTEVLAPGIPPRFR
11492	25393	A	11591	404	152	MGFHVSDGLDLLTS*STLLSLPKCWD*CWDTREPLCPGHFAISFNKVVLTNTTVLYFYLIILHCIYCPYKLLFFFFIY
11493	25394	A	11592	311	386	TVYPPLAGNLAHAGA*AGIVGTALSILIRAE LQPGALLGDDQIYNVIVTAHAFVIFFTAIPIIIGGPGN*LVPLIIGAPDIAFPRINNISF*LLPPSFLLLASSIVEAGAGTG*TVYPPLAGNLAHAGASVDLTIFFLH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11494	25395	A	11593	39	397	EGCPLFFVFVFFFFFGGKKIFFFFPRG GGGAPHKIPGPPPPGGNFFPPPPPLRG GKRGPFPFPGFFFF*KKGGVSLFPRGG VFFPSFWRGGRGGFPFPPQKKIFLKG PPFYKKK
11495	25396	A	11594	243	46	GILSCCFHDSLNSL*CD*WVISLCLS YLVSIELGQCGLIFFIKRBSFWLLLLK MYLQPLSFSL
11496	25397	A	11595	327	2	PRAILRTQFLWLPMRPYVMWSQPCSLCF CHTAKTVPTSRPLLLLGFFSLPGIAHISM WLVLSTYGLGFSSEKVLWPGVVAHVCNPS TLGG*GGWIT*GWFKTSLANMVK
11497	25398	A	11596	292	384	LGTVAHTCNPSTLGGQDGWIT*IQEFET SLR
11498	25399	A	11598	125	2	PFGQQRSGGTRGPGVAHTYNPSTLEG* GGRIT*GQEFETS
11499	25400	A	11599	302	408	TGGWLGVVAHACNPSILGGRGRQIT*GQ ELETRLA
11500	25401	A	11600	409	131	GRSGGVPKSGVLKPPGPPGGTFFFFKKP KITRGGGQPPPLFPLQVRVPCNLSLGS GGCH*TKLPPCPSTWGAQ*KLVSKKKCC EGGGRIYS
11501	25402	A	11601	196	330	HHCMLAWVTGRPYLNIYICITYADIYIHI YICITYIYTHRVYIYLLAI*YIYIVYMR IYIYIYIVYIYTHYGYIYIY
11502	25403	A	11602	41	252	TPGRARGQRLGHSS*TGDLDLTS*SACLS LPKCWDYRREP RPAPEDIKPMF*AILSE TILVRGVRSRATPS
11503	25404	A	11603	271	440	KKKKRGRGRFKESKFTSAGLQGNIFFTGP PKLIPRAAV*QRGDWKNLGVTLNRLCH FSFFFAEKGCVCVSQAGFKLLSSRDLP SAPHLGIRLLGRRLQEDPPSPGV*GCSE LQSRCLCTPAWITKRDVPS*KFKKQKTKT HTH*RKPTKGQDHQYHCLPPPHVMPLKV FRGSNVHGAVRTGRSGRSIPELSHAVPH AP
11505	25406	A	11605	113	2	TEATHLVCTYKN*KLGWAWIMPVIPAL WEAEVORLL
11506	25407	A	11606	301	3	WMVCSVKNIALGHACGKFHYEGRGKPA EHPSPWLLVLESLOKKLFLSYFLTFTLL QPPSPRLT*PVFRFFFRDRIMLCCPGW SAVVPERVGRAGNSE
11507	25408	A	11607	117	431	SCDFCLSFSLSLFFFFFRKGIFFLGPRG ENKGGNKIKWILGPGGKNSRSPSPKGG GKRGGPPPGANLDF*KKTGFPPQGGRGGE KPPPPGGRAGGAPQRGKPKAG
11508	25409	A	11608	277	88	RRTTSSWLARNCIQGPAGYHTGS*TPDL KGSACLSFPPKWDYRWRLDL
11509	25410	A	11609	200	27	VRLKPGDSRDPDMQWYIY*ENRPARCGG SLL*S*HFGRKRKADHLRLGVQDTRSSA R
11510	25411	A	11610	17	414	TVWLVMQDPENEWIVSGWGKKEPGRYF MCEARSSSSMDRVFFFF*KKTLEFPFPGG GGAKIWNVGIPPPQGSPLSVAYPLGVWE KKGPPIHPhKKRVPPV*PGGVLFSEPGN PPPGPPKGVGRSSPSPSVL
11511	25412	A	11611	296	428	RIYENWRGTVAHACNPSTLGGQGGWIT* GQSLKTSTGTVAKP

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11512	25413	A	11612	20	362	NFVRGVARGSRGGATRCBFWGLRPFVGMA YGRSPSWLL*VKPSAASHRPPLPRAADT PGTAPAPITPTPAPAAPALTPSSGPGSA ALTLEELQBAIRRAQRWGLTMLPRLAS NS
11513	25414	A	11613	158	2	LMLSRTPLQQL*YTLELELPRLLAPDL LSNSSSLKDLKWTNSNYRASKETK
11514	25415	A	11614	3	410	RSEVYGLVLTITWYQVNRVPWTHKAARFT RVSRWARPRSKISESCYWLPOAHRKS* PLVRTLGLCSLLGFHPLLFSLLATDLV PLPSFALLLLELFLPGMPKLAP*STP KRSFSFYFFRDRVLCCPGWSQTP
11515	25416	A	11615	189	397	YKVLFLVEKNGFFFLFFETKPCCVAPTG VQGNPFG*LQAPPPGLPLFSALAAPEVG ITNGTPPPPRFFF
11516	25417	A	11616	158	1	KGKPTPKTFFCQKQIFFLVFFF*TESHS VARAGVQWRDLDSLQAPPPGFTPR
11517	25418	A	11617	319	425	KVWLYSQAV*KVWLYSQAVAHTYNPTL GGQGWRIA*AYEFKTSL
11518	25419	A	11618	94	2	CLTISWLGTVAHVCNPSTLGG*GGHITR SR
11519	25420	A	11619	381	9	FFPLPLPLPTVSLFPRSPSDAEPKLDCT AAISAHCNLPA*FSCLSLPSACNCRAP PRLTASASRGAGIADGVSTQCSCMVPRL ECGVISAHYNLHLPATSLGLPKCRDCS LCPDEIVDPRI
11520	25421	A	11620	144	431	IVNVIVGKGEKGRKIPE*LIRCNWGN*S WDRVVAEDHVLREPSNRRLARVRCLTP VSQHFGRRRLDHEVRSRLRPACATWRNS VSTYNTKSGWAC
11521	25422	A	11621	174	449	VFSLPFLGGASQLGYLEVRDPLEEAVCP FSDLKPHAGRTTTLFKAIRQGHLSLQRF LLPFVWLCPAPRGGVYRGRQASLS*GGL HPVRASRP
11522	25423	A	11622	316	412	GGPSAVAHACNPSALGGRGGRIS*GQEF KTSL
11523	25424	A	11623	183	2	PKQVYLRNGLLSHSCNKHINRLKRE KIQGVVAHAYNANTLGGQGRWIT*GQE FENE
11524	25425	A	11624	355	168	DLLIVCYDPNAINL*SLLRRLKWEDCL SPGG*GYSEPRSCHCSPAWAAPDPVSK KDRNVEFIYCC
11525	25426	A	11625	154	3	TADVFLGQAGRGNFVVMKKNCRPGTVA HACNPSTLGGRG*ITRGLFEK
11526	25427	A	11626	412	3	IFFPPPKDKRTRGGQKKNIPAPPNPF LGRGNFPPPKPFPPPL*IFPRPP*C KGSIPPLFLPLCFQKKKTPSFFLPNGS PPICBKI FLFPKGF LKFKPRFLKKG PFFFFFGNAVLLCQPGWSAVAQSQ
11527	25428	A	11627	290	423	VFEYFFKFKKNNSWPGVVAHTYNPSSL GGQGWIT*SQVLRPP
11528	25429	A	11628	213	3	LSGIYSGNRRLVRYSKSVSVIHHINRLK KKNHIIISIDGKPLEIQNSFMT*KRN KLKWEDHLRPADA
11529	25430	A	11629	152	2	FQKNRDLEPSKAGWPGMVAHACNPSTLG ARGQIT*GQEFETSMVNMVKP
11530	25431	A	11630	422	189	PLSGFCPSTWGAKQRLSKKKRSEAGH SGSL*SQVLGRLKQKDHSPGGRGFSE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LLNCTPAWVAKQDPVPEKRLK
11531	25432	A	11631	239	424	KEDNNRVFVIGPLGGLNELAHDKAFKPTQ NHHWLGVGHAACNPSTLGGQGRWTT*GQ EFTTSL
11532	25433	A	11632	343	401	AREREHKSAAQC*GMERSVIKHCHVATE *EREQKRERQERASEKERQOESERDSK RERARESERERESTRAQLVRKIVNQIS
11533	25434	A	11633	125	371	FOGCAKICLTNTLLPYAHGYLIWRHDGK GCHEKMTAKI, HSCKLSPDAL*SQLGVP L*THTHTHTHTHTHTHTHTFSEKKGLVP
11534	25435	A	11634	235	433	AALTSTSGPFFSFCSYLINTLGKPNFHE ISTT*FTLQRL*KIIFWPGMVAHACNPS TFGGQGRWIT
11535	25436	A	11635	93	385	FTLKSERRKHSVPQGGKQNKIKLLSPDC KLENKRFGWARWLTVPVIAL*EAKAGES PEGNGEREEATEPFGSIILGFFFTQIA HLHRSDYEPNEDS
11536	25437	A	11636	190	398	NTKKSQKAFPKTQGGKPPPLDPKKASKK TKFFLPKKISTRKFRITGWRGTNPSLKK AKKNLGKTRKKIFP*RPFFPSISLFWP FFFFLFF*KDKVPLCHRGWSAVVQSOLT ATSIQMY
11537	25438	A	11637	190	380	TPKKWPKAFPKTKGKPSFPHPRKALRK TKFFLPQKFF*NPLSPLIPALFWPFFFF FFF*KDKVPLCHRGWSAVVQSOLTATSI SQMY
11538	25439	A	11638	261	91	EKTLWAGHGGTCL*SQLGLRLRWENHLN LGGRG*RSRHCTPAWVTERDSVSNK*IN K
11539	25440	A	11639	1	334	FRANRTVKDAHSHGTNPQYLVEKIIRT RIYESKYWKEBCFGLTAEVLVVDKAMELR FVGGVYGGNIKPTPFLCLTLKMLQIQPE KDIIVEFIKNBDFK*VQCSLANIRGM
11540	25441	A	11640	193	457	DGILLCGPGWSAVAPSQLCSTISAYCN LCLPGSSSEFVSAP*YLGLOACAHAPLM FVFLVYTGTCMLPLSAHHSRAANSSHP YPLL
11541	25442	A	11641	257	373	NTISCFRSLRPVAHTCNPESTLGG*DGQI T*AQEFETCLG
11542	25443	A	11642	211	367	DTTSHPFEWL*PKSRK*RVLDRIWGN* MLVHCWWEHKMVQLL*KTVWWLFK
11543	25444	A	11643	112	367	LQIKTIRYHHILTRMAKIQNTDTNKCYQ ECGATGTLIHCWWEFKIIPVIPALWEAE VGGLLEVRSSRPAPWTRENPIFTKIKN Y*KYKNTPYIIR*LQIKTIRYHHILTRM AKIQNTDTNKCYQECGATGTLIHCWWEF KIIPVIPALWEAEVGGLLEVRSSRPAPW TRENPIFTKIKNY
11544	25445	A	11644	310	335	YHLIAGSLGDIERLSML*IGKAVCHNKY **GCGEPGFLHCWWEWKMVQSL*KIVC QILQT
11545	25446	A	11645	143	455	KRKGPSLWLLGKSMGGIRFF*KKVFFSG FKSLWFFFWPLWKPLERLN*IKISFYPP AKKKGQORQAQFFFFFPRSFSLAGCSG SISAHCNLCLLGLSDSPTS
11546	25447	A	11646	182	458	SRGGIRFF*KRVFFSVIKSIWFFFWPLL KPLGRVN*IKISFNPPAKRGWERKAQF FFFFLPRSFSLAGCSGSISAHCNLCLLG

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						LSDSPTS
11547	25448	A	11647	319	3	RSTKYSPRGWEPMSWFLFLHVFSLPFRS ILGFPPLGLTPLRGSPPPPPFEGKGFY GLTFFFP*EPPCBIFFFFFLDRVLLYCP GWSAVVQSAHCSLELKDVKCI
11548	25449	A	11648	165	2	DQSGRPRKILCAHTHTAHMHTSLGQT* QDPV*THHTHTHTHTPLLYAAQRIN
11549	25450	A	11649	290	3	SKONTTHWATLKSYYTSPQFWRLGSPSS RWQLDGLVRLALFLVCRQPPSLRILTNW EKTEERKRERK*DRERERNEIERNERE RERERETQRMV
11550	25451	A	11650	220	2	TPTLPKGTGLTALDRIPGRDPGPRRAGR PF*AGVAENCPDPAEGGSTRPLGAPGR GSAPP*RHPGPAGRR
11551	25452	A	11651	29	387	FLIFDVTIVIDLACHEPHSYKMAHLINV VCULTAPPTSYPFISFLGPPYSLRHNDI EIRPINNPRTSQCSSERKSHTSLTLNQ KLEMTTILSKDGMKAKTG*EPGL*C*TV SQAVNAK
11552	25453	A	11652	267	2	KFFFPVFSTSKLNFYPGTFPPLFLFSFF FFFFFPMREGFAVTWVGAVAPGAVLA HCSLELVGSGKPPISAS*GAGTTGMHYH TRMY
11553	25454	A	11653	50	411	EAVAGGMEKSMNNLPKGPDTLCFDKDEF MNEDFDVDHFVSDCRNRGQLELRDNPQ LYYKLLKTAMVELINKDYADFVNLSTD VGMEQALNQLSVPL*QLREEVLSL*SFV IERISPPS
11554	25455	A	11654	303	403	VRNMVEVLGVAHAACNPSTLGGQGEQIT *GQEF
11555	25456	A	11655	356	653	SVSPCPFPGPASTLSFLVADFRRRGVDV SQVAWQSKGDTTPSSCCIINNSNGNRITV LHDT*GPRASPCYNPPIISWLNQFPHSFP WASQLPPSVASVYQK
11556	25457	A	11656	442	2	GRPILMRPAVL*SEPRTPACVDIQQQIM TIIDEVVKACAKVQTLAPINSASRMQS IRHVYVILKDSSARPAGKGAIGFIKVG YKKLFVLDDREAHNEVEPLCILDIFYIHE SVQRHGHGRELFQYMLQKERVEPHQLAI DRPSLV
11557	25458	A	11657	109	474	DINMCGRVVLVAERM*KKRKDKYNYEET E*VL*KKVRHSQKQENVAQNAFVVQNA AYIDQPSPAHVGGQGLSKLPSRPGDQGV EPQNLRTLQGRSVIRSATNTTLPFMLMS QRVIAPNPAQLQQRGPPKHGICRTTTP NMNPANV
11558	25459	A	11658	342	3	ENQLKNGEHSKSSQSSAPPNDHNTSLAR A*KWAGAEAEIALLTEAGFGRWVIMNFA ELKEHVVTQCKEAKVHDKTQELIAGFE RNITYLM*LKITREPHIAITSINSRMA
11559	25460	A	11659	204	17	STCTPLPTA*SQSRPHPPPTPTPPAPWR SSNGPLSRGSSSRNSTSSWSIALATGPW THRSEL
11560	25461	A	11660	505	514	GS*GNHFNPDGASHGGPQSDRTGPRGP CLPSPWGAQILRDWYPQEMGTLGKQ
11561	25462	A	11661	80	374	FLFDIYNRCYLIFINII*YLSSNFD*IF IIYLVAIYRLCLGLPRAPRQCKHPRP QFSFNKIGTKR*AWPGAMAHTCNPNTLG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GLGAQIM*GQEFET
11562	25463	A	11662	142	437	GQRVQIFFFFWKRFPPFFAQQGTEGAQFR LIKPSPSGLKEIPPPNPPRKGE*RDGPP FRGDFVFLRKNGVPPCGQGGSKPPAPGE PPFFTTPRGNNRG
11563	25464	A	11663	120	353	QALQVMLKHVNNFFFLFFLFWKQSFVPL PRLECNQATSVHCNCLPG*RNFPASAQ EFRIAGSYDHAICPPASGKGE
11564	25465	A	11664	1	404	NTWSDLTISYFHPRPSAFLRQGLALSP RLEYRGTTIGHYSLDLWGSSDSPASISR VAGTTYRCM*FQLLGRLLRRENHLSRGR GCSDP*LCPYTPANVTERDPVSKKKLRG GGNSLLSSQTMV
11565	25466	A	11665	493	3	NIWIPDVLPGHLARQ*LGSPGKLSAGF* PLQFPQTLSSARAPFFCLPRLQVRNTVG FLPSPHTSRPSSHCLPACPLPSRTQPPWP VKPGPTACRGFLQHPPTPGSPSP*SPQG SSWWDTDLRALECLLRILRGRNCSVFT TQQLSHEGMNKEFLLTCAKKK
11566	25467	A	11666	3	401	CMERAVTVLLPGSATQSPFVYAPRALAR LWLTAAMMISGFADYEA*SSRCSSACP AGDSLSEYHSPADSFSIMGSPVGAQDFC ADLGVSRANFIPTDTDMSTSPDLQWLQV PALVYSVGPSETIAPHPLGVP
11567	25468	A	11667	1	446	LSCAKPPQRLRHTGIKIFNVFEETRAN KHLGVSGLKPRGFPALFLSVSSFGQKK HVPQWLQSHSHILVISLDDFFFFFEEK KPPFFPPGGRERDQTPFN*TPPRGG*RE SPFFPSRGGGTQGWAPHCP11FRFFQKK GVFPLRAR
11568	25469	A	11668	18	403	DPLQRPQYRGGLRSVGCGLQSPTRGES GRWNPQAQARGPGEAQAWAPGGGPREA FSGQGRPPPLGLHPHRRRGAGPPGPMGP *HEGQGSC*GASCRGGLACTAFAASSP PIFGGLTPENLNFEE
11569	25470	A	11669	157	1	PRPQGFVVFVFFFMQFGRLECSGAISA H*NLHFLGSSNSPASASHVYAPLY
11570	25471	A	11670	396	7	EKVGQARDKSACEGHSCADARSCLHLRV DQGGQHGSHGACPGRRRLRGPDTHRQSCY QCRNRSFDRQLQPGRAGTP*CAEAAEP DAAVHPGQAPAPRLPPALPGRGLLPLPH PGGSQRVYCVRCIGSKLR
11571	25472	A	11671	209	3	DDLGTTHRPKGSQVRVTPREAGENPSAVL PCYLHLVFPV*EDEVKPEDSIPDMPGNE YAREFLAHAPLY
11572	25473	A	11672	270	101	LSLNRWILGAYIIFETESHVAQAGVR *HNLGLLQSLPPGSRRLPAFKVAFLEIG
11573	25474	A	11673	421	592	SSCTPGV11KIPCVRSNHMKLPGPGMVA HTCNPSTLGGQGGRIWSE*FKTRLGNM A
11574	25475	A	11674	176	6	LTFVYMPFCFALSSIMTYGLAM*FHFH SMTLFIIGVLSVALAIYQ*WLDVSRVSV
11575	25476	A	11675	1	418	NTVCVCVCVCVCVCVERKAGHRLTDSFP IQAGPGAQARTLCLRESTGGALSSGLPA SRYQDPGRGALHFCVWTPRCWNWRLNY PPARSPSREAVCYFRQTLKKWRSRPGQG GRILLRVIRTASTFRDTS*TESACLGARP CLDGK*VCESVPCFSLHHTHTHTHTHT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
						HCI
11576	25477	A	11676	305	698	SFMGRSPRKIDQFCNSRNMVHGSVTFRD VAIDFSQEBWECLQPDQRTLYRDVMLEN YSHLISLGSSISKPDVITLLEQKEPWPV VVSKESTRWYPGK*E*SRQGRAIIVPDS PCAQRGVTPLRGLENFLQ
11577	25478	A	11677	107	397	GGDGRETLRAPADDGCI*QERAETPLAI SCPRSSSTCRGRARRYDGCRTRDGHQLI QRGQQQESSRRTAQPGSSKLCRGPGGHR PSLGTGVGHGCSL
11578	25479	A	11678	514	554	RAKPTFP*GGEGQNFGLLKPPVSGLP LACTPPKRWKPKPPPPAPPHFLFF**K RGLIF*PGEVFNLRNWKLPPSPQRRGN KGRNQPPPRGTFMF
11579	25480	A	11679	266	3	GPPLFLGLKN*TFPSPTKV*IFPSQVPS SFPQGLKGGVREIFFFFFF*DRLECNCT ISAHCNLRPLPGSSDSQASAGTTGVCHYT RMY
11580	25481	A	11680	1	408	NTCALRHRDHFSFWSDGRTKEGERIVQ ENWLISWNNSFVSPETLLTSLCPLGKEGM PGEDGTAGAGKVPGEDKIPG*DGTAGED GTEDENGTTGEDETAGVGKTPGAGGTTG EDDTESDGTGDETAGKGGTAG
11581	25482	A	11681	244	420	KDSESTKAYIRDNISSTKKKSWPGAGA HPCNPSTLEGGG*IT*SQEFETSLANM VKL
11582	25483	A	11682	294	443	QMNTCTHIQPAYVH*EKYFRPSAMAHAL NPSTLGGRGGWIT*SQEPQTRP
11583	25484	A	11683	346	1	YNTNQFTLRGTQASVYTCLTALIVLKLL NQPYTLTSAVLLNAGNQPFHAFSPPSLH PDAFHSKIMSHIIILLGFIPPLPASQS LTLSPSLERSGTISAQCNLCPLGSSNSP ISA
11584	25485	A	11684	140	423	SSHQASSPPTTASHSMKISVAATPFFLL ITITLGTKESSSRGPVHPSECCFTYTT YKIPAQRMIDYYETNSQCCKPGIVFITK RGHSRWNTPK
11585	25486	A	11685	163	3	IKIPCNRLKFGPPSCCGFFFPPLPPFF FFETLSRSVAQAGLQWRDLGSLAL
11586	25487	A	11686	179	1	PIVFLGMLFVAFAPRGPFESVTKPPNFF FFFEMESCSVAQAGVQWRDLGSLQARPP RST
11587	25488	A	11687	192	1	EQGFDGHLASWISLKD TAKWNGDELCS YYQSCCTDYTAECKPQVTRGDVFTMPED EYTVYDDG
11588	25489	A	11688	89	3	SGGYCCCLCCRCRSRYSCCCRLREGPTK
11589	25490	A	11689	168	2	QDRLQPHESKRRLGPAPQLRRESSTPS VVNFQSTESQLMSKGEDETKDDSKETV
11590	25491	A	11690	301	397	HFVFSLVTGMNPLSPYLNVDPRYLQVR LRFY
11591	25492	A	11691	18	421	TKALQITCYLHSTMSEESDGKLIEDSLI QLRCHFTWKLLIEAPEIPDLENRIWEEI QFLDTKYNVGIHNLAYVKHLKGONEEA LVSLKKAEDLIQKEHANQADIRSLETWG NFAWVYYHMRGLAEAQTYLDKV
11592	25493	A	11692	188	3	PLQKGFGAKERGQKGFRLRGVVRASRP RPPFGPSLFFFFFFETDSHSAQDGVQW CDLGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11593	25494	A	11693	24	391	APRADAMGHFTEEDMATITSLWGQGNVE DAGGETLGRLLDVYPWTQRFFDSFGNLS SASAIMGNPKVKAHGGKGLTSLGDAIQH LDDLKGTFSQLSELHCDKLHVDPENFKP LGNGLQTALQ
11594	25495	A	11694	138	425	NSGVKAAFQLNPGNPNLEGKPGPGFKTH PGQLGETHFLFKIHYLSGLVGKPWESQL LGNLNRNHWTPERGGPRDLRHCHGIQIP WATNGNFVLKKK
11595	25496	A	11695	158	838	CGTVHSCDAGQRQATAPSHPCDHGNQQ PILYRVLCCQLFWILCFVFSHSIMSTKC PSVSPVSGEMKKRKAITLEMLKIQAQ EGGKPVMAIARELGWLQSTISTILRDKK QISDAKSSASVKSTVITKKRAGPIDDM EKLVMWMEDQIQKRIPLSLLMIQAKAR SLFNMLKDRASDPTTYTQMFKASHGWFPQ FKRRHNFHNVKITGEAARAGNEGAIAFK EQL
11596	25497	A	11696	834	1431	SSACQGSQGWPPRQFWMMWGSRRAPS VTHRTGERCSTSGSAPLPLLLSSLCSSL PRSWEHSTLRQPPHPLPPGCLPPGRE AQRSLGAGHGPGRPAASYPDTQADR KQQQHHPGPDQHVGHREGLALEDAAATHL GLVAALSCWLLGRAEAGYQVPHGHDPK DQHPQADGGQIRIVRAIGLGLGHHVSGRR ARP
11597	25498	A	11697	143	1	ISKERGASRFGSPWVFFFLFLESRSVAQ AGVQWCNLSLQAPPPGFT
11598	25499	A	11698	58	459	KGKEEKVKRKEAEQNFSPYAQDKQERIK GNENDEKTKQKGTIIDIELPKGLDETG ENMDSTLRTTPFEPLNNKQILVLGLDG AGKTSVLHSLASNRVQHSVAPTILGFHAV CINTEYSHMBFLEIGGSKPFRS
11599	25500	A	11699	215	1	GTKKALWAGGGGFFPYLPPMGPLGPICG GVGKGSFGLGCPFFFFFFFETBSCSVA RLDAQWPDLSLQSP
11600	25501	A	11700	300	420	KFKILFGNVFAAPHMENLKRGETVAKE ISEAMKVKAMC
11601	25502	A	11701	351	466	RIKNADLSQAQWFTVPVIALWEAKVGRS LEVRSSRPVW
11602	25503	A	11702	172	400	SNRLRNKIQGVFLNDSSISPFILRKQSI GQAWWLTVPVIALWKAESGSPEMDSTT LLPSSSQVPSLVKMEKLNYS
11603	25504	A	11703	284	408	ASVFSSFFVCLFVFEMESRSFAQAGVL WRDLGSLQAPPPG
11604	25505	A	11704	20	447	LPGADYGGGELSLRLFHLLLASAAWVPD ESQVTLNSAICVLSTVLIMEFPDLGKHC SEKTCQLDFLPVKCDACKQDFCKDHPF YAAHKCFPAFQKDVHVPVCLCNTPIPV KKGQIPDVVVGDDHIDRDCSHPGKKKEK IFA
11605	25506	A	11705	1	455	HSCSLQFTPTAWDCTGSVSSEQGERPAA AMKICSLTLLSFLLLAAQVLLVEGKKKV KNGLHSAKVRSEKQDNLGNTQIKQKSRPG NKGKFTVKDQANCRWAATEQEBEGISLKD ECTQLDHEFSCVFNPTSCPKAQDERV YWKQVARKLRS
11606	25507	A	11706	1	428	DAEADKMAAAVRGGRSGGSGGCSGAGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ASNCGTSGSRSGLLDKWKIDDPVKIDK WDGSAVKNSLDDSAKKVLEKYKYVENF GLIDGRLTICTISCFFAIVALIWDYMHP FPESKPVLALCVISYFVMMGILTIYTSY RE
11607	25508	A	11707	1	422	RSQARSSAAAAARASVPLRGSPGPSAIM PMFIVNTNVPRASVDPDGLSELTQQLAQ ATGKPPQYIAEHVVPDQLMAFGGSSEPS ALCSLHSIGKIGGAQNRYSKLLSGLLA ERLRISPDRVYINYYDMNAANVGWNNST
11608	25509	A	11709	88	423	AADAMKQAEAMGAFMRLAYQELQIDRL KEDKMLLNLEGNKREHAERLGMGLVSRS SVSHSVLSEMLVIEHETPVSAKSSRSRL DLFDDVGTFCSGPSKYTDNPFSLWESIG
11609	25510	A	11710	393	130	NPSATAQSFHAAKRLSTLDRPGSQAPQ KMPSPKPGVVLPASTNAVPTPLAETP SKAHPAISLLSTREGIFKAVPSPASSCS FLHV
11610	25511	A	11711	331	440	KIFFLNFLISRAWWCAPLVLATWEAEVG ESLYPRRS
11611	25512	A	11712	122	478	SGLCPQQPFRANSCPPSSMASCAEPSEP SAPLPAGVPPLEDFFVLDGVEDAQGEE EDEEEEEEDDLSELPPLEDMGQPPAEAA EQPGALAREFLAAMEPEPGSPVPKWL DILGNGL
11612	25513	A	11713	102	2	TNLGNPRRPPPPFFFTVSLLAQAGVQW CDLGS
11613	25514	A	11714	126	2	FFAPFLKIFPPPPFSEMESSCVLQAGVQ WHDLSLQNEGSQ
11614	25515	A	11715	178	449	LSGGLNLFGIILLYCAIIGGKLLGLIKL PTLFPPLPSLLGMLLAGILITNIPVINDN VQIMHRWSYSLRSIALAILVRAGLVLE SKALEK
11615	25516	A	11716	48	417	GSGGNHVSCCDTMEGGGGSGDKTTGVLA GFFGAGEAGYSHADLAGVPLTGMNPLSP YLNVDPRYLVDQTDDEFILPTGANKTWGR FELAPFTIGGCCMTGAAGAMNGLRLGL KETQNMASKP
11616	25517	A	11717	103	2	PKSPTQWLMAVIPALWEAKAGGSRESRS SRPAL
11617	25518	A	11718	1	413	WPSGQVLVGCLSFSLYCWKRSILKRKNPG FEVLLKIFLKNHPRCHTNRMILQTLATPV SALADEPAHIRATGLIPFQMVSFQASLE DENGDMFYSAHYRANFAEADLNHAAS LGGDYLGDLALRLCTLEPVFPQSY
11618	25519	A	11720	116	462	AGMLPAVGSSVDEEDPAEDCEPVLPIE TTQSEBEEKSGLGAKIPVTITGVLGAG KTTLNLYILTEQHSKRVAIVILNESGEGS ALEKSLAVSQGGELYEEWLELRNGCLCC SVK
11619	25520	A	11721	167	407	EIYSLTRFIEVKMSKKISGGTVVEMLD EMTRIIRETLKEKLIFPVESHLSYDL GIENRDATNDQATKDALEAFNKP
11620	25521	A	11722	254	423	NQLSSIMAMFKKIKSFVVFNDEPKVYG SGEKVAGRVIVEVCEVTRVKAVRILACG
11621	25522	A	11723	3	424	VSCDTMEGGGGSGDKTTGGLAGFFGAGG AGYSHADLAGVPLTGMNPLCPYLNVDP YLEQDTDEFILPTGANKTRGKPELALFT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IGRCCMTGAAGFAMNGLRVGLKETQNMMA WSKPRNVPIILDMVTRQAGALWANTLGALA
11622	25523	A	11724	2	343	AFGTMKWVTLVSVLFLFSSAYSRGVFRF DAHKSEVAHRFKDLGEENFKALVMIATA QDLQQCPFEDDAFTSEVPEFATTCQDD DHFEDRCRRVHTLVVVQLCTPATLLET D Y
11623	25524	A	11725	1	359	HAFTMKWVTVISLVFLFNSAYSRGVFRF RDAHKSEVAHRFKDLGEENFKALVLIAT AHYHLQCPFEDHVKLVNDVTEFAKTCDA DESAENCCKSLHTLFGDKLCTVATLQET YGEMADC
11624	25525	A	11726	1	349	GAMSDRKFSAPRHGSLGFLPRKRSIRHR GKAKSFPPKDDPSKPGHLTGFLGYKAGMT HIVREVYRPGSKANTNEVARAVTIVETP PMEVDIAGYMETPRGLRTFNTAFAEHM SDEC
11625	25526	A	11727	81	349	TKGSVVSCCVCLCVCLCTWSHLCLRLVTW LPDMDDDLWLQWVTSQVPTVLMCLLP ASRSQMPVSSQQASPTPEQDWPCWTPC SPEGC
11626	25527	A	11728	264	388	QADPKDIMKFPGLLENQRLSFLLEKAIT REAQMWKVNVRKM
11627	25528	A	11729	2	471	PGCSASWSKRGSGPDMSSMAAGSVKA ALQVAEVLAEIVSCCVGPEGRQVLCTKP TGEVLLSRNGRLLLEALHLEHPIARMIV DCVSSHLLKKTGDGAKTFIIFLCHLLRGL HAITDREKDPMLCENIQTHGRHWKNC SR WKFISQALLTFQTQIL
11628	25529	A	11730	160	377	LQGFGRPSVYHAAIVIFLEFFAWGLLT PMLTVSIAELGLCFVRERDKFLGTYHCV CLDTCLGVALDSDLKQ
11629	25530	A	11731	45	438	KLGRKEATVTKESCKSKSRKVGSPDRF RSPQKRSKGRQDCFTLFCFWKVLDKNME LISPTVIIILGCLALFLLQKRLRRPP CIKGWIPWIGVGFEGKAPLEPIEKARI KVCGRGRRLQRRQCFLF
11630	25531	A	11732	169	292	DSILLVNLAACSAVISAHCNRLPGSSDS PASASRAAGGAHL
11631	25532	A	11733	473	600	KFWEKRTGGRGSKSKNSETGEIVSISA LSTTEVAMHTSTSS
11632	25533	A	11734	19	349	APSPDAMGHFTEEDKATITSLWGTVNVE DAGGETLGRLLGDYPWTQRFDSFGNLT SASAIMGNPKVKAHGTIVLTSLGDAIKH LDDLKGTFAQLSELHCDKLLVDPENF
11633	25534	A	11735	234	359	FYHLKSFTVSSVQSRWLTVPVIALWEAB AGGSPEVKSSRPAS
11634	25535	A	11736	15	372	KLPLKALTGEEKTHINIDIIGHVHSVKS TTGHLIYKRGIDERTIEIFEKEAEM GKGSFKYACILDKLKAERERGITIDISM RKFETSKYYVTIIDAPGHRDFIKDMITG TSHADCA
11635	25536	A	11737	1	357	IWKAAMASPAAGSWARPPRPMREFQTLM PTNAAEDQKLKLERLMKSPDLAVTIPEK MSEWSPGPPEFDRDVMGSRAGAASGEF HVYRLLRRREYQRQDYMDAMAEKRILDA EFQRRLE
11636	25537	A	11738	24	335	APNANAMGHYTEEDKATITSPWKGKNVE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: In USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DAGGKTLGRLLDVYPWTHRFDRFGNLS SDSAIMGNPDKAHGQKVLTSLGDATAKH LDDLKGTFAQLSELHCDKLH
11637	25538	A	11739	141	335	MQFLPCIPILKSLKSVASHSQTVHSDI ISTVEFNHTGELLSTGDKGGRVVIQRE QESKNQVHR
11638	25539	A	11740	7	337	APSPDAMGHFAEEDKATITSLWCKVNVE DAGGETLGRLLAVYPWTQRFDSFGNLT SDSAIMGNRKVNAGHTKVLTSLGDAIKH LDDLKGTFAQLTELHCDKLHVDPENF
11639	25540	A	11741	182	360	SRHSISPPVNQIQLGASVTELTVTVTKT ARVSRQWLMFVTPALWEAEAGESPEVR NSR
11640	25541	A	11742	174	1	HFSDHSLFVCVRQDLTLLPRLECSSLIT AHCSLHLLGSGDPPPTAASWVSGNTGVHY HA
11641	25542	A	11743	75	218	KIILGRAQWLMTVIPALWEAKVGRSPVS ASQSAWDYRREPPCPSCTI
11642	25543	A	11744	168	2	LAPLWSLGPVLGGVGGSPGPGFFFFF FFFFETESCSVARLECSGPILAHCSLR
11643	25544	A	11745	83	2	REQRFLPFVQLCPAPRGGVYRGRQAS
11644	25545	A	11746	156	3	FHSGSGRVENPSFFFSFFETGSCSVTQD GECTGATLAHCDLCLGSSNS
11645	25546	A	11747	244	330	KDRAQWVTFVIPALWAAKAGRSLEVRSS R
11646	25547	A	11748	201	1	TSQPLIRITLSTFFFSRDGGLTMLPRL DPFLPGSSNPPSCSASRVDTTGMCHHT RLIFFSQTDDK
11647	25548	A	11749	262	3	VYTSLTPPPISVNLLTQVSPRSVSYEQN ILCLLFVITYTCTFFVCLFVCLFVCFK MESCSVAQAGVRWRDLGLLQAPPPGFTY TT
11648	25549	A	11750	225	3	PIINFSVPQFLHLYNGIITESTPPSCCI LKQSLGQAQWFTPVITTLWEAEAGRS EAWTLKILANMAKPHL
11649	25550	A	11751	185	2	VSTPFNSFPSPWDLVFLKGFPPPPPP FFETEFCSPPRLERNAGPLAHCNLRLPR SSNSP
11650	25551	A	11752	261	336	DRVSLWSPRLECNAGTSSHCNLRFP
11651	25552	A	11753	282	381	TDLLYKKKCGLGAVAHAYNPALGGQGG RITCS
11652	25553	A	11754	202	45	NPRKVKLQWALILPLPFLGGLKSRFQ KKKKKKKKKKKKKKKKTLVVIC
11653	25554	A	11755	293	357	LTPVIPALWEAEVGGSPPEVRS
11654	25555	A	11756	264	1	TLPINVVCCDHSTGPSLISLPLSLPYS LRHNNIEIRLINNPCTACKYSCLKKSHK SLTLQKLEMIKLGEEGLLKAQIGQKLG LLHQ
11655	25556	A	11757	126	1	ILPGFLKELKIELPFNPAILPLGIYPKE KKLLYQKDTCTHMF
11656	25557	A	11758	399	226	IEKGTGRVWVLTMPALPSEAKAGGSPE VRSRPACIGLLKFYYRCEPQHPARLS EI
11657	25558	A	11759	235	380	DTTVLKLGLITLQWASKCSSERKSRTS LTLTQKLEMKLSEEGMSKGD
11658	25559	A	11760	249	357	NRASGQTWCPTPIMPALWEVEAGGSLEP RSLRLTWA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11659	25560	A	11761	168	372	KLHCLLCFFYLSEFFVFCFLETRSLVAQ SKCSGTVITHCSLKLCCSDPATSDSRV AETTGTGYHAGL
11660	25561	A	11762	303	377	QFAGCRWLMPVIPALWEAKADGSPE
11661	25562	A	11763	135	1	ATTPGLFFIFYPFFETESHIAQAGVQCM ISVHCNLCCLPGSSDSPV
11662	25563	A	11764	219	2	KLRSSQLSEPEVRPDSTLSMLMHAHAHT HTHTHPHLFLPHPCSRPHTSTPTCMPIV THSPIYLKFKHSHTYIL
11663	25564	A	11765	102	1	NRPINNPTMASMCSSERKSHKSLTLNQK LEMIKL
11664	25565	A	11766	245	3	PGEPEEDQLVKFRPSLLWVFMFLFRLR SLALSPRLCSGVECSGVISAHCNLCIT GFKQFSCLSLLSGNDYRHVPPCPS
11665	25566	A	11767	350	97	GSVPASQVTRPTLMTSLADKWFSLCLT SLRVNFGVALILSGSHSVSQDTLLDLTL FSTHLGLPKCWDYKRVPPCSAQFLVTFL
11666	25567	A	11768	188	391	LGSVAGDLLCFGGVIFPCSFMPFMSLC YYLYIWYNSCVFLFKTEPHFVTHSGVH WCDGLLQPPPPN
11667	25568	A	11769	131	2	YTLVTPNKSPIENTQLSWAQWLVPVIPA LCGAETGELLEPRSS
11668	25569	A	11770	165	1	VLIPLIHLCIYIYIYTYICVYIYTRIYT HICITHVYIHIYVYIHTYIYTYMYTY
11669	25570	A	11771	72	1	ILLFFFFFEAESCSVAQAGMQWCN
11670	25571	A	11772	121	3	TSFVLFCFETEFCSCCCGLCNGAILA HCNLRLPGSSD
11671	25572	A	11773	152	3	HVCLNLTLPFLFEKNIFSLCVCVCVCVC VCVLCKKKCKEKFYFERTF
11672	25573	A	11774	190	2	GFSPRQRGAPRVPPPLAGFPPIFFFFF FFEMWHSVAPAGVQWCNHSLSAALTSP DSGDPP
11673	25574	A	11775	287	1	GAHRRKLFITPGESLRDKQIAGFEHRGG EKKKTLFYKKKKKKKKKKKKKKKKKKM LPKCNITMKNHQVPYSIRPTRECADLRV FYFIKFQILKY
11674	25575	A	11776	121	3	KCASRDLSKPPFFFFFLETESRSVAQAGV QWCDLGSQAL
11675	25576	A	11777	142	1	EKTLHVRNTIHNSEGSLVIKIHGRIGVV AHACNPSTLGGRGGQITRS
11676	25577	A	11778	179	3	SHQVPVPGTLDLPRGPQKLQSTSEAESEA SMSEASSEDLVPPLEAGAAPYREZEAA KK
11677	25578	A	11779	147	6	KTPGLKKNSNFFFFFFFETRSHSIARA GVRGCDLSSLQPPPLGLK
11678	25579	A	11780	184	3	GFGFYIIPNYRLFFFSLLIGPFFFLIFF ETEPCSARLECSGVISAHCNIRLLGSC DSPA
11679	25580	A	11781	120	319	VKSLAKFLVNYQLHRQTCGQAGRGALR QRFGRPRQVDHLRPGVRDQPGQHGETPS LLEVRLSSG
11680	25581	A	11782	91	3	YICLSLIYTHTHTHTHTHTHTHIYIVC V
11681	25582	A	11783	221	332	SRLGMVDHPRSGVRDHPGQHGETPSLLK IQKLARRSG
11682	25583	A	11784	243	379	LKYSVPIKNCKPWPGTWDHTRNPSTLGG QGGWITLDQKFETSLAN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11683	25584	A	11785	327	5	GRVDSQPIYPKNPPGSFPIYPGSFKTL FPYLQSRHSFSIPRSKLARFHQAKPLFC SKPSQSLSPHSSELKKDLQARWLTPVI RALWESKAGRSPEVRSSRPTWPT
11684	25585	A	11786	245	359	FKGMDRLRSGVRDQPGQHSKTPSVLKIQ KLAGHGMRL
11685	25586	A	11787	356	67	RDIASITARLRYDRGVGITRLEVLKSD EYTKGSVLDFSRETEPIGYIYIYIYI YIYIYLHSLPLNHMEISLGHPLSNK VQNFDSPKLSYH
11686	25587	A	11788	103	3	KYIIPVCIFPPFETESCSVTQSGVQWCE LRRRG
11687	25588	A	11789	136	1	VHQPTIRILNYYYYYFFETESYSVTQAG VRWCNGLSLQPLPPGFK
11688	25589	A	11790	291	163	SLLLLPRLCENSTISAHRNPRLLGSSDS PASGRSLEPRSSKLQ
11689	25590	A	11791	107	2	IFMYVFFETESRSVAQAGVQWRYLGSVQ APPSGFS
11690	25591	A	11792	329	3	KNPRNIIGKSRGPYITNPPGDKGPKNSS PRGNDLSINKNWAQAFQPRGQKGLFFPK KKKKKETQSRSIPLRECNGPTLAQCNLK LLASSNPPTSASHSAIISMHS
11691	25592	A	11793	213	3	ISPWLFLLLQATLFRSQYPGFPFPLSLS PYLFPFKQLGSGFFFFLFFFKTESRF LARLECSGIITAQ
11692	25593	A	11794	1	400	KRAAPQPAPEQRDLKKKKKKPPLAPSSL FRFWEKLLPSFQFRQPRGPFGLTRGVSF AFHRRRFQYGNMGEKQTWGNPGSSSNP PPGTAGSLSGNRGPGWGGKIADRFWLYA RDSFGHSRGLKGSCECAHLGK
11693	25594	A	11795	3	769	RKEQTRNARAEVLROAKANFEKEERRKE LKRRLRGEDTWMLPDVNERIEQFSQEHVS KKKKKKDKHKKAKKEKKKKSKKQKYEK NNSSDSSSSSEDEWVAVPSQTPDKEK ANKVKDEKSGKDDTQIIKRDEWMTVDFM SVKTVSSSSSLKAEKETMRKIBQEKQAL EQSMEIFQSKLEDAEKAASKEDYRRER WRKPTYSDKAQNCQESRESDLVYGFCS RDRYATDTAKNSNNEKFIGDEKDKRPG SLE
11694	25595	A	11796	110	13	HTHTHTHTHKHTHTHTHTHKDRSGKIKC VPTV
11695	25596	A	11797	184	2	SEIFGKFHVFIYILTVHFMPTQVYVERD VLGQEQLLTPVIPALWEAKAGRSPEVRS SRPA
11696	25597	A	11798	83	387	GERRRRRRRLWAPLQKKKKKKKKKKK KKKKKKKKKKGGAPLKKPPGGPHFSGG RQKNIPPLKGGELKRAPAGDFKNPGRGK IARGGFEEKNLWSGGEK
11697	25598	A	11799	153	2	IPWEDTVYSGYPQFLFSHSFFYFYFFE TGSCSLTQTGVQWCNHSGLQPR
11698	25599	A	11800	93	3	VWGRAWWLTSVISALWEAKVGESPEVRS S
11699	25600	A	11801	115	1	NPLFFFFFFFEMESCSVAQAGVQWCNLS LQPLPPRFK
11700	25601	A	11802	295	137	RCFIFILFINKLYFVYLFYFFEMESHT VAQAGVQWRDLGSLQAPPNNKLYF
11701	25602	A	11803	287	1	MGPAPFKGTGCGFQDFRKNLEISAGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						THSPLLAQNFRVGVAPSPRYSPPRFGSKG GGGFFFFFFFETESHVAQQAGVQWCD LGSLOALPPGF
11702	25603	A	11804	202	3	WSVCCFKQGLGLSPRLCNGAPGFKQSF PLSLLSNWGYRGPPLNFFFFFFFEMES CSLAQAGVQR
11703	25604	A	11805	3	315	FMLLILTLFLLRNDRLVQCDVRSSVVC GFLGLWSVILYPLMAAFMPTMWIFLFI FSMLFFYVFFLFLFLFLFLFLFLFLFCF FFCFYLFRRFFFFFFLIFSSP
11704	25605	A	11806	126	3	KRGFFFFFFFETESRFAQAGVQWC DLGSLQALPPGV
11705	25606	A	11807	130	2	QSIKMTCSLYFFIKKNVAVWLTPVVP LWEAGAGGSHEPKS
11706	25607	A	11808	149	1	GGKAILFFFFSLSPRLCSGAIPTHCK LCLPGRSRHSPASAFRVVGTAG
11707	25608	A	11809	258	3	KYYYQGNRQIKFVNAKSNKNLPSYSQKA SWFSSRNIRMMGQHQPMLDNPSTFIKK LGQAWWLRPVTIPALWEAAGGSLESRL
11708	25609	A	11810	153	285	CASPIRSHQKLNKNGWVQWMPVIPVW EAETGGSLLQRLSSRLA
11709	25610	A	11811	160	3	NHLFLLLNRYKSIIFGRVQWLMPVSSAF WEAKAGRSFEPRSSRPAGQHGTKL
11710	25611	A	11812	89	2	FFFFFFFETVSCSVAQGGVQLCHLHSLQ LN
11711	25612	A	11813	254	336	LLGQPWLTPVIPALWEAAGRPFSEVR
11712	25613	A	11814	108	2	CVGVLGFFVCLFFETESCSVAQAGMQWH DLLGSLH
11713	25614	A	11815	166	289	SHSGWNAVWRDGSLLQPLTPGFKRFPCLR VPSSWDHKCAPPC
11714	25615	A	11816	192	2	DKDPGKVTREPFLLCIFYLFICFLRRT LAVSPRLEFSGRGCSSEPRSHRCTPSWVT EQDSCRK
11715	25616	A	11817	228	343	LLQVSIQNEADAGWAWLTPVIPTLWEAK AGRSLEVRSL
11716	25617	A	11818	322	407	VLRLMLHCLRECKLVQPLWKTWQFLKD
11717	25618	A	11819	119	1	WEKIVRGKKCKQKENTHTHTHTHTHTH THTYRESKRERLV
11718	25619	A	11820	269	1	FVQVFYILWTQSFCLTCCQWFLGYHLS SVSNRFRMRSGKSTFFMTSEFFFFEMES RCVTQARVLECSGSISAHCKLHLPGPRH SPALV
11719	25620	A	11821	217	389	EHIETVYGLGISEHWGKGLFNKWLTI WKKDYSWQWMLMPVIPALWEAEGGSRV H
11720	25621	A	11822	188	1	GSHMPCRVISSVHESMNEFFAVPTSYPA NPOPRERAWRNQREKEDKKERSQRSVGR VQAGLV
11721	25622	A	11824	126	3	KLQGVQWLTTPVIPAPWEAAGRSPSEVR SSRPASTWRNLV
11722	25623	A	11825	224	3	ALIIKKEVSAMELEGSNRIQAYGVQST GARDYHAAASRVPAIKGTHHARVIFVF LVETGFHHVGQAGLDSC
11723	25624	A	11826	3	364	HELPEPLRLVLTARVAMAPGSRSTSLLL AFALLCLPWLQEGAVQTDPLSLRFDHA MLQAHRAHQLAIDTYHEFEETYIPKDQK YSFLHDSQTYFCFSDSIPTPCNMEETHQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KSNLELLR
11724	25625	A	11827	2	376	ARELPEPITVLRTAHLKAMAPGSRITYLL LAFALLCLPWLQEAQAQTDTLYMLFDH AMLQAHRAHQLAIDTYHEYDETYIPKDH KYSILHDYQTSFCFSNSITTPYNKEBTQ QKSNLELLRISLL
11725	25626	A	11828	288	3	IHTKNPSVHHHQRPKVDKTTKMGKKQS RKTGNSKKWSASPPKEHSSSPATEQSW TENDFDELREGEFRRSNYSELQEBIQT GKEVENFEKN
11726	25627	A	11829	107	1	KRSGVRLQRLVLRWLTVPVITLWEABVG GSFVRC
11727	25628	A	11830	220	354	QGNKSFKNIIAPWLGTVAHACNPSTLGG QGGRITGHEIETILANM
11728	25629	A	11831	273	352	ENLKTGQIQWLTPVIPALWEAKAGRS
11729	25630	A	11832	239	488	SQTHCSGKTENSEGTNSDRNQVPTALHK RPSSPARFLTRAVPVPVDYLSVAFA VSAVASQWERTGKPFNPLGETYELIR
11730	25631	A	11833	189	294	DQTRWLTVPVIALWGAKASGSPVRSLL HFPLLF
11731	25632	A	11834	1	332	GTSPEPLTVLWTGDLAMAPGSRISLL AFALLCLPWLQEAQAVQTDPLSRFLDHA MLQDRAHHLAIDTYHEFEETIYIPKDK YSFLHDSQTFSCSDSIPTPSNMEET
11732	25633	A	11835	330	175	PRELAQLGSPNVRVSRVKRGPQPMFFF FFWRQESCSVAQAGVQWHPEQQE
11733	25634	A	11836	96	1	VFVETGSRSAQDGGQWCDLSSLPQPP RPPRA
11734	25635	A	11837	267	334	SWVQWLTPVILALWEAAGGSP
11735	25636	A	11838	180	2	SVLEKKEKNLYKNLFTYKLLKKVQGTQ CEGRAQICSVCVCVSVCTCVHVCAYV SSC
11736	25637	A	11839	183	2	AAPLTSSAPQAPGWKPHLAPNSPKNFT GRGQAQWLMVPVIALWEAKVGRSPEVRS LSSC
11737	25638	A	11840	54	330	DPNGQLPEPLKGLWTAHLVAMAPGSRIS LLAFGLLCLPWLQEAQAVQTVPLSRFL DHAMLQAHRAHQLAIDTYHEFEETIYIPQ DQKNSFLD
11738	25639	A	11841	117	344	IQYVQINETEMRNNESYLNHSTLTTI HTLCMGSYLEHFQNCGRARRLMPVI PALWEAKAGRSPDVRSSKEA
11739	25640	A	11842	750	968	RAQGPRIWIKIPFSSPFRFLPLPLVFL YNPPPLFPFPTNATNNSPFPPLPPP LPFSPPPPPSPSRPPPS
11740	25641	A	11843	757	1000	VVELVWYCCLESPFFPLPSPPLFPFPFP SPPHSFPFPSPFRPLPLAPTRPPFPFS LFQAPPLLPSCSPFPFPFPPLSFL
11741	25642	A	11844	278	361	TLLFFFFFEMESHFVARAEVQWRDLGS
11742	25643	A	11845	260	2	GSCLEGLTNRKDIHTKNPSVHHHQRP PKVDKTTKMGKKQSRKTGNSKKQSTSP PKERSSSPATEQSWMENDFDELREGEFT RA
11743	25644	A	11846	194	2	TKFAKEPSPPPCWQEVFKTSPLGFFFCP RSFPVNGFPRLKNLFFFETESCSVAQA GVQWCARA
11744	25645	A	11847	219	1	SLGHTLKQSESSLFSPPGGTPLLFEKPS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VYDPSVPPFQVSKGCGVFFFFQTESC SVAQAGVQWHDLGSPRA
11745	25646	A	11848	126	3	RFFFFKGLFLHFFFFFCFETESHVA QAGVQWCDLGLV
11746	25647	A	11849	216	339	KCFKVGKVKYKLNRETFFYLAQNFFDRNWA TQKMVVKTLLELI
11747	25648	A	11850	190	334	VSYHIEMSFEEVYNEKIHDLLVCKDENG QRKQPVRLKQPIICFEBFLFL
11748	25649	A	11851	198	352	SRQGTWGIHGLECFVCLFVLFETESH FVPRLECSGAISAHCTLHLPGL
11749	25650	A	11852	371	1	PPKKLGIQVFTFPAPRAFVPLVFKKKG FPQGNLVLPGFFSKVSIQGVPPFCRKP SGWGEAFQIGFFINRGKKFFPLGFFL KKVFLKFLAKFFFFFETESHVAQ AGVQWRSGLV
11750	25651	A	11853	176	3	KKGFPLDWNMVKNIIVKFGEDLQISK LHTFFFLTESRSVAQAGMQWCDLGLH SC
11751	25652	A	11854	281	375	QLTFKKYFLGWARWLPVIPALWEAKAG RSP
11752	25653	A	11855	146	356	KCGALIAEIEVPLFSELDRFLAYSMT ELCFKRCVPSLHHRALDAVDDCLHSC CTDYPINRSLMNAV
11753	25654	A	11856	136	1	LSILCEFFNWLIEMEYRSVSQAGVQWCD LSSLKPPPPRLQOCHSC
11754	25655	A	11857	277	361	IVLRGAMWLTPIPTLWRAEGGSPVVR
11755	25656	A	11858	295	152	VVFGFGFFETESHFVAQPGVQWQNLGSL CSLRLPGSSNSPASAFQVA
11756	25657	A	11859	1	342	GTRLPEPLTVLWTAHLGAMAPGSRSTLL LAFALLCLPWLQEAQVQAPVSRFLDH AMLQAHRAHQLAIDTYQSEETIYIPKDH KYSLLHDSQTCFRFSDSIPTPYNMEDTQ HK
11757	25658	A	11860	244	332	TIEMMLDIKQIQVIFLFEFKMGRKIART T
11758	25659	A	11861	1	339	GTRVVTICQVQLHAYAHFLYFFEMEARS VAQAGVRWCDLGLSQPPPGSSSSSSSS S
11759	25660	A	11862	311	394	GMLGAVAHACNPSTLGGGGLGWITCSQEF
11760	25661	A	11863	130	1	VPPSVRTFFFFFETESRSVSQAGVQWH YLGLLQAPPPGSTSC
11761	25662	A	11864	3	320	IMMYALFLLSVGLVMGFVGFSSKPSFIY GGLVLIVSGVVGCVIILNFGGGMGLIV FLIYLGMMVVFYTTAMAIIEYPEAWG SGVEVLVSVLVLGLAMEVGLVLW
11762	25663	A	11866	165	309	GLILLPMLCSDRISAHCSLYLLGSYDP SDSGSHVAGTTGTCHYAWLR
11763	25664	A	11867	208	314	GSRNKLSGQAQWLTPVIPALWEAEVGG SPEIRSSR
11764	25665	A	11868	102	1	KKFFFFETESHVAQARVQCNLGLQA PPPRFT
11765	25666	A	11869	126	3	NNALQLHSSYCKKPPFFFLKTESRSLTK AGVQWCDLGLLQ
11766	25667	A	11870	1	273	KQLPVNVLNWRLELTGLLCTNLKPC MIFIILVIVKYWFLFCNIFKNHIFSA QWPTFVIPALWEADMGSGHYWITTIVD FMCATLT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11767	25668	A	11871	126	2	FPKALLVVVFFFFFFETESRSVAQARVQWHNPGSLQCPLR
11768	25669	A	11873	269	9	QVSGKFWPDI FYKTGEKGLQCPNFPQGHPPRGLKKKSFSKSKKKKKKKKSIAVGQAQWLIPVIPALWEAKVGRSPEVKSSRPACP TW
11769	25670	A	11874	114	1	LEAKPGVFQSGVLLVIFFFETESHVSQAGVRWC DLG
11770	25671	A	11875	146	1	GNHLSSRVGVQDQPRQHGKTL SLQKI QKVAGPGGAHLQSQEVQVGGSL
11771	25672	A	11876	2	159	SLQFFFFFRWSFVLVAQAGVQWHD LGS PQPPPPGFKHSPASASQVAGRGG R
11772	25673	A	11877	124	240	FRAPSSGQAWLTPVIPALWEAETGGSL EARSRPDWRT
11773	25674	A	11878	135	5	QVLFYFYFSDSFTLSRPLECSGVTLP HC NLCLPGSSDSCASAS
11774	25675	A	11879	170	2	GFFFEKKGWYKNSFLCFFFFFEPEFC SVAQAGVQWLHLGSLQPPPPVFKVDAAP
11775	25676	A	11880	97	267	GHGHATLRGLCVLSLFHHIPAPSVSGTS DAERCCLCVIYRLICGYISRNCLYFSDH R
11776	25677	A	11881	1	292	LPEPLRVLWTAHLQAMAPRSRTTLLAF ALLCLPWLQEGADQTVPLSRLFDHAML HAHRAHQLAIDTYQEFQTYIPEQKYS FLHDSQTYFCFSD
11777	25678	A	11882	93	2	KYQMGWAWLTPVILALWEAEAGRSPET SC
11778	25679	A	11883	145	2	PPLGLRLQVQAPTGGFFFFFETESRSP RLKCKGAILAHCNVCLLLV
11779	25680	A	11884	202	1	TWWRWGVTVLVRVLMNCRPCDRHKSASQ LIGRVRQENGLNARVGGCSEPRSRHCTP VVWTSNPSSC
11780	25681	A	11885	42	155	GERGSLSPGVQDEBPGHSGTSSIQKILK LAGHGCTCP
11781	25682	A	11886	215	1	STMARHCPLSPMLFNSAMEVLVRAISQE KEIQGIQIGKEEVQLSLFTDDMIFNLEK RKDCSKNLLQMLNLV
11782	25683	A	11887	214	1	GYFFGLNEVLGKLEKPSLVKVPQNPSPKR PFFLGFFFFETESRIVARLECSGAISAH FNLCPLGSSDSPVSC
11783	25684	A	11888	215	3	WGPGFPPFFSFFFFFLRQGLAVIRLKCSG TITAHCSLNLFLGSSDPPASVSLVATTG HEPSITQFHS HGSC
11784	25685	A	11889	118	1	RFFIMGENPTKFFFFFETESLLPRLECS GVISAHCNLSC
11785	25686	A	11890	267	83	HCLRSVGVQDOPGQHGKNPSIQIKIQLAT SFKKS LKIVIPPLPFKNKDTDSKSSCSS LSPHS
11786	25687	A	11891	134	2	DRLAVLPRLECSGMIPLLEPLSRFKRFS CLSLPSSWDYRGAPRA
11787	25688	A	11892	116	1	SKGVGHFLFFFFFETESRSVAKTGVQW CDLGSLLCLV
11788	25689	A	11893	397	475	RFVCSSTIKVLRDLSSDRSNPGRFLST
11789	25690	A	11894	115	331	KNVCLFVFMKNHNLNPGDEGCSKPRSR HCTPSWAAQQDSISKYICYRYLYLDIY LSKLVVRLRINQLPNS
11790	25691	A	11895	134	251	INPPVSRKKKKKKKKKKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKKKKKGGGL
11791	25692	A	11896	186	402	PGKNLTLENVPRENKVGEKAPGQNEPPV LGGGEYQDPGGNVKGVPPAPGFGKDG PKRLADTFDLIEGDGD
11792	25693	A	11897	100	2	KGPPPPPPPPPPPPPPPPPPGQSGQVKLK SPKCK
11793	25694	A	11898	92	3	SVARIMPYALFLLSVGLVMGVFGSSKPS
11794	25695	A	11899	283	362	MTYTMITIVHALWASVCLLLNHAHDPLD
11795	25696	A	11900	248	1	VMSAQPLSVILRFMGKWSNWTGMQYTE SEVERYRDRGRARETERQRDRERERENP RNRKLFYGRFKHSQDFFMPQKVHF
11796	25697	A	11901	253	2	KLQENPFKLLNFIINLCSVSLNVPITLN INIKPSFIAPKPRCPSKFORNYIYIYPS IYLSIYLSIYLSIYLPITISKVLKDVE
11797	25698	A	11902	179	3	LAVTKNEIMGFSTTWMEMGDINFFFFF ETKSHPMVRLECSGVISAHCNLRILVSS SC
11798	25699	A	11903	1	403	GTSSQESFGGCCVSGLIAMGTKAQGERK LLCLFILAILLCSLALGSVTVHSSEPEV IIPENNPKLICAFYDLSSFFSSFSYFF HLSFFIYYPYLLFVSCFTFYIVILLSFI YSHHLSSVSYSYVLLIYTFIL
11799	25700	A	11904	37	242	KGPTRDQLQHPKARLEAPLRVLWTAHLA AMAAGSRTSLLAFALLCLPWLIDGAS HIVSLEMLFIIF
11800	25701	A	11905	1	298	GTSQHRGRKDSRTGSHSSSDHPGAKLLS TEEQAAETMRPPSAPPRGCI PWQGLL LSSS
11801	25702	A	11906	225	30	ACYLQKDGAFAILPDVLPDMFKGHSSLY PCQHAECDHIKNIYNCVCVCVCVCVC IVICKLV
11802	25703	A	11907	196	320	HSSSSTTPSQDTHTHTHTHTHTHTHTH HKIPORELLPSVD
11803	25704	A	11908	130	3	NGPVFSPPPPPPPFEMESHSVTQARVQW CDLGSLSQSLPPGFK
11804	25705	A	11909	381	2	ASICGQKLIFQHWKKIILVQQVGLQKK NSTLKRAWEFLSFPQAPPLGSLPKGIN ILNKGAKLKGKTNFPPIVFFSVLP FFGLKKFQKKVFHQGKSPFFFFFETE SRSAQAGVQWHD
11805	25706	A	11910	138	2	SVPLKEFIISQARWLTPITPALWEABAG RSPEVRSSRPASTWRNP
11806	25707	A	11911	231	54	IRASFGIQIRICLTIFFFETEPHSVTQ AGVQWRDLGSLQPPRRQEQNSVSKQTK TN
11807	25708	A	11912	3	461	DAWGRVEGPPLRPPATSRRWAGPTLWRM EVTGDAGVPESGEIRTLKPCLLRRNYSR EQHGVAVSCLEDLRKACDILADKSLT PVTLVLAEDGTIVDDDDYFLCLPSNTKF VAMAINKWAYNNSNGGTGWISQESFDV FEAYSGATLLFF
11808	25709	A	11913	318	407	LCGRLWWLMPVIPALWEAEAGGLLKLS MR
11809	25710	A	11914	340	5	DRVAKFSEARLFRLFFPPFFLKI FCFPR GPKIFRGVCPLLFPPEFWGLFQKGPGR LFFPPLGGFFFFFFFFFFFSFFFFF FFPFFFFFFFFFFCHKNKILLKVVHNSI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11810	25711	A	11915	274	385	IKPQRWGETRAEKLKSLKIRVPLLLQRN AAPHQQWNK
11811	25712	A	11916	259	441	DTKLKPVNIKLNHFKKKKKKKKKKKKK KKKKKKKKSSSLRG
11812	25713	A	11917	254	402	LTVSVIDFLRWRLPLLPKLECSGMISAH CRLRLPGSYHSPASGCQLLGR
11813	25714	A	11918	223	1	NTNSPRKKFFYEVSVPVFFGVFFPSP LKGSFRAFLKLAWRPPLPLFFFFLEMSR SAAQPEVQWCDLGSLLQPP
11814	25715	A	11919	97	3	KPEFFPFFPFFFEIESRSVTQAGVQWRD LGS
11815	25716	A	11920	154	384	KEFFLMLFFFLPPPPPPFFFLGKGLF FFPPGGGGGQFFSIGPPPPRGKDDPP SPPKMGGRGTTPPPPGYFFFF
11816	25717	A	11921	225	369	GTLNLLTYIKSWGAVAHYNPSTLGGW GKWITSGQEFETSLANVVKP
11817	25718	A	11922	116	372	MEYTNWKMAMSYNLHIYQTYKNSVIEHP TGVLPHSRVIMVNNIVLCISKQLKELLR RLMWEEHLSPGGGCGSEPRSRHCTPAA T
11818	25719	A	11923	271	409	KKKKKKKKKKKKKKKKKKKTGGGA
11819	25720	A	11924	121	228	KKKKKKKKKKKKKKKKKKKKKKKKKKR GGGFKKKPWGGQK
11820	25721	A	11925	55	423	NKPKKKNFLKKKKKNFFFPYPLKFFFF PKSLNFFRRVVPKISPPKKKFFFKNSPS VFFFPPLKKKNFFFLTPLKFGPPKNFFK RPPPLFFFFFFFFFFFLSGNCIEKL
11821	25722	A	11926	253	443	YQHQRPKVDKSMKMRNQRKKSSENSKNQ NTSSPPKDHNSSPARQONWMENEDGLT EVGFRRW
11822	25723	A	11928	175	413	KKKKKKKKKKKKKKKKKKKKKKKAGGG A
11823	25724	A	11929	490	182	RKQKIKGCKKPNPLAQGGVKKKGKGGPP FNFFLKQKGQDFLKNWNLGQKKKIPPP QVPSLRQKGAFFPGRIFFFFFETESCS VAQAGVQTLSTYKKNKIK
11824	25725	A	11930	110	2	KKIPRKPPFFPFFPFFFKAGSHLVAQAG VQWHDLS
11825	25726	A	11931	169	987	YLEKIMSEHSRNSDQEELLDEEINEDRI LANLSAEELKELQSEMEVMAPDPSLPVG MIQKDQTDKPPTGNFNHKSVDYMYWEK ASRRMLEEERVVPVTFVKSEBKTQEEHBE IEKRKNMAQYLKEKLANEIVANKRESK GSSNIQETDEEDEDEEDDDDDDEGEDDG EESSEETNREEEGKAKEQIRNCENNCQV TDKAPKEQDRPEAQEQSEKKISKLDPK KLALDTSFLKVSTRPSGNQTDLDGSLRR VRKNDPDMKELNLNNIENIRK
11826	25727	A	11932	161	389	SVQTHPNLRSCSVLKNAMHFYLLGYVIS GCTEPAKAIKPIDRKSVDHQICSGPVVLS LSTAVKKIVGNSLDAGATNI
11827	25728	A	11933	134	289	ASTQNMGMRLRLMSPTLLSLSLSHTHI HKHTRMHTHTHTHTHTYPTKKV
11828	25729	A	11934	128	1	IKKGEFFFFFETESHSPRLQCSGTI LAHCNLHLLGSSNS
11829	25730	A	11935	131	19	MYIGWVQWLTVPVIALWEPKVGASLEAR SLRPARTSE
11830	25731	A	11936	104	3	LKGQLIRAQWLMVPVPSLWEAEMGRSPB

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VGSSR
11831	25732	A	11937	146	2	GGRLGIYHAWNPEGFFFFFEMESCSVG QAGVQWCNLSLQPPHPGFK
11832	25733	A	11938	149	1	DKCFLCVCCLFIFYLLIYFFETESC SIAQAGVQCNCNLSGSPQPLELA
11833	25734	A	11940	176	380	QSVQQLPRLECNGMILAHCSLHLLGFKR FSCSLSPSSWDYSRLRNYQGGRWSKTH QAWCQSLTILWN
11834	25735	A	11941	133	415	KKKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKSG
11835	25736	A	11942	222	420	QGDKPLDNNNSTILYMERKKKKKKKKKK KKKKKKKKKKKKKKKKKKKYSR
11836	25737	A	11943	163	425	KNPPKNSQLSPSTLKKKKKKKKKKKKKK KKKKKKKKKKKKKKKTG
11837	25738	A	11944	143	3	KMGKKQSRKTGNSKKQASAPPPKERSSS PAMEQSWTENDFDELREE
11838	25739	A	11945	200	3	QNSQVGYKGAPHKEKTMALQARVNLGPP RGPLKRPALFFFFETESPSVTQDGVQW HDLGSMQPP
11839	25740	A	11946	221	3	RKIEGGPSTSRKSVRGVRCFQPLGLGFP GGLFFFFFYETESCSVARLECSGVVSA HCILHLRSTNEGRGR
11840	25741	A	11947	68	177	ISSSFKNKCLCEKKKKKKKKKKKKKKKK KKKKKKR
11841	25742	A	11948	210	329	RHTHTHTHTHTHTHTHTHTHTHTHTHT MYFLAFFDLRS
11842	25743	A	11949	183	20	LGTVAHSCNFVFSLSRGFLHVGNGLRL PTSDDPPTSASQASAGTTGMSPTWPE
11843	25744	A	11950	232	329	VGIKMSSISDEVNLFVYRYLQESGFSHS AFTF
11844	25745	A	11951	412	239	LFYEKGSRFVVSQAGLELLELQSPCFGL PKCWDYRHEPPRQADLPFCVPSSAWASW L
11845	25746	A	11952	310	393	PHTDISGTPEIMHYVHVHVRTTQPRNKP
11846	25747	A	11953	193	3	LSSWPTLISGAFKAENAVEGNDSDRIL RGFFVLFCFVLFRRQSLALSPRECSGV ISAHCNL
11847	25748	A	11954	185	416	SVQTHPNLRSCSVLKNAMHYLLGTEPA KAIKPIDRKSVHQICSGPVVLSLSTAVK KIVGNSLDAGATNIDLKLDY
11848	25749	A	11955	100	1	AHLSKVFPFFFFFFFEMESHVTRLECSG TISAH
11849	25750	A	11956	35	521	KEKEFFFHAGVYWGPPRNFLKRAPLFFFF FFFFFFFFFSEFFS
11850	25751	A	11957	214	1	KKKIFFFKEIFYPKLSRKKKNFFRGAGK ILNLSIFPEKKKIFSPFSFFFETESCTV AQAGVQWHVLGSLQP
11851	25752	A	11958	114	1	RYFSGQAQWLTPVIPALWEAEAGRSPEV SSSRPAWLTV
11852	25753	A	11959	188	12	SKCQCTFFSNFKKTEMESHYLAQAGLEL LGFSHLPTSVSQTVGITGVSHCAQPNNAH LY
11853	25754	A	11960	241	556	SSIFPLPNKHLLSFSTLSSSLGREVSIQ DMCQGTQKQPPFPPLPHVPHLSIRDGE LCVGRDVHLCQTDLAQVFCVCLFVLGVL LSLPRAGVQWCHLSSLQPPPP
11854	25755	A	11962	362	462	KIGQALTPIIPLWEAEAGASPEARSSR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SAWET
11855	25756	A	11963	43	2	CCCYCCCCCYCC
11856	25757	A	11964	30	415	GLGFKQKIFFFFLGQGNFDLLRAKKR PFLPPPPFPKNPKNRGVFLGPGSGVPKP RPRQGDVPLKPRSLGVFLTSKKTPLGP WANPPPPPGDGP
11857	25758	A	11965	149	2	SKTWLKLAKYLKNTYPGWVRWLIPVPA LWQAGAGELHEPRNLRPAWAT
11858	25759	A	11966	179	3	KKNIFPPPPVKFGPPQGFKRPPPLFFF FFFFFFFETESRSVAQAGVQWLSIGSLQ AP
11859	25760	A	11967	245	382	DVTDSKMHDPFRSSHVKMWLGVAHACN PSTLGSGRQGEFKTSLAN
11860	25761	A	11968	264	10	LSTLECKGVSPGVFSPKGRKGLGYIFS PFLEKPHIPLGISMYPFFFDGVSVAQ AGVQQRDLGSLHLPSPGSSYS CASASLS S
11861	25762	A	11969	326	406	RLKGWALWLTPIVPTLWEATVGRSPE
11862	25763	A	11970	120	1	KGYGFPPFPKPLGPPFFFFFATESCSV AQDGVQWRDLGS
11863	25764	A	11971	84	370	RNGAELKTPLAGQTQITINCRYSWVTLV LGDLESILCWHIFKKTNLFCGFFSSFL LGAGRMKSHCVRLCEGRMISAHNRVCL LGSNDSPCSAF
11864	25765	A	11972	196	3	SRGKMGEPFVLFKNPSWAKAGGNKGNP FFFFFEAESCSVAQAQVWCNLSLQAP PPRFTPRA
11865	25766	A	11973	559	644	KIGCSAYGVAILLFLYFFNKLAPTLWKK
11866	25767	A	11974	3	391	HEAQLPEPLMVLGTGHLAEMAGGSRTYL LLAFGLLCLPWLQEAQAQTVPLSRLFD HAMLQAHRAHQLAIDTYQLEETIIPKD QKHSFLHDSQTSFCLSDSIPTPSNMEET QKSNLELLRISLLIE
11867	25768	A	11975	138	365	LKFECHSTLCANHGKQTTFVFYNKFL KYTFYFVSVLTAINWYIKNLINVFKKKK KKKKKKKKKKKFKKKK
11868	25769	A	11976	275	433	MSILDLSKARNFPLSFLETGSCSITQAG VQWLNHSSLQPTPGLRDPPASAQ
11869	25770	A	11977	108	3	RCGLFFFETRASPCRPGWHLGSLQPLP PRFKRP
11870	25771	A	11978	270	408	FENNVLGRAQWLTVPVLPALWEAQAGRS PGPENQNHDPYKGNPWPY
11871	25772	A	11979	228	441	QALKFVIEMLLSLKKCLDVSVINRHHK IELLQKKKKKKKKKKKKKKPSQKKKD SSRGKDS
11872	25773	A	11980	2	447	GALALNKTADVWRLNFLVSLGHLWKRWL QQTSLSKWVKIKECSILKKKKKKKKKK KKKKKKKKDKK
11873	25774	A	11981	124	445	KYGEMSQNPARGGPKFSKNQXYSEHLRI HCCPPPTFLISKKEIGDRKYSICKSGCF YQKKEEDWFCPCQKTKTSRRAKSLKRP KQKPVAPPGGVKAPKPRSLPRF
11874	25775	A	11982	48	429	KESNGSQDRLLPKIHSPDVSGGKSGGMS QNPARGGPKLSKNQKSSSEHLRIHCCPPL PFLISKKEIGDRKYSFGKSGCFSQKKKE DWICCPCKTKLKGKIRPPPKKNGPGGS LNGRTTWVSGLFVHN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11875	25776	A	11983	419	500	SLLVKVEKQWPGAVAHACNPSTLGGPG
11876	25777	A	11984	362	496	LWSPIRILLRWAHHVPTVPAIWEAEV GRLLLEPRSLCNMVRPIS
11877	25778	A	11985	142	433	RFVCSSTIKVLRDLSSDRSNPGRPLSTSN SSLKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKGGGVKKFLGGPIFGGGG KEKFFFFGGGFIN
11878	25779	A	11986	177	2	CQRRWVTLSSHHTSITRPLGQLKKGWSP GAVAHTYNPSFLGGQGGWVTYVHTRGR TR
11879	25780	A	11987	178	443	DKKKKKKKKKKKKKKKKKKKKKAGGGLF KKI
11880	25781	A	11988	329	410	LIFFFIFFERESHVAQAIQVWHDLGS
11881	25782	A	11989	146	1	DRASALQPGRQGRNFVSKNNNNVIYII NTLTTTIFLGTTYDALSPDL
11882	25783	A	11990	240	420	GVFAPLLGDVSSQSGYTGFDRDPLEBAVCL FLELECHAERTTALPRAVRQGCCLSLQNL SVAF
11883	25784	A	11991	239	410	GTLFIYLLGDLFIYPRNKSLTLLPRLEC GGVIVAHCSLDLLSGGYPISALPSSWD C
11884	25785	A	11992	126	3	YTGEYKSFCHKDCTHMTAALFTIAKT WKNPNRGVGGRV
11885	25786	A	11993	300	22	SQLLGRLRQENHFNWGGRCSEPRSCHC IPAWATRANSIFCGEQASSVEVRRSARK KLFSIDILKRHTISWRVSGLLLVDSYFG RLATPVRAQ
11886	25787	A	11994	303	2	EGEETFLPSPFPFGQENPGSNCSPPFLF PFGTFLDIRVAGSHKVQAGVFKRPPS LHLFLIKKRFFFFFETESRSVPQAGVQ WRDLGSLQTPPPGFKR
11887	25788	A	11995	171	457	SFSDHLILGWIGFCNNLSKIALCSSPIK NKNDLQKKKKKKKKKKKKKKAKASS SYQDSS
11888	25789	A	11996	357	204	EKTGFPHVGQAGVDLLTSRSTRSLPKC WDYRHEPMRLAGHLYYFYPMK
11889	25790	A	11997	219	1	PRVFWAPPRIYPPGALFWAPRPVGSVLG ARAPTAKGPKQKGARGTFFFFFEMESHL SPRLECNGTIWAHCNLC
11890	25791	A	11998	254	1	AHLRGNRQLPKHTFFQYMTNLKCAFSV GRQSYSIPWRSFYTSLPFKYSCVFHTHT HTHTHTHTLYFQIMVLLPSLRKKGS
11891	25792	A	11999	167	2	NFKSFFQGLSRGVLNPKVNLFPLETES CSVSQAGMQWGDLSLQPPPTRPPTRP
11892	25793	A	12000	104	3	RPWTFFFPSETKRSRVAQAGVQRDLCS LQPPP
11893	25794	A	12001	178	2	KIFQRGAKNSPWGLPFRGGENKKGAPPC QKGFGRFFFFFETESRFITQTGVQWCDL GP
11894	25795	A	12002	163	282	GIGGEWCLSKYVIKYVRKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKK
11895	25796	A	12003	195	2	KWGRIPKKGGFCFTKKKSGQTLLIKSP PPAFVFFIFFFLETESRSVAQATVQWC DLGSLQAP
11896	25797	A	12004	152	1	CFVDVSAEKLRPKDFMTKTPKAMATKAK IDKWALTKLKSFTAKETIIRV
11897	25798	A	12005	359	1	EVVPIWPPPKRRVLSKVSQKQFFISAPIR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						KKPFPQCQVGLILAPFRVLLIGRPFFFFF GVLVVEIQWRSFISLVVVVRARIMMYA LFLLSVGLVMGFVEFSSKHCPVYGALVL VSIIGRV
11898	25799	A	12006	189	12	DGRLPGSVCCYLIIFLRQSFLLAQAGA WCHLGLSLQSPPPGFKRGRVSRIRAVRG DQ
11899	25800	A	12007	131	3	KIFFFFFFFFFEMESHVAQAGVQWRDLGS MQDPPPGFMPLLFY
11900	25801	A	12008	150	2	IILFLVPDIEAVFFFFETVAEAGVQWHNL SSLQPPPPGFKQSPASASRVA
11901	25802	A	12009	305	3	KFFFSKLKASIRGRWGLFFTPPKRGFLP KIPHQVFKGGPLWEKLQGLKAGNLGPGY KGFFKGAARFFFFFETESRSVAQAGVQ WRDLAHASVHASAHAS
11902	25803	A	12010	263	517	DKGFLPPLPRWCPGQDPLFFYGGIVFHGG YGPFFFFFFFKAESRLVAQAGVQWQDLG SLQPPPCRTRGSP
11903	25804	A	12011	107	374	WMGTWGSPLVLLTTRSTCPPRSPLHRR TGATIWIFFRLFFETGTVLPMLECSIVIM AHCRLQLPGSSSSPTIASQVAGTKAHL DCFVY
11904	25805	A	12012	144	261	FPKKINNFYFTFLQDPTGIFSLDKTIGL GTYGRIVLVS
11905	25806	A	12013	371	3	IFHLRKIFTPLPGIFWPIRLSEKKKPK RFFWKIKKKFNGYPLKNPINPKYKGRPF FFKGEKNPNKGVPVLKKIKIPSFSKALG FLQKKASKPFFFFFFDTECTVDQSGVQ WCDLGSLOAP
11906	25807	A	12014	101	3	RGAFFFFFFFFBTRSRSVIQAQGVQWCDLGS LOAP
11907	25808	A	12015	205	2	VFNPSGINVMYVDAILNKRILATRIQOH IKQRIHLDQVGFHGMQGWFSIRKSINV IQHINRPKDKN
11908	25809	A	12016	168	1	GCVCQFQKKLNGGNGNGFFPLFFFFFF EMKRSVVQAGVHWRYLSSLQTPPEFK
11909	25810	A	12017	311	2	RGLRFGQWKTQMENTPFSALRPGQLS SIRSGLLHTYPGLGDRSEPLSCSLSSS KYVVWQAVTSALSSNKPQASQGHWKDDF FLFFETESCSVTQAGVQWH
11910	25811	A	12018	383	247	LVEMGFRHVQDGLDLTSQSAHLGLPK WWDYRREPPRLATIEVL
11911	25812	A	12019	2	379	RVLWTAHLAAMAAGSRTSLLAFALLCL PWLQEAQAVQTVPLSRLFKAMLQAHRA HQLAIDTYQEFISSWGMAYITKEQKYS FLHDSQTSFCFSDSIPTSSNMEETQQKS NLELLHISLLIES
11912	25813	A	12020	3	389	PEPLRVLWTAHRGAKAGSRTSLLLGFA LLCLPWLQEAQAVQTVPLSKLFDHAMLQ AHRAHQLAIDTYQEFETYIPEDQKYSF LHDSQTSFCFSDSIPTSSNMEETQQKTN LELLRIFLVLIELWLD
11913	25814	A	12021	247	386	PMLGHVSQSGNGVRDPLEBAVCPKAKL KHCSGRSTALFRAGRQKR
11914	25815	A	12022	17	371	PLRDLWTAHLEAMAFSFTDLLLAYALL CLPWLQEAQAVQTVSLYRLSDHAMLQAH RAHQLAIDTYHRIEETYLKDKYSFLH DSQTSFCFSDSIPTSSNKEETQQKFYLE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LLPISL
11915	25816	A	12023	3	359	LRALWTADLGAKAPGSRFTLLLASALLC LPWLEEAGAGQTVPLSKLFDHAILQAH AHQLAIDTYQELEETYPKDKHSLD SQTSFCFLDSIPTPSNMEETRQKSNLEL FRTSLLL
11916	25817	A	12024	2	363	PEPLKGLWTDHLGALAPSSRTSLLLAYA LLCLPWLQAGAGQTVPVYTLFDHMLQ AHLAHLAIDTYHELDETYMPEDHKYSF LHDSQTCFCFSDSITTPYNMEETQHTSN VELLRISL
11917	25818	A	12025	314	393	GQAWWLTVPVPAFWEAKGGRSLEARS
11918	25819	A	12026	80	392	PLIACSFLLFLFFFGKILFLPPRWKG GGGIWVNGNPGFRGQAFLLASSKKPGM GGPPLTPGKRFVELKKKGFSPGGPGGSK FSAPGTPPTGPPKGWEIPAK
11919	25820	A	12027	165	2	WQKLLFHFGTESCSVARVGVQWRHFS KPPPEPFKQLSAPASRVADRRPPDAW
11920	25821	A	12028	1	338	VFVALKFLMCLLSVCIFSLNIIYSNLP QKNCLPLIFFFLFFEMEACSVTQAGVQW GDLGSLQPPVSHNLGGGGCCPECHC TPCSRPGDRDFVFNKVTMIQDNHLMELT
11921	25822	A	12029	2	315	HEERERERERERERERERERERVRG GVGETYKAELPRVGGAQKRAHFSARGR LFMEICGDMCGEKGPKPPHSLTEELSR CGERFFDTSLAITRGCAQSV
11922	25823	A	12030	216	3	ERIIPRGVRQRNRLFSGRDTASPPFY PPRQIHKRGVEDREHERRGERERERERE RERERERERARAAR
11923	25824	A	12031	114	329	QTERNSININKKDIHTKTPSVGHQHP KVDKTTKMRNQRKAENSKNWKASSPP KEHNSSPAREQNWMS
11924	25825	A	12032	177	1	IKKKTFFWQNIPLFSKKTCRQKFFFF FFETGSLPLRLVCSGAVLAHCSLCLPGS AFL
11925	25826	A	12033	127	1	PSFFFFFFFNETESRSVAQAGVQWRDL SLQAPPPGFITPSC
11926	25827	A	12034	47	314	GAPVASVISCPSCSATDGVVRNGKSTA GHQRYLCSHCRKTWQLQFTYTASQPGTH QKIIDMAMNGVGCRTARIMGVGLNTIL RHLKN
11927	25828	A	12035	15	408	GAIPGAMGHFTEEDKATITSLWGMVNA DAGGETLERLLVDYPWTQRFDSFGNLS SASAIMGNPKVMAHGKKVLTSLGDATKH LDDLKGTFAQLSELHCDKLHVDPENFKL LGNVLVTGMAIHLGKEPTP
11928	25829	A	12036	122	2	KLVDVLPPPGGARVFFFFFPLETEHCS VAKAGVQWHDG
11929	25830	A	12037	154	1	GKPPPKLGFWGGPRQRVRGRGPPFFFF ETESPSVAKAGVQWCDLGSLLHPL
11930	25831	A	12038	58	254	DPRVRQORTTAHCSLNLGLQRPPLSL PSGWDYRHAPLCATQKILAYRVAQRERS AHGSYYQAS
11931	25832	A	12039	270	124	DGVLLLLPRLECNCAISAHGNLRLPGSS NSPASNKTQNNKKTLNKF
11932	25833	A	12040	63	355	LGRGTAHRLWRPLSRPASRVSYLSAAT NKRSPAPPSRAFWDNKGWGGFFPET GSHRRRPGRMECSGAIHAHCSLDPPGSE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=-possible nucleotide deletion, \=/possible nucleotide insertion)
						MGFTMFPSLVNS
11933	25834	A	12041	184	3	GVSRLGGVSQGLGYMGVRDPLEEAVCLF SKLKHPGRTTALPRAVRQGCLSLQKFL LLFA
11934	25835	A	12042	118	3	DRVLLCYLGWECSGTISAYCNLHLPQSK RFSCLSLPSS
11935	25836	A	12043	40	436	LSEGKLTNRKDNHTKTPSVHHHQPVPK DKTTRMGRIQSTKAENSKNESTSPPKKE HSTSPATEQSRMENDEDELREDFFRSVI TNESELKEDVRTLCCKEAKNLEKRLDEWR TRINSMEKTINDLMELKTM
11936	25837	A	12044	101	2	HLGQVRWLTPVIPILWEAEVGGSPPEHRS SRPAW
11937	25838	A	12045	123	3	LTVIKELPLGQARWLTPVIPALWEVKVG GSPEVRSSRPA
11938	25839	A	12046	3	432	PIFGGGERIFPPFFPSQGGGVFPKPT KNKGFFPFLGFFFKIFLRFNFFLFFPFF FLNPFYFGAPPFFPFFPFGGFFPFLPS RFFKFFQNFPGFFFGGFFPFLGFF FFFFFL
11939	25840	A	12047	325	164	KNKRNRGQARWLTPVIPALWEAEAGGS PEVRTTGVSHGTRPHLLNTVSEYI
11940	25841	A	12048	187	381	LMDKRVSLWGDENILKVESNSGCTTLYL LVCFEMESRSITQAGVQWRDLSSLQPPP SRFRKFSCL
11941	25842	A	12049	84	464	SYRVPSHPDITLVLSRISAEAGEKSPFC FPERVWPCPRPLSDLGRLKLECGPDL DSTFLSFFFGGLKGTGSHSGALECSGVI RDHCGCLCSGSGDPPISACLRVAGTTGV SHHCIFCRQDLPGS
11942	25843	A	12050	232	20	LLQCSSRAKIHTSLTGNQKLEMIKLSSE GMSKAEISQKGLGLHLGLVANAKQRF KVIRSATPEFRHAE
11943	25844	A	12051	401	518	FFETESCSVTQAGVQWRNLSPLRA
11944	25845	A	12052	191	1	LFPLKKEKIFFLGPGTNGAPPMFFLKAP PLFFFFFFFFFFFVNLFL LSFLHILEP
11945	25846	A	12053	12	369	PLPIYSACTEVGSNPGPGIDAKSVSHN NCYLKEKKKKSNGSQNNLLPKIHTPNG SGKKTGEKIQNPPRGPKLSKNQKYSKN LKKHCCPRLTFLISKREKGNRYTFGKS GCFYQKK
11946	25847	A	12054	89	513	NFTVRGSIPLNNIPMANLLLLIVPILI AMAFMLTERKILGYIQLRKGPNVVGPI GLLPFADAIPLFPKEPLTPAPSALFALC FAAPALALPFALFLCPRPLGRP
11947	25848	A	12055	158	3	SQLTWPIMAQTDMSMCLWVYFDNIGWA WWLMSVITLWEAKVGGSLHNS
11948	25849	A	12056	113	1	KSHGGHGVVSVLVGLAMEVGLVLVW KEYDGAALA
11949	25850	A	12057	44	263	ARIARSAHEGKMERKYTGARKNAENRPO RELQLKASRSTIDLAEHACNALWYQLEFL ISVGSWKNYILFYLYT
11950	25851	A	12058	142	1	KKIFFRYKKEGFSFPKFFRISLFFFFFF ETESRSVAQAGVQWRDLGS
11951	25852	A	12059	12	347	QTERNSININKRDIHTETPSEGHQHQRP IVDKSTMRKNQCKKAENSKNQSSSPA KDHNCPLPAEQNWTENEFHKLTEVGRI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ITNSVELKEHILTQCKEAKNLEQRLEEL
11952	25853	A	12060	245	3	MPEGSFFLEIPETRIVFVKPKGKFLGGV GPSLLFFFPFFFFFMQRSLAVSPRLEC NSAISAHCNLCLLGSSDSRSSGSR
11953	25854	A	12061	94	3	KGGIFFFPFFFLRQSPSVAQAGVQWCD LG
11954	25855	A	12062	108	5	NNLSSGVRDQPGQHGETTSLTKIQKLAR HGGRHL
11955	25856	A	12063	298	1	KKKKINTHAQKRGPPFFFKPPPEKGKAP PPQRTVKKGKDSFIPKRREKKNPPPL SFFFLVRVHVRERERARERERERERER ERERERERERERERAR
11956	25857	A	12064	122	1	VCEGVCVGGWVRDRERERERERERERER ERERERERERAR
11957	25858	A	12065	126	1	ATCTKFRNDNRALLRVRFERERERERE RERERERERERESR
11958	25859	A	12066	48	351	FFFFFPFKKGPKIVPPGGGGGGDPFL EPPPPPLKKFWGPPLRGRNKGGGPFGW VNFGLFLKKKGLPWGPGGVKTPAFKGS GTPPKGGNNRKNPPFW
11959	25860	A	12067	1	365	GTRLTVLWTAHLVAMAPGSRSTSLLDFA LLCLPWLQEAGAVQTVPLSRLFDHAMLQ AHRAHQLGIDTYQEDEETYIPKDHEDSF LHDCQTSFCFSDSIPTPSNMEETRQKYH LELLRISLLF
11960	25861	A	12068	174	1	PAWVMQHNPSVSLFFCFETESRSLTRLE CSGTISAHCNVRLPGSSDSPVSPSRVAA RA
11961	25862	A	12069	270	375	TRIKRCNGGRAQWLTPVIPALWEAKAGE SPEVRSS
11962	25863	A	12070	197	350	KKIYIFLTINTIMDLIIPFLLDNILGFW LGAVAHACNPSTLGGRGGWITRS
11963	25864	A	12071	3	378	HEGQLPEPLKGLWTAHLGMAPGSRSTSL LLAIDLCLPWLKEAVAVQTVPLSRLYD HAMLQAHRAHQLAIDTYQBIETTYIPKD QKLSFLHEYQTSFCFSDSIPTPSNMEET LHKSHLELLRIYL
11964	25865	A	12072	219	1	FSHPFPFGVFQTPLVFPRPWEVLGSPGG GGGPPKKWAGVQKWVFFFWEMESC SVAQAGVQWYDLGSPRA
11965	25866	A	12073	134	3	VFGPPFFPFFFCETESHSAQAGVQWRD LCSLQAPPPGFMPSC
11966	25867	A	12074	175	357	MPINQPVKKMCVCVCVYIYIHTPLYI RVYMYCMYICVYIHVYIWMCIYIHTHV STYVW
11967	25868	A	12075	193	350	KIPHLTSLYHTQNYLKYCIGQANWLTPV IPALWEAEAGGSPVRSRPAWFW
11968	25869	A	12076	252	1	GVFGFPFKGGFFVWKGFLGTPQIFWVG VFPKKKGALWVKGLLKPPPPPLFFFF FETESCSVARAGVQWRDSVKKKITIARA
11969	25870	A	12077	273	366	IFIYLFYLFETESCSVSQAGVQWPNLG RLR
11970	25871	A	12078	127	2	KKKKTLFFFFFFFEMESRSVTQAGVQW CDLSSLQPPPLV
11971	25872	A	12079	206	334	HNRVTIVNNLIVHFKITKRCWTQWLTP VIPALWEAKAGGSSE
11972	25873	A	12080	135	2	KMKRKFGEDSQIPKTLQTFPFLTESRSV AQAGMQWCDLGSLSHC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11973	25874	A	12081	147	3	ATTPGLFFIFYYFFETESHSTAQAGVQCM ISVHCNLCPLPGSSDSPVLV
11974	25875	A	12082	106	2	YFIPINEGYCFIYLFFETESRSVVQAGV QWCDLV
11975	25876	A	12083	164	346	CPYKKRKKANQAKWLTPTVIMLFGRPRRV DRPSSGVQDKPGQHGETPSLPKIQKKSQ AWWCA
11976	25877	A	12084	186	1	KSLFSKGNPLPKGPPPPPPPPPPFFETR SRSVTQAGWGAVIMAHCCNLNPGPSDPP TPAPRA
11977	25878	A	12085	98	2	CPFFRVNFFFFEMESRSVAQAGVQWRDL GSRA
11978	25879	A	12086	154	2	SPTPEKGVWELSPFFSWGPKIWGCIF FLYETESGSVAQAGVQWRDLGS
11979	25880	A	12087	326	3	KTSVITCGLPMGWSWGPFPKGPWWCKKF CVCKFWANQTLKKNLGAGRFPQKPPSAAA FLEMGGFPFKFRFFQGSQFFFFFPFET BSCSVTQAGGQWCNLSLRPLPP
11980	25881	A	12088	154	3	KEFSFFAPGGKQGEIRSLRGPFPQVKP LFFFFFFETESRSVAQAGVQWR
11981	25882	A	12089	174	2	SWKAILQYSLEIILVLPSTFQIFLCFSHT HTHTHTHTHTHTLSQIMVLLPSLRKK GS
11982	25883	A	12090	265	30	WFIVYSEISQLWGLPSFNTLGTWQSLSF IFVAEMRSCCVTQAGLELLASSDPVSA SQSARIRAMSPSAWVPIGRSR
11983	25884	A	12091	257	1	GSVMRMHTEQYPENKVEQSSSGFIRPH LVYRVCFYLSVCLSVCLSIYLSIYLSIY LSFFLSFFLLRKSLSIFLSFFLLSPR V
11984	25885	A	12092	311	404	LYHQNPWLYSVFFFLETESCSVAQAGVQ WCD
11985	25886	A	12093	331	83	GDDYKGARENSRDDLFYVLIMVVIQ HVFVKIHKTLQNGYILLCKLYLINLTK NNFQKPKTNSQKTLHIFHPDSTAANI
11986	25887	A	12094	82	2	LREPNNLNPGECECNARWCHCTPAL
11987	25888	A	12095	255	393	HGILFSSFCNINQFLSQHLMVPVIAL WEAEVGGSLPRSSTLAW
11988	25889	A	12096	80	3	FFFFFFFFFETESRSVARLECSGMI
11989	25890	A	12097	367	1	PRVDKPTKMGKKQGRKTGNSKKQSPSAP PKERSSSPATEQSWMENDFAKLREEGFR RSNYSELQEEIQTGKEVETFEKNLDEC ITRIPTTEKCLKELMELKPKAQELREBC RSLRSRCDQL
11990	25891	A	12098	94	236	MMADYFCMSPSIDGLKKKKKKKKKKKK KKKKKKKKKKKKKKGGAP
11991	25892	A	12099	410	212	NSLHPSTSLFRFSSHFIKLISGQAQWL TPIIPVPWEAKAGLLETSSRLAWAAQ EDPISMPVCK
11992	25893	A	12100	140	324	NLGOAQWLMPVIPARPWEAEVGRSLAVR SSSNSPASASQSAGTGPSHHNWLMFLQ LLTRL
11993	25894	A	12101	247	357	KQIQGRAWNLTPVFSPLWEAKAGESPEV RSLREAWPT
11994	25895	A	12102	245	2	DVLVGGCLCPAGGTLHLTSIFLLSGCWC GSKDEEAPCKQRISVQRESQSRTRLRAGV SPKKAHPCEMCGLILEDVLHFPDLQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11995	25896	A	12103	230	379	KEASFFETESHVSQAGVQWRSLNPLGS GNPPTSTSRVAGTTGMSHHVWL
11996	25897	A	12104	86	2	DGVSVLSPRLCENGLILAHCNLRPGSS
11997	25898	A	12105	116	2	SQKTPFFFFETVSLLLPKLECNCAISAH CNLCPLGSSD
11998	25899	A	12106	271	416	QFTFSKAFNLVFIKPSFHISFYRTHYSQ AWWLTPIPELWEAEAGGSP
11999	25900	A	12107	194	3	HVLGTVLVAEDTASNKIRSLQGLLLPL LFSVLEVLARAIKQEKIKVIQIGREE VNRRRGR
12000	25901	A	12108	142	3	LCLLYWDCKRHAWWRGQVRWLTPIPAL WEAEAGGSPEVRSRLPAW
12001	25902	A	12109	233	346	HQRSLIGWAQWLMPIPALWEAEAGVSP EVRSCLKPAWP
12002	25903	A	12110	234	349	GFSPFYDFCLFVFETESCCVVQAGVRWH DLGSLQPPPP
12003	25904	A	12111	136	333	RLNFFYFYFFETASCSVAQAGVQWHDLA HCIPAWETEQDSISKNTVQKRKKCVTRA GISKTKNENF
12004	25905	A	12112	345	110	QDGLCLVMTLQETQPIILAYSLWFFPIVFP TTKACNVQGDSEKLLKKYLQGVQWLMPI VIPTLWGADVEGSPLESLLEPA
12005	25906	A	12113	108	285	YNAMKNRFLKTIILNNKNSIGWARWLMV IPALWEAKAGRSPEVKSSRSRPGAVAVQV DAA
12006	25907	A	12114	1	364	RVVAAEMGKFMKPGKAALDLAGRYSGRK AVIVKNIDGTSRDPYSHALVAGIDRYP RKETAAMGKKKIAKRSIKSFVKVHNYH QLMPTRYSDIPLDKTVVNKDVFRDPAL KRKARREAK
12007	25908	A	12115	120	3	TQIWGAFLTLFFFFFFFEAKSHSVAQAGV QWCSLGSLOA
12008	25909	A	12116	120	3	TQIWGPFLTFFFFFFFEAKSHSVAQAGV QWCSLGSLOA
12009	25910	A	12117	231	1	FLSPFSCYSAITKLLSLSYFLLGHTILL LGSTPEAAQVQVVSFADSDIVPPAST WVFPTLIGIMHHNKQATENAKE
12010	25911	A	12118	216	1	LIFPPLNFCYGEVLGFGGLALFFACM FFWPRFSPKTFFFFYEFHSAQAQGV QWCDLGSLOPLPRGFK
12011	25912	A	12120	267	1	KKKKKAFFSPPLGCFIRLQKHLGLIV YRSHLISLLCLEGIIISLFIATLITL NTHSLLANIVPIAILVFAACEAAVGLAL LVSIS
12012	25913	A	12121	167	372	ISGQDLLKETKRVKRPQDDVPFINIF VPTPGAPRSLRQILELRGKTDPSPIIVG DFNTLFSALDRS
12013	25914	A	12122	124	2	GLLKFNIFAPFFFFFFSETESHSVTQAGV QWCDLGSLOPPPP
12014	25915	A	12123	121	1	RPTAASANSQAVSAAVGYMDPGSEIIE SVPPAGPVSSVV
12015	25916	A	12124	176	2	RDLRGFSRFSNYKFWNFRVGGIFKFPVF GKGVKRFFFFFFFETESCSVAQAGGQWRD LG
12016	25917	A	12125	137	2	KLGGFFGGGGKIFAPQKNFFFFFFFEE MESCSVAQAGVQWRDIG
12017	25918	A	12126	103	3	LEENLGNTIQDIGRGKDFTSKTPKAMAT

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						KAKID
12018	25919	A	12127	212	351	LITFEILNICLGDNILDGLARWLTPVI PALWEAKAGGSPEVRSR
12019	25920	A	12129	187	3	RGSTMQQTINRTPGVRVLYYILMIATMA IPYIPMANLLLLIVPILIAMAFIMLTER KILGY
12020	25921	A	12130	13	329	ASRVITRVMASNSTKSLADAGYGEQEL DANSALMELDKGLRSGKLGEQCEAVVRF PRLFQKYPFFILINSAFLKLADVFRVGN NFLRLCVLKVTTQQSEKHLEKI
12021	25922	A	12131	231	330	MDTDEIYLGRAFWLTPVIPALWEAKASG SFEVR
12022	25923	A	12132	95	2	KGKCFPPPPFFETESRSVAQAGVWRDL SSL
12023	25924	A	12133	129	1	DLALLPRLWCSAMIMAHNCSELMSSSDP PISASQIPGTIGMCH
12024	25925	A	12134	196	361	TIMYYAAMKKKSESPLLHFQGGKLNQD GGWAWWPTPVI PALWKARTGGSLEPRS
12025	25926	A	12135	120	1	PPPPGLFFFFFFETESYSVAQAGVQWCN LGS LHPPPEFK
12026	25927	A	12136	235	3	KKGIRIERDRKLQSVQCFQAKFPPPF PSGVGEKQNPFFKKKKKKKGRAQWLTPV IPALWEAEAGGSFEVRSSRPA
12027	25928	A	12137	185	1	IWCPFFCPGFCISFRCHEFFFFFFFFFF LEAETRSFAQAGVQWCDLGSLSQSSWVTE LAAAS
12028	25929	A	12138	158	1	LRRGGVFSIFFCGTMVLSPADKTNVKA AWGKVGAGHAGEYGAELERMFLSF
12029	25930	A	12139	76	3	KVLARAIRQEKIKDIQIGKEEVK
12030	25931	A	12140	157	2	FFSSPRLLKRRPGNPLGARENFFFFFS ETBSPSIAQAGEQWRDLGSLQAP
12031	25932	A	12141	234	388	LSQLMSANLFFVLLFEAEFHSVNRLECS GMIWAHCNHLPGSSSESPASTSQ
12032	25933	A	12142	112	453	LGRRQAASMRGSIHVGGAGVHIGNAC WELYCLEHGIQPDGHMPSDKTIGGGDDSD FNTFFNETGAGKHVPRAAFVDLEPTAID EVCTGTYRQLFHPQLITGKEDAANNYAR G
12033	25934	A	12143	44	443	AKLGTTRKLPKAKMKEITLINIVVIGH VDWGKTTTGHLYKCGGIDKRTIEKLE KEAAEMGKGSFKYAWVLDKLRDRRGI TIDISLWKLDTSKNYVTIIDAPGHRDFI KNMITGTSHADCAVLIDAAGV
12034	25935	A	12144	3	386	REAAATMRECICIHVGAGVQNGNACWEL YCLEHGIQPDGHMPSDKTIGGGDDSDNT FFSETGAGKHVPRAAFVDLEPTGIDEVR TGTYRQLLHPVQLITGKEDAANNYARGH YTIGKEIIDLVLDRI
12035	25936	A	12145	3	386	AGATYIDRLRVALFEATFTLWVRPELS SGEATMRECMSIHVGAGVQNGNACWE LYCLEHGVQPDGHMPSDKTIGGGDDALN TFFSETGAGKHVPRTBEVDLEPTGIGBE GTGTYRQLFHPQEHMM
12036	25937	A	12146	3	385	GRATYIDRLRVALLEATTSTLRLRRELG SREATMREGICIHVGAGVQNGNACWE LYCLEHGIQPDGQMPRDKTIGGGDDFFN TFFIETGAGKHVPRAAFVDLEPTDIGBI RTGTYRQLLHPQLI

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12037	25938	A	12147	11	381	HTPEGRTRVPVLIAGVVYQAEALRDWGR VTASSTGAMAFLRSMWGLTALGRSGAK LCTGCGSRLRSPFSFVYLPRWVSVLAR CPKKPVSSYLRFSEQLPIFKAQNPD AKTTELIRRIAQR
12038	25939	A	12148	321	509	YSMDQYFIPFYCQIMHLCFPLKTRVSL LLFPWLECSGATSACNFCCLSSNSPASA SRVTGIT
12039	25940	A	12149	51	400	AATMRECISIHVGQAGVHIGNACWEL CYCLEHGIQPDGQMPDKTIGGGDDSFNT FFNETGAGKHVPRAVFVDLEPTVIDE VRTGTyrQLFHPDQLITGKEDAANNYAR GHYITGKE
12040	25941	A	12150	25	399	EATTSTLGLRHQLGSRESTAMRECIS IHVGQAGVHIGNACWELYLEHGLH PDGQMPGDQITIGGGDDSFDTFFSET GAGKHVPRAVLVDLEPTVIDEVRTG TYRRLFHPEQLITGPEDAANNYAR
12041	25942	A	12151	1	402	TKHEELCLACRQRADGGWRSQMNAG SDPVGIVSAARTIIGSFNGALTAVP VDLGSTVIKKVLKRATVAPEDVSE VIFGHVLAAGCGQNPVRQASGGAG IPYSVPAWSCHMICGSLKAVCLAV QSIGIGDST
12042	25943	A	12152	3	400	TDLRLVALKKTTSFPCFPHLGSRE TAMRECISIHVGQAGDHIGYACWEL YCLEHSLQPEGQMPGDKTIGGGDDY FNTFFSETGAVKHVPRAVFVDLEPT VIDEVTGTyrQLFRPERLITSKE DAVNIY
12043	25944	A	12153	2	398	GRCALDRNTFIFARFGCYLIASGH PGEKLMMDMSPLRPQNYLFGCKL KAENDYHFIVANDENEHQISLTAS LAGANDDMNI VEAEMNYEGTPIKE TLATLKMSVQATDSLGGSEITPPSV LRLKCGSR
12044	25945	A	12154	203	405	FTCPSPRIICVISRRISPCCAPDLN PMLSANAMLDVFVTFVEDPGGWD SKNLQKKWSHYSFLTGIRPKI
12045	25946	A	12155	229	397	TKIAHHKAGFALISKITKNLKMFL SKFLPIHALWVTGSSGMQPYPLVW GHYDLGK
12046	25947	A	12156	2	399	GGVPHCVWATAWGMRLPGPTGLCA QTSRRGQKSVLKQKESCGIWQLYH FLSRKQEPRWEPCVSGSSSGEGAV ADLADELRGYPALCCTLPVHSYRS WAGIRPQIMNGPLHPRPLVALLD GRDCTVEMPIL
12047	25948	A	12157	85	414	ALLPQSEALQGAVTMPHSYPALSA EQKKEVSDIALRIEAPGKSI LADES VGSMARLSQIGVENTEEN RLLYRQVLFSAADREKKCIGGV IFFHETLYQKDDHGVFPVR
12048	25949	A	12158	85	407	GLLPHSEPLQRAVTMPHSDPALY AEHKKDVSDIALRIGSPGKGI LAAYESGMANPLNQMGVENTKQ NRRLYRQDLFRAEDREKKSLAG VIFFHDTLYHKDDNGVP
12049	25950	A	12159	85	406	VLLPHSEALEGAVTMPHSYPALSG EHNKELSDIALRIVAPGKGI LADES VGSMARLSQIGVENTEEN RPLYRQDLFSAADRGKKSIGGDL FFHDTLYQKDDNGGP
12050	25951	A	12160	275	146	EKTFTISFFFFFETESHVAQTGV QWHDLGSLQAPPPWFRRIA
12051	25952	A	12161	212	2	KRSRPPFFFFKEMGSCYIAQVGM QWLFV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GTITACYDPBLLGSKDPPTSASQVTGNT GTHHTQLIFVFLV
12052	25953	A	12162	253	2	GRVDSECCLANGNAEKSTFCCLLVLYFY LSSRQSHSVAQAGVQWHDLSLQPPPPG FSLLSRVAGTTGARHHDWLIFFVLGET
12053	25954	A	12163	228	1	LLGLWFEQLGRFTKIAKTGERSQTQSG HSMDMRVPAQLLGLLLWFPGSRCDIQM TQSPPAVSASVGDRIITCR
12054	25955	A	12164	122	1	RLFFETESRSVARLECSGAISAHCSLR LPGSGSSPASAS
12055	25956	A	12165	239	350	GQARWLTVPVIALWEAKASKSLEVRSLR LAWAGHGGG
12056	25957	A	12166	235	359	TDKATSKRDLVLRREIIFEMESRSVAR MECSGVISARCNL
12057	25958	A	12167	209	396	QFSGIPFDQYKCGKFNYYIYYIYYIYI YIYYIRKYTRAYTKRYMCVFSRATHNIV YLCAYI
12058	25959	A	12168	327	130	GGVGLGGPGGKPPRPSPPFFFFFEKES RSVPQARVQWPDFGSLPAPPFGFTPLR ESFLFSSLM
12059	25960	A	12169	317	422	RGEKPLFFFLQKKKKKKKKKKKNIKKG GRRYKPS
12060	25961	A	12170	260	375	EKVTCSWTQWLTPVIALWEAKAGRSLE FRSLRSAAWI
12061	25962	A	12171	304	3	KFFFFFFKGFFFLGGVGPIFPPPKRFFS KIPPGVFFFPPLKKKIFFFPVPVILGPP RVFFKGAPLFFFFFFFSETEFRSC CPGRLECSVAVSAHCK
12062	25963	A	12172	105	3	LIFLRQSSALLPRLECNCAISAHCNLCL TGSSD
12063	25964	A	12173	146	17	RIFFFFLGQSLAVAQAGVQQRDLGSLK APPPGVHAILLPQY
12064	25965	A	12174	234	2	LFPRKPKPSVLSLSLSLSLRLRLKLS FMRHNNIEVRPINNPAMTSKCSERKSL VSFTLNLPKGMIRLSEEGMLK
12065	25966	A	12175	292	380	VRGLGRVAHTCNPSTLGGQSGWITGGQE F
12066	25967	A	12176	109	1	GRIKKVIKQQAQWLMFPVIALWEAKVGG SPKVRSSR
12067	25968	A	12177	170	291	LINFYFYFLRQSHSVTQTGVQWCNLSL QPPPAARRRRRG
12068	25969	A	12178	260	380	LTYIALFTFLRRSLTLPRLECSGMISP HCNLCCLGSSDS
12069	25970	A	12179	54	166	PKRGFHRVTQEGNLNLTGSPRLGLPKG WDHRQDPLP
12070	25971	A	12180	273	359	APAGHGGSCLSQHFGRRLQADHLGSGV R
12071	25972	A	12181	27	225	IGQAQWLTVPVILAFWEAKAGGSLEVRSS RPAWPIYFLVLLASYLRRFCLIQGHSDL LYTSSTRGS
12072	25973	A	12182	1	155	VHKIFIAKYSGFTVFRGRAWLTPVI PALWEAKANRSPEVRSSRSRGRG
12073	25974	A	12183	91	2	FNLEFFFFFETGSRSVARLECNCAISAC C
12074	25975	A	12184	122	2	GQAQWLTVPVIPPWEAKVGKSPEVRSSR RTRGRTRGRTRG
12075	25976	A	12185	389	20	TDRGRRARRACFCGKVFDELSFALKLA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						REMGRPDWRAMLGMSSTTEYADWHRFYS THYFHDVLLDMHFSGLTYTVLSLFFSDP DMHPLDLSLLNRREADREPDDVLMQKA AGLAGGVLEFI
12076	25977	A	12186	180	393	LNPSSGGCGEPRSRHCTLAWTERESVS KNKIKIKINKQIEEGFLFQPPGQGFIC YFPAKEFIILSKT
12077	25978	A	12187	37	443	PDFPIPFPPRKVQHLARPSPKTARPAWT IRRILPPPPKKRHPGLARGKFGPRELA KAGLAKECPAGGPTPAVRPATPTRGGGG RVAGFQTPMGIPMGKARLGLLTFLGFAS GWIGAYRPRETLCCGELVDTLQF
12078	25979	A	12188	3	411	AFPENATGSTFQDFVPASKGRAEVGNM RLSVAAPISHGRVFRMGLGPESRIHLL RNLLTGLVRHERIEAPWARVDEMRYAE KLIIYQKLGDTNQRAMRMADFWLTEKDL IPKLVLQVLAPRYKDTGTGFTRLQ
12079	25980	A	12189	2	414	QEFGRKRATFISLLFFSSVYSRGVFR RDAHKSEVAHRFKDLAEBTLRALTLIAF AHYLHQCPFADHVKLGNRATEFAKTCVA DESAENCCKSLHTLFGDKLCTDAPLRET YGMADCCAKQEPERNECLLQHKDD
12080	25981	A	12191	3	514	PRLLMEAGPHPRPGHCCKPGGRLDNMHG FVHHIRRNQIARDYDKKVKQAAKEKVR RRHTPAPTRPRKPDQVYLPVRHDVSAH PRNPDIYESGESSSSGGSELEPSGHQLF CLEYEADSGEVTSVIVYQGGDDPGKVSEK VSAHTPLDPPMREALKLRIQEEIAKRQS QH
12081	25982	A	12192	182	3	RGLFFIPPPPIKTKIWPFPKVVFMGFG PPLFFFFEMESRSVAQAGVQWHDLSLQ ALP
12082	25983	A	12193	53	400	PETPSWLGPVRRFYFIIKSVWKKKKK KKKKKKKKKKKKGGGPFKTLGGDKFYW GVKKKIFFFLGSSKKHPWGFEEKLFFG GGKCGAPPPKDISCLWGKKNFLGAIGBK TCCC
12083	25984	A	12194	182	3	KGIFIQIAPPKKKKKNWGLWKVVFKGFG HPIFFFFEMESRSVAQAGVQWHDLSLQ ALP
12084	25985	A	12195	200	378	KSSKSQWLGYLFIGLLIYLFIKFFLETR SCFVTQAGILAHCNLKLGGSDPPTSAS QAA
12085	25986	A	12196	341	54	SLSFHGGLSVLCIFSTYKLSQEQLWLT VISVLWEVKVSRSPQVRSRPGDPPASA SQSAGITGVSHHARPHLSLNPRLEMIL SEEGMLKRMGT
12086	25987	A	12197	1	462	GGPPRPFMRKAVALTLAVLFLTGSQARH FWHQDEPPQSPWDRVMDLATAYVDGLKD SGRDYASQFEGYALGKQLNMLLDNWD VTYTFSLRQLGPVTQEFWDNLDKETE GLTHEMSKDLEDVNAKVQTYLYDFQKTW QKELTFTAESVP
12087	25988	A	12198	80	1	SNKVFFLETESCSVAQAGVQWCDLGS
12088	25989	A	12199	221	3	TMGIMLDKKEIQAFSFKFMGHAVAET TCNINNTSGPGTANKVTQWWFKKCKG DESLEDEHHGRLEV
12089	25990	A	12200	239	336	FGALPITTCFKGKKKKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						KKKKKKKKKK
12090	25991	A	12201	279	366	KKKKKKKKKKKKKKKKKKKKKKKKGFK
12091	25992	A	12202	153	40	GFLFLIFFFFTKSRSTIQAGVQWCHLG CTLAWATETD
12092	25993	A	12203	317	406	LGKLCNGAVSGHCNLRPLGSSDFSGSA S
12093	25994	A	12204	2	925	RSGPDHELTLDGKGTCTRMVPASAAASE DRRKLP IIVEDEGGPTRSRACSSPARGS RPPPSAIGCSPVAQASDSAAGPARRTAL QSLSSNLGYQIDRHSVPVYVFKSPFSV IMAPKHSSDAGNDRPKRSRKVLPLSE KVKVLDLIRKDKKSYAEVAKIYGKNESS IREIVKKEKIRASFAVSPPTAKVTATV RDKCLVKMEQALHLWVEEMNRKRVPIDS NMLRQKALSLYQDFSKGCSETDTKPFPA SKGWLHRFRHRFSHYKKKKKGIMAQVA VSTLPVEEESSETRMVVTVFLVSALESM
12094	25995	A	12205	272	1	KMARAGLLVIEGKVWRTVYRFATREER EGKMTNLMNKLDITIGFDNKDLLISVG DLVDRGAENVECLELITFPWFRAVRGNH ERQPGQ
12095	25996	A	12206	166	478	ISASGLLPTSPLTGTSKLQDPNEHLNLL MLNRVSLLLPRLECNLTILAHYNLRPLG SSNSPDSAFQVAGITESFTCEINALKDS SQVALWSFRCEMDHSSICNR
12096	25997	A	12207	102	497	PLLALLFGSQKTFCLCLQLSLKPTRSSLL SPGSAGNPENBAPCPQLNPEATSLKKKK KKKKKKKKKKKKKKKKKKKKKARG
12097	25998	A	12208	131	2	FGFLGGDKAGKGPFPFPFPFPFPFP VAKAGVQWCDLGSLL
12098	25999	A	12209	221	499	QTRHKLTSNRSGRTGLQILIKEQHSSGR WCGTGDILWQSLEDITICYSVPKSLDLFL LFIYFETESHFVTRLECSGAISAHCNLR LLGSSDSPA
12099	26000	A	12210	297	398	HNFFFFLKTESCISISQAGGHWDLSSPQ PPPPG
12100	26001	A	12211	341	452	NWSPGLKQSSRLSLPKCWDYRREPCLA GLLAYLFR
12101	26002	A	12213	214	468	FFFFFWGKGVFFFPPLGRGGSVYV TPPPRGKKNFPLGLGKMGNNPPPPPR FFFFFKKGVFFLPGPGVKTPSLRETP P
12102	26003	A	12214	223	477	CPTETQLQLIFAREKHKPSVLDDLDLY GFFFEMESHVSVPLECSGPISAQSNLYL LGSHNSPA
12103	26004	A	12215	263	55	TPKRYGKMQTATYLPKSKYIYIISDLRK QDYIVYKQSKKPEGWAQWLTPVIPALWE AKAGRSPKVRSSR
12104	26005	A	12216	328	471	GVIHAQVLHAHTHTHTCTHTQVHAHS
12105	26006	A	12217	434	1	WDHSASPPTS SVGTPLRADGPHPRLTAPG HVGSSAMLSAPAAGRRGLSLGRWCDRD KLSQRGPQPKWILWGNLPGGGLHRHI HKPLPTIPSTVRGEEVLQQLHSASF ILFIFIFLDRVSLCHPGWSAVARSPTT TSTS
12106	26007	A	12218	304	43	EKPIGVAPSRVKKRAGGGEKTECCLLKG PLQGFQGVKGLKPLKNGPLFFFLRRS LALFRLECNGTILAYCNCLLGSSDSPA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SEI
12107	26008	A	12219	171	365	ALVQPRAGREAVTVPACCSQSDVFLYET NKVARIQSINYGTIKFFHVIVFSYVSKE HLKRKLEK
12108	26009	A	12220	171	452	ARYKFLHPKFAFGLYPSSSQIQGARHQL WILIKCSFYLLFLRQCLTLPLQLECSNM ITAPLQPLPGLKQSSHLPLPSSWDYRH EFP
12109	26010	A	12221	323	458	FRVQRSFLFIYFFETESHPPVQAGVQW HDFGSLHRISP
12110	26011	A	12222	189	56	DRVSLVQPTLECSGTISVYCSLNLGSS DPPTSASPVAATTGGI
12111	26012	A	12223	246	494	FLCSSYAYDDHFLRPFPIHLILDLITAF SQDTIISNLLFQDACSVPKKAANLGOAQ WLAPVIPVLWEAEVGRLLLEVSRSPAW
12112	26013	A	12224	55	353	RIQGCSCWVKLCPEKWKVQRTDAEQES QTKAEIQDMKQELSAVNMDKFAARSARL ERKINKMMNKLKTHVKVQTAQSGMLKWV ISVAFYKLPQTVIRL
12113	26014	A	12225	199	23	LKLSSIIYVPGTILKYFTGWARNLLPVI PALWEAEVGGSPVRRSSRPANSTSWIER HQ
12114	26015	A	12226	369	14	DCVRVGLSYBQTVCPSCSVRKAPFSSR PHRGVLESQGPCKSRVDIFFSMERER DRERERERERERERGQKTRRVWGGERE KLGYSYHAWGWRGGRGLGWGGMCGIPPPC TSDVHQ
12115	26016	A	12227	206	2	QNGHMNGGCPVSLSLFLETRSFLFFLA SLSMLECSGAILAHCNLRPGSSNSPAS ASQVAGITGACH
12116	26017	A	12228	231	501	RSWEGQALHGSDDLASCTRIQSNYMALQ RINQELDKLYRMGQHYEBEKRLASHBI VALNSHLLLEAKVTIDKLSBDNVSAAHW PMEDCR
12117	26018	A	12229	86	455	DLPTFFVPPHPGFGSGLLQSELPNSCQ TGGRSHLSVSVLCPTLATTPLGLDFPTC GTSQPLPLQLAHRSELAGLSLPLST NCTSQRPLPDRPHRSDAPHTHTHTQHT HTHTHTPATVT
12118	26019	A	12231	211	96	KSHFKAGGGGPPRYSPFFGGGGGGVFRV GGFPPPGLTQ
12119	26020	A	12232	228	3	KRWFIKGFSLKGLGPPPPKFLGFFFPF FFFEQSFLVLAQAGVQLECSGTILVHFN LYLPGSSNYPASASHPRV
12120	26021	A	12234	137	3	VPLPGTLKNHSMVPCFLFVCLFVCYETE SHSVAQAECSGAISAH
12121	26022	A	12235	139	1	FKLCFGQAWWFKPIIPALWETDASRSLE VRSSRPADAWADAWADAW
12122	26023	A	12236	80	1	VLLIFIFLEEMGFHHVQGQGLDLTL
12123	26024	A	12237	187	494	TERNSFNINKKDIHTKTPFVGQHQRPK VDKTTKMGQRNQSRAENSKNSTSSPPK DRSSLPATEQSWTENDFDELTEVGFRRS AITNFSSELKEHVLTRTE
12124	26025	A	12238	252	503	CQVGADDLQSQAEIQCELCAESIDRFD ILFFFFLGLGPPHKNPPPTPQKWPGK APPLALWDIPRGAKGPGRQPGRAIHTC
12125	26026	A	12239	2	471	RIALCPAVRIRHEERERERERERETP GHTQLSPGARRTPPLERERAFNDCFSLN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YPGNLCPGDLIEVFRSVYQHCALYLGDG YFINITPVYGIAPFTSAKSVFFSRALE KTHLLKDVVGS DTYRINYICYETLPSLS VEEII TRSEFVIGQEA
12126	26027	A	12240	14	149	FMTACRIRHEMGRGLRLGLWPLHIVLWT RIASTIPPHVQKSALPH
12127	26028	A	12241	588	671	RSRFSFQEQAFESSQKYKEGKYIIBLNH
12128	26029	A	12242	384	464	RGGQVWVLPVVPALWEAKAGRSLEAG
12129	26030	A	12243	325	459	TYLFIYLFYFETESCSVAQAGVQWRDL VSLQPLPNSPALPTN
12130	26031	A	12244	323	457	SLQRECGPADTFFEMDSCSVAQAGVRWC DLGSLQNSP
12131	26032	A	12245	241	466	GALFFFFFFFFFFFFFFFFFLSNKAVY F
12132	26033	A	12246	385	37	QARRRCLQTSRMEALGRWSYKVTIEFPL QILFPFPILKYKVFIGIKITPNPHFLER YEEGQRLGKSTVSVWFNEDTRLINIWNR HITVNPRTNSQNRMLKMAHESKYSQVPP PLQA
12133	26034	A	12247	318	456	LILKYFMYVCMVHMYVCMYIKSCSVAQ DGVQWYDLGSLQPPPPGL
12134	26035	A	12248	362	473	SPCQNNMNSAKTEARTNIKFMAKLMWKN GAIIDALQK
12135	26036	A	12249	310	463	FSIKTRKNALGKLQSLLRCHQFYLYVCV CVCVCVCVCVCTRTRYAILTCIAV
12136	26037	A	12250	169	54	EAKSGQARWLTLPVLPALWKAKAGGCPEV RSSRLAWPIW
12137	26038	A	12251	49	449	GIPATSTSCVQVILLPQPPLLLGLQDSF LPQEI I IKVEGEDTSLTIPSGEWNFK IVTVDFTRREEQGTCPNAQRTLDRDVILE NHRDLVSWDLATAVGKKDSTSKQRIFDE EPANGVKIERFTRDDPWLSSC
12138	26039	A	12252	130	428	RWGLAMLPRVLVNSWSQVILPPQPQVGA TFGGFPNPPGHWKLLGGISSGEEAGVEE AEEGQALGFLGQFPSSPQLLLQTSWCL RTTRTCRWSLLWKAH
12139	26040	A	12253	204	54	PGMHKTQKSDLGQVQWLTTPVILGLWETE AGDSPESRSSRPAAWKHKIVR
12140	26041	A	12254	375	470	SLCLFFSFFFQTEPRCVAQAGVQWRHLS SLQP
12141	26042	A	12255	432	512	GQVRWLTTPVIPALWEAEGGRSPPEARSS
12142	26043	A	12256	232	1	KGALS KKTQSFWGGQKFFPRPGVFKGVF FWGGGFCFFVFGGFFFFFFFFFETESCSV AQAGVQWCSLGLSLQPLPPRFK
12143	26044	A	12257	22	123	RFVCSTIKVLRDLSSDRSNPGRFLSTSN SSSTRP
12144	26045	A	12258	71	362	QTERNSISINKKDVHTETPSKGHQHQRFP KVDKSTKMRKKQRKKAENSKNQNASPP KDHNSLPAREQNWTENEFDLTEDFRFR WVTNNSSELKEHV
12145	26046	A	12259	375	3	SPNIEAPPKAFFFFNQRHFVFCFFSCRA ENTHEIVWVKVYFNSQSKAKLFFSFFV QRDRSSPDSYLMPLQLQMWDTAGQERFR SIAQSYYSANALILAYGITCESFRCL PEWLRQIEQYA
12146	26047	A	12260	98	1	KYQIDLGGRGSSNSPASASRVAGITGTH HHTQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12147	26048	A	12261	125	3	LFLIQKIYITGQERWLTTPVIPAPWEABAG RSPKVRSSSPA
12148	26049	A	12262	228	385	SCLYLQMIPISSIEKSQGMYYKATRGRRAR WLTTPVIPALWEAGAGRSPEVRSSR
12149	26050	A	12263	227	369	MLKHKSNNKLNQDLGQMQLTPVNPVLWE AKVGGSPVKNRPAWPTW
12150	26051	A	12264	102	487	QNNRFFGTERTGRGTGRGVSSFPQLSPGS LELASSPSPSVGRLGSAASQSRSGGQER PKAQLRRPPRESSSPRLRGRENCAHAR TPGGILDRPPPTLTGNTLLKGRPAWMA NPPEAKHTANGPGEQA
12151	26052	A	12265	391	476	PRSYRVECSGISAHCNLGLGSSNPSS
12152	26053	A	12266	378	476	MSSRLGSLEVGILGRAWWLTTPVIPALWE AKEGG
12153	26054	A	12267	166	58	NEFFFFFETDSCSVAQAGVQWHDLSHCN LCLPASSN
12154	26055	A	12268	209	49	TPPNFYIKISRSQQAQWLTTPVIPALWEA EAGRSPEVRSSRPASPTRRNSISNS
12155	26056	A	12269	127	1	SSSFPLKTFGLFFFLCFESESRSVA QAGVQWCHLGLQA
12156	26057	A	12270	154	27	IQTPGKKEFFFFFETKSCILVAQAGARL CPKKKEKENSFVL
12157	26058	A	12271	180	22	VLKIHNIQRAQWVTSVIPELWEVKAGGS QALRSSRAARTWDACNFVEKTQVY
12158	26059	A	12272	207	422	GDSSTRGADEKPKGVKTDNNNLINLKV MGQDCSMEQFKIKSHIPAGYGGSHRESQ HFVMPRWADHLRSGV
12159	26060	A	12273	59	479	NSLGGGGVYGSFRFTFPGRALSPWRV RVQRRRCMSTMPADTLLIVFISVCTAL LAEGITWVLVYRTDKYKRLKAVEKQSK KLEKKKETITESAGRQKKKIERQBEKL KNNNRDLMSVMKSMFAIGFCFTALMG
12160	26061	A	12274	354	439	VKTGECSTAKTWNQPKCPTTIDWIKMW
12161	26062	A	12275	366	499	TRAQYFVVVVGIGSQCVTLCSGMIMAH CSLDLLGSSDPPTSAS
12162	26063	A	12276	136	37	KFPQGVHWLKPVIPALWEVKAGGSPEVR SSRPA
12163	26064	A	12277	419	48	DGKLNVSFLTSSSGCFLIFLLIVRPPY FLRYNNSEIRPINNPTMTCKCSSKRKSR ICLTFNQKLEIIKLSEEGMSKIKTGQNL GILCHVSQVDEQHKFVKATKSATAKIN LSISKYIMSGA
12164	26065	A	12278	190	1	RKGVFSQMGPGLGKGSFPLAKLNFPF KKTFFFFFETGSCFVAQAGMQWLDPS DANADAW
12165	26066	A	12279	276	389	WFNLSFFCFCLFFETESCSVARLECSG AISAHCNLT
12166	26067	A	12280	425	1	PPHPPPGKPPPPRPELFFPKTKNKKER VLFFSPPPKKNFFSLTTPRFFSPPQKK KKKLNPPPKQGPVPIKPPPLFFFF FFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFSGLTVRVIMTCWLIVDIGLL I
12167	26068	A	12281	253	90	IWPPQGSFKTAAPFFFFFVFLVEMGFCH VVQAGVKLLTSSSPPASASQTAEKLF
12168	26069	A	12282	61	387	PKSSSSAPFQISSWFSLPASTSASTMSI RVTQQPYKVFNSGFWAFSSSSYSRPSA HISSLIVSRVGSSTSFQGGGAGMGLP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in US 9,515,126	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12169	26070	A	12283	186	305	LHSSLANRARLSQKKKKRGGRSKEP LHHSTVQVREEEHKSLHTQVHTHTTET HPLVIMSSHS
12170	26071	A	12284	2	190	PRVRFDVRNNRSLNPLISRTMRIEPIPE NPKFSVKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKGGGA
12171	26072	A	12285	17	197	SLGVGGGQGGGVHFPCKPFIVLSPVS LSKHCSYLPKKKKKKKKKKKKKKKKKK KKKKKKKKKKKK
12172	26073	A	12286	158	405	GVASYAEQRYFLEMEYFPGGEAISIVE MTTEDLHYSINLDDKAPTGFERYVSHFE RTCTDDKMLSYCITCYRIFCERNKL
12173	26074	A	12287	364	142	GCAFFLGGLKERRKRAVPPLFFFNFF FETESCSVTQAGVQWNLGSLQPLLIDW WQPGTVAHACHPGTLGG
12174	26075	A	12288	171	380	VFBAGHAWLQENLTSPDFWGFSSFFPDT GMLEKKKKKKKKKKKKKKKKKKDR
12175	26076	A	12289	194	2	GPRGFQFWVTKGFFPKKGFVKFYPPAG GWFFFFPKRGFPFPSLFFFDRVWLCHP GWISVARS
12176	26077	A	12290	179	416	LIFLETFAVCFQLARFHKIHIETAL RCLIIILSCPFTPLKMYREGQARWLT VIPALWEAEVGGSPVRSRLPAC
12177	26078	A	12291	3	408	LAYGFHRTTYDTPSALMMVLVDELIT GNKNGSGEAPYLPEDFRDGEDDAAVTL EKQEDLTTLVTLPTLGEHQRETQLE AKLLKKRLELGSLLDLVEDLELIQLKK KKKKKKSPLWGAPFKGPLGAPI
12178	26079	A	12292	119	278	PKSTIAGVKSVDHPLPKNKATHLSCKK LKKKKKKKKKKKKKKKKKKKKKKKKKK KKKK
12179	26080	A	12293	119	3	MLFTGFHTKVMSLNSITGWAWWFTPVIP ALWEAEVGKS
12180	26081	A	12294	205	1	ILHFYSTETKQPKGLFALFYSDCEQEK RKGGKLLKIFKKAQGQARWLTVPVPAFW EAKVGRSPEVGS
12181	26082	A	12295	215	1	AFKIKLTMHIFSSPLCLPQDEFHPPFTEA LLPHVRAIAYTFNQLARKRYFKKHEK RMSKEPHGARLEGNO
12182	26083	A	12296	185	411	DVPLMPHVLHLHSDFRISTEIGVETVG KRVLHRIILLLLLLFFEMESCSVTHAG VQWCDLGSLQAPPPGFTPF
12183	26084	A	12297	281	388	RILFFFFFETKFCSPVQAGVQGRDLNSL QPPPPGFM
12184	26085	A	12298	178	3	TLLSVTQVPILPGSASSPLLSRKDIKI PTSVFFSFQTEPRSVTQAGVSWCDLGSL QP
12185	26086	A	12299	199	450	TLIRHMICNYFLLSHRSFPSSVDYFLCY REIYSLIKTLNKLIGGGFFLNLIKVMYD KPAASIIIRSEKQKAFPLRSCTIRICPL
12186	26087	A	12300	3	407	EFKDHSTAMDEPNPGTSSVSTTTSTT TTTTTSSSRMQPQISVYSGSDRHAVQ VIQQAHLRPPSSAAQYLQQMYAAQQHL MLHTAALQQHLSSSLQSLAAVQASLS SGRPSTSPGTSVTQSSMVQTSI
12187	26088	A	12301	227	3	KRGTEGQTLFFPAPRARKSPPPKMPKK VEKEFPKGGFFFFFETESAPSPRLCS GAISAHCSLNPASAHAS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12188	26089	A	12302	292	380	KCYRWARWLMFVPIPALWEAKAGGSLEPRN
12189	26090	A	12303	13	186	VDERHIRLSEMAWVALYLLSLLWATAGTSTQTQSSCCEYDVFPFRRSGKQLPWGRGCDL
12190	26091	A	12304	253	409	ITAVIAAAAAVVGVTIIMTNFRSLPRLECNGAISAHRNLLLLGGSSDSPASAS
12191	26092	A	12305	153	64	GRAQWLMPITIPALWEAKAGGPLDVRSSRPA
12192	26093	A	12306	265	420	GTLMSRNTKLQLCRMNKSRTLQGPPWLTPIVPTLWEAKAGGSLEARCSRPAW
12193	26094	A	12307	295	1	RPCLNKKKTSPhwKKKFANPLFGKAPVFLDKKPKPHYRESRPLKKKNGPKGFFFFFFETESCSVTQAEVQWRDLGSLQAPPPGSYHSPSKLIIN
12194	26095	A	12308	247	421	SWCCLKKKKKKKKKKKKKKKKKKKKKKKKKKGGGALKKKKIFS
12195	26096	A	12309	168	3	GQALLLLCLTVAFSKTTVVCHAPILGWAWWLTPVPIPALWEAEVGRSPEVRRSRP
12196	26097	A	12310	117	3	VAYNIAVFRGGVSLLLPRLECSGVISAHCNLRLPCSS
12197	26098	A	12311	256	101	EPPTPPFFFFETGSCSITQAGAQRDRHSPQQSPTPLGSLNTPAPASRACESGR
12198	26099	A	12312	146	3	FVALCIQLFPLVNVICFHKKHKHTGRARWLMPVPIPALWEAKAGGSPEV
12199	26100	A	12313	207	3	VRVRTTGIVIMALRGLCFSSVEESMTKDELIALRLSLGELNRDVSITGTKEELALRV AELKQELDDSR
12200	26101	A	12314	282	2	NCLAEEKVKFMVSAISLQPGQISILFLSFFBEKESCSVPQARVQWPNFSSLSQSPPPGFKLFFCLSPGGGGCSEPKSCRCIPGWQQNETPSQKKK
12201	26102	A	12315	298	84	KTPQPPVFALSKNFGPPKTAIPFFFFFFFETKSYSVAQAGVQWRDLGSLHSSSLGHRARLHLKKRKRKSNINL
12202	26103	A	12316	124	1	SKGHFFFFFFFSETESCSVAQAGVQWHNLGSLQVPPPRFTTF
12203	26104	A	12317	132	398	VVTNAVFSIVTFSPPSVCHSEVALAAYKWLVCYLLRETYQKLNQEIKPPTLSVPKKKKKKKKKKKKKKKKKKKKKK
12204	26105	A	12318	262	392	PHYCONQPQARRSGSHQHFQKQRREDHLSLGVRDQPGQYSETP
12205	26106	A	12319	168	3	EAPKAINCTTALQPRLOGKNLSQNKEGVQQLCTPVIIPALWEAKVGGSPFVRRS
12206	26107	A	12320	48	385	DLGLSGHSTLASSFISLLLLSYKKCLSPSTMIMRLPLPGSPIKPPFLPKKKKKKKKKKKKKKKKKKKKKTTGG
12207	26108	A	12321	218	83	NLSPIFPEGNFFFFFFFEMESRSVAQATVQWRDLGSLQAPPPRRK
12208	26109	A	12322	197	1	KETWPPFPKKEQGLFSFFPKRIFFFFFFSKKTPSPFFFFFFFETESCSVAQAGVQWHDLGSLQAPP
12209	26110	A	12323	128	36	KGLFFFFEMGVSLLPRLCSCGTTSAHCNLP
12210	26111	A	12324	140	3	ILNSNLKPIKNTFFETESRSIAQAGVQWHDPSKQPPPLGFKR
12211	26112	A	12325	273	369	RKEWFLKKKKKKKKKKKKKKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKK
12212	26113	A	12326	140	415	RTGLLGPGRLQGGPPYGSREYKGSGLLDL NASLLDPEVWAPSLSGPETKPPAHSPSD PGVHSSCSASQGSQGGPGLTPSSRIHEP KPDGFFFK
12213	26114	A	12327	2	506	FVPLSETEAPGCSGSRPPELEPERSLGR FRGRFEDKDEQLBEEEELEEEEEED MSHFSRLRLEGGQDSEDEERLINLSEL TPYLCSICKGYLIDATTITECLHTFCK SCIIVRHFYNSNRCPKCNIVVHQTQPLYN IRLDRQLQDIVYKLVINLEEREKKQMD
12214	26115	A	12328	1	419	FRVPSARCQYLPPLRGASQLGYSGVRD PVEEAVCPFSDLKLCAGRITTLFKAVRQ GHLSQLRFLLPFWLCPAPRSGVYGRQ ASLSCGGLHPVGASWPCLPTQASAMAG TPPPASLPCCSLISDCCASNERGSMGV
12215	26116	A	12329	259	414	NMENSRLCWVVPKLAFLVLFASLLSAHL QVTGFIKAFTALRFLSEPSDAVT
12216	26117	A	12330	302	404	SCYRVSVISQARWLTVPVLPALWEAEVGR IPEVGS
12217	26118	A	12331	94	375	SRDMSPGLLTTRKEALMAFRDVAFAFTQ KEWKLSSAORTLYREVMLENYSHLVSL GIAFSKPKLIEQLEQGDEPWRENEHLL DLCPGWSAMA
12218	26119	A	12332	7	246	NPIVDPSPCGGIRVVRTPAGRGGPALVR PETWEAGEKMPSESLCLAAQARLDSKW LKTDIQNCFITRKISLLPLFCHHL
12219	26120	A	12333	150	1	YIYFFHLVRGLPGSGYDEYFVVVVNTE SPSVTQAGVQWCHVSVSVQHKPP
12220	26121	A	12334	34	426	EPGFLFVFFFLIRGKKTPLFFWGRKNP KSGKPLFTPPGKSPSEPPKSRGGPLFPQ TRSLTPQSWFGGAPKPLGGEPKFW AGLGGDPPTPRAPHRADQTLQPIQAPT RIIQNEQWAIKPPQMPGG
12221	26122	A	12335	185	3	TVITPLHFSLGHRARLWSRVPAAPAE NRSMEGGLGRAVCLLTGASRGFGRTLAPLL ASHE
12222	26123	A	12336	60	316	GWGPIPSTDVTVLSPQKPIILQGERAI TQIKYNREGDLLFTVAKDPVSVGWRGSG RGGILLPGRWVDTPVLPAGNQASHCE K
12223	26124	A	12337	3	167	SFRIQVQGNHTSKHYPKIQYSDQAWLT SVIPALWEAKTGRSLEVRSLRAFAP
12224	26125	A	12338	238	401	RPLSVMCGRLTSIRVEDSGARCWFYLF IYETEFRSVAQAGVRRRLGSLQTPPSG
12225	26126	A	12339	354	433	GWAGWFMFVIIPALWEAKAGVSPVRS
12226	26127	A	12340	238	382	LLIVYNMMLLPDAVFTCNSSLTGGQGR RITRGQEFETSLANMVKPHL
12227	26128	A	12341	101	1	KTKQTNKKTRSVGQTWTFPIIPAYWEA QAGEL
12228	26129	A	12342	276	23	GSCLLLEGKLTNRKDIHTKTPSVRHHQCR PKIDKTTKMRNQSRKAENSKNQSSSSP SKECSSLAATEQSWMPHDFDELREGFR
12229	26130	A	12343	122	1	YMGVNERGCGQSIFKSSLSQLWWWAPI IPATQEAAGEW
12230	26131	A	12344	180	360	LHVYVFFSVGDPLPPPPPLDDSSALPS ISGNFPPPPPLDEEAFKVQVRAEVKVML GKS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12231	26132	A	12345	35	411	TMTIVDKASESSDPSAYQNQPGSSEAVS PGDMDAGSASWGA VSSSLNDVSNHTLSLG PVP GAVVYSSSSVPDKSKPSPQKDQALG DGIAPPQKVLFPSEKICLKWQQTTHRVGA GLQNLGNTCFANA
12232	26133	A	12346	278	386	IIYCYKQTTIGQARWLTTLIPSLWEAKV GGSPEVRS
12233	26134	A	12347	111	2	KSQTGQVQWLTPVIPALWEAEVGGELLE RSSRLAWA
12234	26135	A	12348	215	316	LNKRLMISFIKKKKKKKKKKKKKKKKKK KKKKKKKGGPL
12235	26136	A	12349	265	404	SNISYFLNNFNSKALSLNIKYMISQARW LTPVIPALWEAKVGGLE
12236	26137	A	12350	372	1	PVFPLPPKKLGEQLPPPALARFLAVSPLP KAAHEQEIKEKVLAVHKNPIDPVYGFPG KGPTNFFLPFLPQRFVIFLGAQKGVSWFG FYVKGLSLAPKLGGPPFFFFFTESRSV AQDGVQWCDLGS
12237	26138	A	12351	318	416	QGRAQWLTPVILTLWEAKAGGSSEVRSS RPAPF
12238	26139	A	12352	144	1	NGYATVECVVLFCEVFLRQSLVQAAG VQWCNLGSMQPPSTSLVQAI
12239	26140	A	12353	116	1	SGRVSFKMKCGQERWLASVIPALWEAE VGRSPEVRS
12240	26141	A	12354	102	2	ETRYKKQPGGWERWLTPIIPVLWEAEVG GSPEV
12241	26142	A	12355	112	294	LISPCPMWFSPHGTWLSRLISQHS NLKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKRGGA
12242	26143	A	12356	138	2	SFFLVVFFFFFEMESRSVAQAGVQWCN LGSPQAPPGRHCPVD
12243	26144	A	12357	148	394	PGEPPGEKGGGKGGKPGGRGWGEPPCR GGFKEKFPKGKAPPLKENSRENLGWG TKIPLGKKKPPPPQEQEMILGPPQF
12244	26145	A	12358	97	3	EKFSPCFVRARHTHTHTHTHTLSL GFH
12245	26146	A	12359	204	2	KHYTPAACFAPCLPDEAPIIAAKPATT TSEQMAVPPKYANLGKSARNVFNKGYG YGLINLLKTKS
12246	26147	A	12360	156	391	NRGLFKVEESFSPICSVRCSIHPSALVS PTPPTDTTNWALPFETESCSIHQTGMR WRDLNLLQPLPPGFRFSCNL
12247	26148	A	12361	179	1	ALKKLLIIDDNSHKTNIKHFSPRNF LFLLETESRSIARLECS DANPTH CNLRL SGP
12248	26149	A	12362	218	391	TILKDCITFKMICLSQAQWHIPVVPATWE AESRGLLEPTS
12249	26150	A	12363	2	356	TNSHVDNSITQKPEFCIPRCGYIVCOL QLVERAFIFNFFFFFLKRSFVLLPRLEG RGAI FRVTQEGSNLLTLGPAPLGLPKGW NYRGDHPGPAYFYFLMGKRLLIQGGRG LKRNL
12250	26151	A	12364	94	1	KNPPLFFFFFSESESCYVAQTAVQWHD LGL
12251	26152	A	12365	237	2	YSSLLFKPAESAKGILRHHTPKSTSAI SKILFCFLFFVETELSPGLKCSGAIKV HCSLNLGSSNSPTSASQVPGS
12252	26153	A	12366	340	442	GLFVCFVWFLETESCSVTQAGVHWCDL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SSLQPS
12253	26154	A	12367	208	45	EGGEFFFFFVSFFFFRAGVLPCCPGWS ETPGSSDPPALASQSAGITGATVNST
12254	26155	A	12368	60	443	CSSCVSSKFPQSPHLKKQGD RMGAHLISG GCTEATAGKMRKCLVAWSTCAGARPPS RNRGSQGH SARFQGPRLPTVRLPPPP QAKPFCKWMLGGPISIEPKQHPGPG KKKWAGKAAPRLVPT
12255	26156	A	12370	341	421	SGWVRWLTPVTPALWEAEAGGSPEVGR
12256	26157	A	12371	280	393	NTIDHYVTQWLTVPVIRTLWEAEAGRSPE VRSSRSAPWT
12257	26158	A	12372	268	399	TLCSLSAESIHSYEFESCKDNYLMT NEAYKACMRRAFIPL
12258	26159	A	12373	209	468	EAVPDETSHPSPADSFSTSSNLACGTHH LRRLLKLYVEELEYYPRIQCFHFSFF FFESRSLLLLPRLECSGSISAHCNLCLL GS
12259	26160	A	12374	381	488	TITCLFQKQGRGRARWLTPVIPALWEAE AGGSQQQE
12260	26161	A	12375	276	395	GHVVTKKKLKLIFVFFEMESCSVAQAGV QWHDLSLQPPP
12261	26162	A	12376	295	472	VYSSVALNTFTLLCNHHQPSPEVLTFP NKKCRGAILAHCNHLGLGSSDSPTSASR VAG
12262	26163	A	12377	390	511	PGAVAHACNPSTLGGGGQITRIPSL
12263	26164	A	12378	417	511	AHRFFEMESCSVTQAGVQWRRLGSLQP SPP
12264	26165	A	12379	133	406	KLSLNKRDKYKQVCKETKKKKKKKKKK KKKKKKPGAKKKKSGSPR
12265	26166	A	12380	247	345	HMWSSQLNKGKLNKKKKKKKKKKKKKK KKKKKKKG
12266	26167	A	12381	156	15	NFFPFETESCSSVTQTRVQWFDLGLSLQP GKQEQNVYSKKNQKELIH
12267	26168	A	12382	275	1	KIVFLKGPPLFFFFKKKVFVFLKVGFKG GLNFIKTFFPPGKPISSKKRIFFFFF ETEPHSVARLECSGTISPHCNLHLPSSN DSLASTS
12268	26169	A	12383	43	379	LLGYDESRSLSWICLCLSCGLQLLSFLN LLVYVFCQTCVCFHYFFQYFSTLFLLT FWDNVNLNIRHFGIVPQVLDLVPFSPN KEIFLGQLQWLMPIPAFWEPAGRSPE
12269	26170	A	12384	303	1	KGPPFFFGLSPPFFFLKKVFFPPFFLRT PPPPFFPPFFKNFFPPPPKKKNPPFFFP PPPPFFPPFFETRSRSVAQARMQWGD HGSPQPPPGSSDPTRP
12270	26171	A	12385	141	1	KKEPLRAPPFFOLFCEFFYFETTPCSVTQ ARVQWCNLSLQPPPLRYK
12271	26172	A	12386	31	417	CRLADSPSPNDTGQDSRGRAGIKHIPPL KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKSGGGA
12272	26173	A	12387	291	412	LSSMILLFCFVYFLRWSFTFVAQAGVQW CDLGLLQPPPLPG
12273	26174	A	12388	310	1	MTPCFPLFFCPKKRKAGGGFIKKALFFN PQKEVFLGPPPKGPPFLGFPQTPPWGKK IPRLNPLFWRSSIFFFLLDGVSRLPR LECNGVISAHCNRLRLGSS
12274	26175	A	12389	117	2	KRNPQRGGPLFFFFFETESRSVVQAG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						AQWHDLGSLQ
12275	26176	A	12390	117	319	SFLKKPKDSTKNLLKLINEFSKSGPKI TIQKSVAFIYPNGEHSEKKIREVITFTI AAKTIKCPPOA
12276	26177	A	12391	95	2	SKSWTSLKLRITLGWARWLTVPVIALWEA KAG
12277	26178	A	12393	127	395	IPGSQGFCCLIKQSALHLLNKSSFSFLSF IETQSLSVTQAGVQWCYLSLQPPPPRF KLROKNRLNSGGRGCNKLRAHHTPGWV TERDS
12278	26179	A	12394	252	391	FFCFVLLCFEMESCSVAQAGLQWPG LGSLRQGFAMLARLVSSS
12279	26180	A	12395	275	3	TFRLVILKKSKEVEINCLTKSHSVAR AGVQWCSQDWEEKAGFNWRPSKARRCP TSVLKCHLGWAQWLMFVIALWEAKAGG SPEVRS
12280	26181	A	12396	111	3	GNNVIRGLRIRPLKGWACWFTVPVIAF WEAEAGG
12281	26182	A	12397	124	1	VSRGRTVHQEKPTERAASPRLECNGTIS AHHNLCPLPGSSNS
12282	26183	A	12398	259	387	YQSESFSCFLFIFLFFIFYDTERSV A QAGMQWHDLGSLKPP
12283	26184	A	12399	103	1	KGRFFFFFFYETESRSVAQAGVQWRDL SLQAPP
12284	26185	A	12400	308	416	CGNNFEKAGRVRLTPVIALWEAKAGG SLEVRSLR
12285	26186	A	12401	92	1	HTWGLTQWLMFVIALQEAQVGLFEPR SS
12286	26187	A	12402	265	388	GLSWLFRPQHLFYFIFPFTMSVSITQA GVGCCDLGSLQPP
12287	26188	A	12403	279	1	SLSSKMESGLTFSTIDIWGIITLSCC PGHCRMFSIRGLYPLDASSTSSC NN QNSPDMGTCSLWSQLLRRLRWEDCLNTG GRGCSEPGS
12288	26189	A	12404	387	152	NPPPGFNFGGPLKKNFFSPPRGEKFVFL KRPPPPPPPPPPFETESHVAQAGVHW RDLGSLQALKSFCDLVSAFKGF
12289	26190	A	12405	262	464	IIFHWLACILVIHSSFDGHLFLPLAVA DSAAVKHSCTICLNIEYIPNGIAGSC GISVLNFLRNC
12290	26191	A	12406	204	67	KCFGQAWWLMFVIALWEAAGRSQELR SSRPAAWAKELLNNRTRAS
12291	26192	A	12407	134	1	IQRPCIQLFSTFFLILFYIFTEIDSCS VAQAEVQWHDGSLQPP
12292	26193	A	12408	145	403	TYMYSLINYYKANSHVTKVKNHTARFL ESLLCAHPNPPIKLIIISLLREKKKKK KKKKKKKKKKKKQK
12293	26194	A	12409	65	415	RNKRISQSWNGPSRKQSSALLCGLGH LTSGVRRVSPVQGLVRIKGGSGPSKP KKKKKKKKKKKKKKSSKKKAQKGG ALKKK
12294	26195	A	12410	124	404	PWWEFLHHRNCQMWPGTVAHTCNPGLT G KKKKKKKKKKKKKKKSSSSSS
12295	26196	A	12411	164	2	TGAGLTIMDMVGVPDLLQLRFCFVLFC FLVFFETESDSVAQAGVQWCPNSSL
12296	26197	A	12412	114	3	PGMVAHACNPFSTLGGQGGWITRGQVYKT GLAKTVKP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: In USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12297	26198	A	12413	583	391	LADTGFHHVGQADLKPLTSCSTRLSLPK CWDYRCEPPHLAVPDTVLSTRGLISEKS FLPLCTFR
12298	26199	A	12414	280	2	KVSSMNAQTSVLFSTMLGISETLKYRGR KKRRERGREGGREGGERKDECRKVRSE IEGKKRGRKEYREGRRIEVSANEET PRDHPANK
12299	26200	A	12415	264	352	RFLVHGCDIYICINIYTHTHTHSHSTH T
12300	26201	A	12416	359	485	TDARMDWCYQEGTGSQAWLTPVIPAPW EAEAGGSFVRSR
12301	26202	A	12417	171	1	PLFRWWGFELFPFGYQKKGYPPFFFF ETEPCCVTQAGMQWYDLRSLQPPPEFK R
12302	26203	A	12418	265	1	WHKSNEELAAEASAPVKARASNTILGPH THGKERCPVSLRNVLDEGVKSTNFFSFF ETDSHSVTOAECGSAISAHCNLHLMGSR DSGA
12303	26204	A	12419	278	388	SSLTGFFIRRRNEEPGQHGETPCLLKIQ KLAGCGVL
12304	26205	A	12420	205	413	WNLFVYLYQTHKYARVYSYNIILFTNKK RAIGQAEWFTPIIPAVWEAKVSRLEVER SVRLSLPKWRITS
12305	26206	A	12421	103	2	RSLSKHRTEITLGLPAAVLIILFPPLLI PTSKY
12306	26207	A	12422	372	478	NIFVFLKETPCQSQWLMSVIPTLWEAEA GGSLEPR
12307	26208	A	12423	174	416	KMHYCVLSAFLILHLDVALILSTCSTL DMDQFMRKRIEAIHQILSKLKTSPPK NYSEPEEVPEVISIYNSTRDLQEQ
12308	26209	A	12424	572	733	RFSCLSLPGSWDYKNCLNSGRGYSEPR SHHCIPAWVTEQDSVSKQNKTKQSA
12309	26210	A	12425	123	2	GYIFIFIYFFETGSCSVAQAGVQWRNLG SLQLPPSSSDS
12310	26211	A	12426	224	417	TADFYGVNYISIKLLPKKKKKRGGPFKE SKFTAAGLQKNIFFLSAPNFIALAVLKR RDWETPG
12311	26212	A	12427	115	3	FFETGSHPVTTQTMQWDCNSLQPLTNR LKQSSHLSL
12312	26213	A	12428	250	398	PWAGHLTSLGLSLPIFNIGIAGQACWLM PVIPALWEAAGRSLEVRSSK
12313	26214	A	12429	215	3	KKGLVVGANKLWFTFPQKFFLNQFSGW ALTPRGKSWFSKRRAPAPFFFFFWETE SHSVABAGMQWHD
12314	26215	A	12430	345	2	FSHHPAKPQGGFLPYRQPLGLEKETRPR LNDRFMAGSFPPAQGLRMPFLGKEWER EGCSFVQCPVEGFAMWPYPLGSPPGPRL FFFFFFEAGSPSVTOAECGSGITANCSL EL
12315	26216	A	12431	348	3	LYSSLGDRVKLRLEKTKTNKWLHSHVYS TCKIINLDHYLIPCTKTNSEWIKYLNVR TNSIKLLEEDISVNLHLELGSDNSFLAMT PKAEIIEKIYKLHFIKIKIFHVSEDI EK
12316	26217	A	12432	160	52	NTAIGHPHQAIYLSYLSIYLSIYLSIY LSIYLSIY
12317	26218	A	12433	180	2	GRSKLHICREHSICAIEHVCGCDTENNT NLCQVQWLMPVILAIWEABAWRSPEVRS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LRA
12318	26219	A	12434	193	3	PGAENPPPKGGPPFFPPFRGFPFGVFF LKKKGFPFFFFFDTSRSVAQAGVQW HDLGSLQ
12319	26220	A	12435	321	422	NVEGDFLQRIKNIRYWP GAVAHTCGPST LGGRG
12320	26221	A	12436	116	2	HDRFCLFVYDRVSTLSRLECSAISAH CNLR L PGSSN
12321	26222	A	12437	302	400	THTHTHTHTHTHSGLLYLPKGKQSH EFCW
12322	26223	A	12438	329	399	LALQARLECNIGIISAHCSLCLPY
12323	26224	A	12439	310	2	KPILSRGLFCARPCFRSNNMRSFNPSQS YQVGKDTFGFTVKVTKLKVLPSPGPKG ARQGVHKGKCLLTLPKMLRFLFPFETES CSVTRLECSGAILAHCNL
12324	26225	A	12440	151	401	EGMHLPGSHSSNILKRGRESGREAGR KGRKERRKEGRRERRKSEEKRGKIR RKDRGENEEEEENRLSSKVSLEISTCP
12325	26226	A	12441	276	1	FHPFGRPSVSPRVQPKIGIIHTCVARI EKGGSCKALSLCPQYVGSNFFFFETRS FSVAQAGVQRCDLGSMQPPHFGSSDPP APASRVAG
12326	26227	A	12442	140	1	NSHFPKNLGSPPSFFFFFYLETESRVA QAGVQWLDLRSLOPPPPG
12327	26228	A	12443	310	3	LPPCSWGLYGAFARCPMLDDKQLSQVPL WACPLSTAGRTRLCVACIKAAQKAGQFF FFFETESHVSQTQAGVQWHDLSLQPPH AKPKHTHTHTQHTIPDT
12328	26229	A	12444	337	2	GFFAIVPKKGQKMFSPFPKEGIFSGPC FISSTPTLLGVKKILPNTSEIRPVLS IINTSVHIREQKTTYVGIFTGKSRFFF FETDSRSIAQVGVRRHLGSLQAPPPG
12329	26230	A	12445	112	9	GRVRWLTPAIPALWEAKAGRSPEVRNSR PAWPTR
12330	26231	A	12446	172	3	IPGELLIGRAKFAKNWPAPRGIPLGR QKFSFFFFFETESRSVAQAGMQWNLGS
12331	26232	A	12447	221	418	RKAERLEVFRRRLCQALRPFPFHCLAAA PMPLIVLKKPILGRAWLTPVIPALWEA EAGGWLESRS
12332	26233	A	12448	280	392	PLGRVRWLTTVIPAHWEALAGGSPEFRN LRPAWPDMA
12333	26234	A	12449	410	129	PSQEIFFPYGPFGKTPFFLKKKKKNRGG GGGLPFPFPQKVKKKKFFYPGRGRFKQP KFNLPPPRGEKKNPKPPPKKKKKKEK KRKEKLV
12334	26235	A	12450	159	1	KKKRGGLGLTFIKKTGDPFFFFFE SRVAQAGVQWYDLGSLQAPPPGLM
12335	26236	A	12451	270	1	NPLKFFFFSLFQNLKKDPAIFNPPFFF FPRIFWPPFGGVSKAGIWWFFPPFFFF FFFFFETESRSVAQAGVQWRDLGSLRT RGRTRG
12336	26237	A	12452	249	33	DKLVKLPLILKLNLSFFFFFETESRVA QTGVQWRNLGSLHPPPPGFKPNAYAW AHAWVVPGLPAQNLR
12337	26238	A	12453	190	86	TNDLGWTQWLTPVIPALWDAEAGRSLEL RSTRKA
12338	26239	A	12454	318	2	PPTFPLKTLFFPVFLPKLFSTLFSPPKK FSNPLVSAPPPFFLT LGNSQGVLLKGGP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Value, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFFFFFFFETESRCVSVQGVQWRDLEKK EKKKCNSNGGRHYISTHLKYK
12339	26240	A	12455	204	288	IQLNTHTHTHTHTHTHTHTHTNETGKMW I
12340	26241	A	12456	409	13	QGGAPPPIIMLSFLQEAGLLHVAQPVGK LLTSGDPSPPSKSASWRQRQETRLNLGG RGRSEQRPPPRPAPAWATQQDSVSXTNKQ TKNNKKIRKSLCKKTLEKMLAVMIITK YLLCTDVPSTVLCTHLYLT
12341	26242	A	12457	204	3	KKKSPPTQSASFPLGGGVFFFLVGMRS PFVAQAQGFKLPGSSDPPILASQSTAITG MNHHTSSAPH
12342	26243	A	12458	289	3	KAREKKKVGTAKNIRIVDSLKGRTSLCK KTEMPPVGNRRNQKPQNPSNLRISTRPE TESRSVTRLECSGAISAQVILPGSSDSP ASNWRQSETLS
12343	26244	A	12459	261	388	SWHFGRSKQVYCLSLGVNRNPQGNPVST KTTKISQAWWHAPW
12344	26245	A	12460	313	391	RVGRVHWLKFVIPALWEAVAGGSPEV
12345	26246	A	12461	112	7	HICIFYFETESRSVAQAGVQWHDLSLQ PPPAGFK
12346	26247	A	12462	389	3	ALHEGAARGPSPPGGKKKKRGSPPFPMGN QAPQVPGKLGGFGFWFFKSLPLQPGG KPGVFYKPKKVTPKDPPTLWGWWGT TGGPPLGLFFFFFFFETESRSVTQAGVQ WRHLGPLQPPPAHAS
12347	26248	A	12463	26	349	CIMIDSTGTGFIHCWNECEMAHPFWKAV WQFLFFFFKRGVYFFFPGGIKGPGFGLR EPLPPGIKGVPRPNPLGGDLRPPPPPP INLGFFKKGKVFMVWPVGWNFLI
12348	26249	A	12465	187	54	GYNKPKQAQWLTPVIPALWEAKAGGSP EVRSSRPAPWIWRTRG
12349	26250	A	12466	199	55	I IQLRQNSFLFCFDIESCSVAQAGVQ WHNLSLQLEVPGFKHAPSH
12350	26251	A	12467	107	3	FAHCLIGNSPFSFFFFFFFEVSGCSVAQA GVQWSD
12351	26252	A	12468	120	1	GNWCRAQWLTLVIPALWEAEVGRSPEVG SSTRGLPLTHRPF
12352	26253	A	12469	105	2	YYLYFFIFFLFLETGSCSVTQAGVQWKD LRSVTS
12353	26254	A	12470	238	405	FHICLFIKNQVSKMYTHTVSCSLLEII YCCLLQWLTPVIPALWETKVGGSLEVR
12354	26255	A	12471	425	1	LNPAPAIFFGPPKKKNFFSPPRGDKFFF FKRAPPPPPPPPPPPPPPKKKKFFPPA QKKGRGFPGRALSQWPLAGFLKITQFPP WSRVFSPDLLFFFDMESPSVAQAGVLW HDDLHLPGSSDPPTPASRVAGITGVCHH A
12355	26256	A	12472	122	2	QNKYSELRMNTFRGPWFPTVIPALWEA EAGGSPEVRSSR
12356	26257	A	12473	144	420	GAPRPISRPRGKTPGGGKGRGKPNKNGL GENPFPFKGVKGKNPPIFPFPLQGNGPT PLVLGSANMGFYLYLKRGKPGKGREALR AEPGPFFY
12357	26258	A	12474	80	1	KGGQVQWLTPVIPAFWEABAGGSPEV
12358	26259	A	12475	54	294	LKSWQHRRQRYVSLMSFIFFPCHTWYS QRSPTQTQIILEISDTGKNKYFNCTGSH RKHTHTHTHTHTHTHAHTHTL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
12359	26260	A	12476	364	234	EEMGFHVSQDDLNLNLSWSACLGLPKCWDYRSETSRSLASLPF
12360	26261	A	12477	288	450	PGTVAHACNPSTLGGPGWSETPGLKRIICLGLPKCWDFRRELLPSLPCLLI FL
12361	26262	A	12478	271	396	TISFLSFFFLFLFFFFFWKSGRESRFSQKKKKYKKNIYY
12362	26263	A	12479	289	2	GSCLLERKLTyrKD IHTKNPSVPHHQR PKVDKTPKTGKKQGRKTGNSKNQSASPP PKECSSSPATEQKWMENDFAKLREKGR RSNYSELQEEI
12363	26264	A	12480	323	1	YSMVYPYVFLTAKKDQLQVNNLTQLTKS YQLVHCINHSTLQTHNISTLMILGHIPG LCIPVNLSEAWAATPALHFVKLLLTTLT HHVCRALDIIILAIVSLVALITS
12364	26265	A	12481	279	429	MNGQRKCVYVYTYTYTYTYTYSTLKRK WPGTMAHACKPNTLGGHGGWTA
12365	26266	A	12482	308	423	LTFKNTITGFFFFFETEFCEFPVQAGAQ GGDLSL KAP
12366	26267	A	12483	272	474	MVSWGLSRAKIPWVLSFFFFFEKSHFF FQGGGRGGDLSWEQPLPPRSKGFSCFTL PSTRDYR PAGP
12367	26268	A	12484	84	229	LFKSVCHLLPLSSCSSHVRQACLPFTFC HDCKCSRASPAMLVPQPAEL
12368	26269	A	12485	392	3	TGKKKRFPFPFKKKIFNSKPQFSWRKKK LFKIFSPPGAPFPFPGVQKKKTFFFFP FSPRTFFFSIFFPGKPPKGGGLGPPFF PQKRGGFNSKWETWEKFPPLFFFFF ETESHSVAQAGVQWHD L
12369	26270	A	12486	76	1	KLISWTWWHMPVVPATWRAEAGDFS
12370	26271	A	12487	204	8	FFIFFFFFFFFFPCFKTGSHSVAAQAEQ EWHDHGSLQPPQSFHLSLPCATMPGL FFLFLFLFT
12371	26272	A	12488	96	3	KKPLGQAMFFFFFETESCSVAQAGVQWC DL
12372	26273	A	12489	126	1	KPPHPFLFFFFFETESHSVAQAGVQWC YLGS LQAPPGFTP
12373	26274	A	12490	107	2	IAGRAWMLLAIP TLWEAEAGGSLEPRS SQPTCAT
12374	26275	A	12491	302	2	GGFGFFPREKGGFFQT VLFVPPGFFS PPVFKTGPVFFLGAQKKKIFPPPPGK IWFLLRGAPLFFFFFFFFFFFEMTSCSV AQAGLQWCDLGS LQHP
12375	26276	A	12492	248	398	PTQVTLGITAQSYSRVHINNRYDLAV GSGHPDGA AAIKGSFVQRLKSY
12376	26277	A	12493	341	1	RTSHFREIYPLEHASSLSKKIETGALPC SQELLNSQENSVMNKFCLNQLPFQDVN SCIIRFQTKDTLKHTAIQPEAKTSLPC YTHTHTHTHTHNNHSIFELLCMQCDSY N
12377	26278	A	12494	95	3	PLFFETKSCSVAAQAGVQWQLGSLQPP PP
12378	26279	A	12495	62	420	CAAKLCTEAHTAASADTHTSPHGSVSGL FCFHFPHRRQRSRPGKPAHRLAGR ALSQKPVGSGATPHNLHHQIRTQTNGLI QLLGDRQAPWVTPVLPVLWEAEAGGSLE ARSLRPA
12379	26280	A	12496	58	492	NSPPFPAPSQRTSPAAAAAPTGGSSSA PCPASSWPRSSIALITFYDQPCGLSF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NNLAWKQNVLCFKERLLKMFRRIOVLG LLVWTLIAGTEYFRVPAFGWVMFVAVFY WVLTVFLLIIYITMTYTRIPQVPWTTVC LCFKR
12380	26281	A	12497	2	198	RLQGILSAGFLVPGDTSVSSPRRAAGS QSSTSRVLWKLSCGMLRLVLMGVSAF TLQPAHTG
12381	26282	A	12498	71	346	GMFMTSKETFTHYQPGNSDPAHTATAP GGLSAKAPAMTPLMLDTSRKLVAWDGT TDGAAGVILAVAADQTSTLTIFYKSGTF RYEDVLWP
12382	26283	A	12499	122	59	HQIYIYIHTHTHTHIYIYIYI
12383	26284	A	12500	220	3	PKKESVRCVAMKWLILLCQTSLHWSL PQSSLAATPCCNLGTVDVLQGLGAVAH AWNPSLGGRDGWITS
12384	26285	A	12501	125	1	HVLVLSHFLFVLFLFFETESRSVTRPKR SSAVSAHRNIRLS
12385	26286	A	12502	373	476	ILTRDGVSLPRLECSGTISAHNLCLL GSGDYP
12386	26287	A	12503	440	573	STWEDHLSLGNRGCSPEPRHLCTPTWVT E
12387	26288	A	12504	146	5	HPHLQTMNGAPIPQELTLPLEKERDGLR CRGNRSPVPGIPPRWSRDL
12388	26289	A	12505	140	44	AQGLTPVIPALWEDEVGRSPEVRSRSD WPTR
12389	26290	A	12506	247	420	LEISVTFSCSFGCLPKKHHTHTHTHTH THTHTHTHTHTYIRTIYTLARPLSALH NF
12390	26291	A	12507	346	473	KAYTIGLNCFYETKSHSVAQAGVQWRDL NSLYS
12391	26292	A	12508	87	414	RTGVYRVGKDGSRSPDLLICPPLGLPK CWDYRREPPRPACLPPLSHSPPPHFSF LSPFLSFLPCSPFLYIFPPPLPLPISL RWRLIPEGRFMAPLCLQMLPGHDT
12392	26293	A	12509	386	467	LLLFEMESHISITRLECSGAILAHCNL
12393	26294	A	12510	344	472	KFLFPDPAVSLGLIYPKESKSFYQKDT TRMFIAILFTIANTW
12394	26295	A	12511	424	132	RGEPPRSGLSPVGPGETPPFLKKQK ITRGGGGGFLPPLKRVRGNSFPFGGK SFHGAKFPFCPPPWATKRNSVSKKKKQ TKKGSRIILYNNE
12395	26296	A	12512	351	510	GGTDFCKQSKLQSLQPAVEIFIPGRVQW LTPVISALWEARAGGSPEVRRSRPA
12396	26297	A	12513	362	463	NTITWLGAVAHACNPHTLGGPGGRITWG QEFETS
12397	26298	A	12514	137	1	EEISLLLPRLECNGAITAHNHLPLCSR NRRPGKAVHVRQAYSFQ
12398	26299	A	12515	251	592	GAFTGLAFTMAGGRPHLKRSFSIIPCFV FVESVLLGIVILLAYRLEFTDTPFVHTQ GFFCYDSTYAKPYPGPEASRVPPALVY ALVTAGPTLTILLGELARAFFPAPPLAG PV
12399	26300	A	12516	3	413	SWGGRKFLCPPRSLSGSRELHPAQGDRP GPLSSSGKRETGTHRETIGKKKVSSAPE AQGAGLRLSQALGGLCYDLSPLTEPRLP LAATAFPPPCPALPHPPQPRVTMGSSVSL ISGHSFHSKHCRAQONKLRKSSHLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12400	26301	A	12517	115	2	KSHGGHGVVLSVSVLVLGLAMEVGLVLWV KEYDGAALA
12401	26302	A	12519	444	34	YCLRQKHTEYRRRSNLEMASSCLSGRKT CTFFTLYQNLKMIKLEEGTWQAEWLKS RPLAPNSKVVEAKEKFLKKIKSVTSLNT YILRKPNLSLIADMENILVIHIEYQTSYN IPSSQRLIQSKALCLFNYLEMECRI
12402	26303	A	12520	1088	935	ILIIIFINRCEFLRSKSSSEITQYIQS YKGFVDRTVMYNSNFFLKFLDYL
12403	26304	A	12521	2	347	AMAAGSRTSLLAFALLCLPWLOAGAV QTVPLSRLFDHAMLQAHRAHQLAIDTYQ EFBEITYIPKQDKYSFLHDSQTSFCPSDS IPTPSNMBETQQKSNLELLRISLLIES WLE
12404	26305	A	12522	50	205	VVGESDRQSSGFNASSAHACNPTWVET GGSLEARSWRLQCTMFASVKSTRP
12405	26306	A	12523	105	2	RFVCSSTIKVLRDLSSDRSNPGRFLSTSN SSLYER
12406	26307	A	12524	279	455	KTKNWLALGGPPCFPGQYGETPSLLKNE KLAGHGGAPLYSRLRLRRGNSLTPGD RGC
12407	26308	A	12526	305	454	LYFLLEFPQIINRMVLFVFCFFETES HSVPQAGVQWRDLGSLQAPPPG
12408	26309	A	12527	363	459	CTILGQAWLTPVILALWEAEAGRSPEV RGSR
12409	26310	A	12528	182	36	QHIVVFHKEHGQVRWLTPTVISALWKA GRSPEVRSSNAAWHACRNSA
12410	26311	A	12529	388	530	KSFLNFFPRDGLNCVPPQAGLELGSSDP PASAFRVAGTTSVWHHSQI
12411	26312	A	12530	134	1	GHHKGVLPFFFKTESRSVAQAGVQWCTL GSLQPLPAHATRPV
12412	26313	A	12531	230	1	KKFGFFPQAGPQGGHLFTTLAPWGQAI SQREKPPFFFFETEPHSVARLECSGT ISPHCNLHLPSSNDSQASTS
12413	26314	A	12532	145	3	KKLEILSAIIPPKFRKEIFLFFFYETES CSVAQAGVQWRDLGSLQAP
12414	26315	A	12533	365	2	LFFFTSLIWQITLGLFLILNCPCIPGVC YIQFANTFRKFAFLFTNEIAYNILILPL TKQDYTNLIKLIKHSFFSNFLKQLLFV FCFVFSLFAMESCSVAQARVQWRNLGT LQPPPPRFK
12415	26316	A	12534	313	475	FFWSCSSPQQGFGGGITIIIIILRWILA LSPLERKWRDLGSLQPSPSGFKRFF
12416	26317	A	12535	124	3	MGSLIMGAELSVYRQVCDCKPQGVCVCL CVCVCVCASTCM
12417	26318	A	12536	333	58	ACNPSKVRSCRPAWSNMVKSCLSKNAKI TKEWVANFFVFLVEMMFHHVQGLS LKLLTSSDLAASASQSYGITGVNHYAQP ARTGSR
12418	26319	A	12537	214	3	SDPRACRCPEAKEQQRRLPGGSVPAL SIFFFKTESCSVPLSPRLECSGVISAH CKLRLPGSCVPPAS
12419	26320	A	12538	146	1	MNFLAFTNPPRPQQLKPLLFILRRES HSVAQAGVQWCDLSSLLPPA
12420	26321	A	12539	195	1	IFIPPAQAKRGDPFLSFFFFETRSPSPR LECSDAITACSLHLEPGPEPTTPIPK SWDHSVPP
12421	26322	A	12540	151	334	LLGRLRHKNHLPNGGGGSGTIMALCNI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LLPRSSSSPTSASKVAGITGACHACCLRYFLY
12422	26323	A	12541	314	402	NLNSGPAWLMFVIPALWEAEAGGSPEVG
12423	26324	A	12542	339	3	GSCLEGLKLPNRKDIHTENPSVHHHQRPKVDKPTKMGKKQNRKTGNSKTQSVSPPKERSSSPATEQSWMENDFDELREGFRRSNYCELRREDIQTKGKEVEIFKKNFERV
12424	26325	A	12543	31	365	RSVMPTEDRATWKFNFLKIIQLDDYPKCFIVGANDVGSQMQQIRMSLRGKAVALKGNNTMMRKAIRGRLENNPALEKLLPHIRGNEGSVFTNEDLTEIRDMLLGKNV
12425	26326	A	12544	278	410	FSFKNVTAGRVWLMFVIPALWEAEVGGSPVVKRSRTTLANMVK
12426	26327	A	12545	88	276	EVPOAHRKLPAPQLRPLQAISTKGPCPPQSPQPSRPEGSSAHSRGKRTREGRKEKRKKK
12427	26328	A	12546	251	3	PVEDNSKRRFQTGEEKVTQEEQALTPWRTNFFCFSDRVSAQARVQCDSGSLQPLPGSSDLPTSASQVAGTTGMRHHAC
12428	26329	A	12547	106	2	DEHLPLTSTFETESCSVAQAGVQWRDLGSLQAPP
12429	26330	A	12548	225	1	GFFKKKEPHPRCKKRTPPKLPKPFWGGLNKKIPLSEVFSKKGPLPKKFFPPFFFFETGSCSCHPAGVQWCDHGSLO
12430	26331	A	12549	218	3	VPPFGLVPGLPQIIPKGFPTKGPCKGPPGDKQKSGPPNKKNFFFLRRESHSVAQAGVPWC DLGSLQ
12431	26332	A	12550	276	24	GPLKMEAPPQNPLSPKNKIFFFFFFETESHVAQAGVQWRNLRPGSSDFPASDSRGAGITGARPHVQLIFVFLVKTGRKR
12432	26333	A	12551	331	440	KSASSWSFNSKGGWWLTPVIPALWEAEVGSLEVR
12433	26334	A	12552	136	1	RHTGSKTTATALVDVFLLLFFETESHLSRLKSGTTPGHCLNLYE
12434	26335	A	12553	84	1	IFFCLFSFEMESHVAQTGVQWCDHGS
12435	26336	A	12554	3	349	HASGPEELSKDPSLVSQGPQHRKPGPKRCSSRPLGPPDKLGEGKQGLGFTLWLSGP I KPCDDEEKNKKKKKKKKKKKKLGGGPFKKLLFFPPGGGRNFFFLGAPKFFWAGR
12436	26337	A	12555	257	417	KQLHLLQGRFLSPSFLPSISKLFFFEMESRSVTQAGVQCDLASLQAPPPGFT
12437	26338	A	12556	268	403	YMRLSPQDLVMFKDVAVDPSQEBWECLNSYQRNLYRDVILENYSN
12438	26339	A	12557	286	426	DMLIKTCCHLVCEKKKKKKKKKKKKKKKKKKKKRGGALKKKPLPPP
12439	26340	A	12558	114	1	PLKBIANRHMKKCSSSLAIRQMQIKITMRYIFTPTVMA
12440	26341	A	12559	106	1	FFFFFFFFFFFFFEMESRSVAQAGVQWCDL
12441	26342	A	12560	118	2	KNYSNNLKTNAGRAQWLTPAIPALWEAAGKSPSEVRNW
12442	26343	A	12561	196	2	MCCFSKNWQEGAQMTPGFEPQDNSEKTKLSDTRLLFFFFERESRSVAQAGVQWRGLGSLQAPP
12443	26344	A	12562	128	3	RAPFFFFFETEFSLPRLECNGAISAH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NLRIPGSSDSPAS
12444	26345	A	12563	277	370	WSFTLVPOGAQWCDLGS LQPALSRFKRFSR
12445	26346	A	12564	55	251	AMVIPTVPPNITINSKPLGHISFQLFADKPKKTGENFHTLNNKDKGPGSCFHRIIP EFICQGDDE
12446	26347	A	12565	129	3	KYSVLRPGTVAHTCNPNLTGGRGGQITWGWEFETSLANVAK
12447	26348	A	12566	172	1	PPPKKKKPRPPKKKNFFFFFGAISAHCNLCVPGSSDSPASPSRVAEITGSRCHABPY
12448	26349	A	12567	257	380	GICRPLLGGVLQSGATGVRDPLEEAVCP LAELKHCAGRSTA
12449	26350	A	12568	120	1	GVFLFCFVLFETESCSVARLECSGMISAHCNLRLLGSSNS
12450	26351	A	12569	250	2	IGKPKTPQFWFLKTKRGGFNAAFSFKKFFQQLKPPPRVFLKIFSCQKKIFFFFFFETESRSVPQARVQWHD LGS LQAPPFGF
12451	26352	A	12570	338	3	VSTPEKNFVHTRGFSKSSSKYKVCNFF FQKILGSPFPFLSKKVFPGKPPYSCCSGRVSTAPYFLNPGPSTKILPFPFGPLGPPEKFLSFFFFFEMEBCRSVQIAGVQWCDLG
12452	26353	A	12571	5	556	ICCCCLCFKINIFQLHFNKINFFCVTRSGPVTQAGVQWCN LGS QQPQLSSKQS
12453	26354	A	12572	115	2	DRVSLVLVAHCNLC LRGSSDSPASASRVAGITGARHD
12454	26355	A	12573	279	377	GQVQWLMPPVPAFWEDAEGLLQPSSSRPAWAT
12455	26356	A	12574	117	1	KTPLEFFFFFEMESRSVAQAGVQWYDLGSLQAPPNGFT
12456	26357	A	12575	253	374	SLPGMVVHACNPSPLGGRGRRITWGRKF GTSLANMAKPCCL
12457	26358	A	12576	130	2	KFPGPFLGFFFFFEMESRSFAQAEVQWRDLGPPQAPPPRFT
12458	26359	A	12577	132	3	RVPGPPLLFFFFFEMESRSFAQAEVQWRDLGPPQAPPPRFT
12459	26360	A	12578	3	370	LRKNCLNLGGRECSELRS HHCTPAWVTERDSVSKKKTLSVLMKWP NPLRPLALS RKKFPRGPPEQVTHLVKEVVS LTKPCCA EGADLD CYDERTSPLFAKSWERNFPFPVHPGPVEGC PK
12460	26361	A	12579	131	2	FIYFLFYFLFLETESLSVAQAGVQWHDV GSLQTPPPRFTPTRA
12461	26362	A	12580	202	2	RMRKNQHKRAENSKNQNTSFPPKDHNSSQTR EQNWME NFD ELTEVGFRRWVITNS SNLKEHV FSC
12462	26363	A	12581	109	2	KIFFFFFFFETESRSVPQARVQWHD LGS LQAPPFGF
12463	26364	A	12582	105	375	LIMILLPLQLVHSGTFCFLPFGFETEFHSTPRLECN GVM SAHCNLC L PVTSPAS TSQIS
12464	26365	A	12583	106	3	RPIFFFFFQTESRTVARAGEQWCDLGS IQPPPP
12465	26366	A	12584	484	700	SSSWNRAFSRKKDKTWMHTPEALSKHPI PYNAKFLGSTEVQPKGTEVVRDAVRK LKFARPIKKSEGQKKKK
12466	26367	A	12585	301	1	TOPKVRTOMKNNIFEHAFLSSTFPNPLP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						NLPADFYSATSQTKPDILQSMQKAFKNS GIGQAWWLIPAI PAALWKA EVGGLLEPR NLRPAWVYGKTL SLQK
12467	26368	A	12586	76	379	PLHPPASCAPAPSLSC LIPGSPSDPLFSD SARPGWGRGWGRAPQLPPSPFLYNLIK KWSRFCHQKKKKKKKKKKKKKKKKKK KGFFFWRAPPPFFFGGGFFS
12468	26369	A	12587	109	376	LEFFKMSGVVPTAPEQPAGE MENQTKPP DPRPDAPPEYN SHFLPGPPGTAVPPPTG YPGGLPMGYYSQQPSTFPLYQPVGGIH PVRYQ
12469	26370	A	12588	323	1	KKFCPPRFFPPLFGFQKKGTNPISPFSG GFKNLGGFNPPRPWPSPQIGFPLGRS KELILGLFPTRIGIGGFFSFFFCETKS HPVMRLCSGVISAHCNLRLLVS
12470	26371	A	12589	262	1	GDPPTTSGPQTNQPK EHL MNFKSDSOLY EDTLAGRSVLIKNLTPQTLQPRWTGPYL VIYSTPTAVRLQDPPHWHRSRIKLCPS EKK
12471	26372	A	12590	284	374	TESRNWGAQWLTPVILPALWEAEAGGS PE
12472	26373	A	12591	297	387	GQAWWLTSVIPAFWEAKEGGSPDVRSSG LA
12473	26374	A	12592	206	407	VKPQNPRKAQKLGLVYIHIYVYIYVYV YIYIYIYMYICRYISLTVVYTVNSKEKG LDTAAHTCNSR
12474	26375	A	12593	222	379	LTTGSGIMGNFSFLILVYTRKVMG SVQWL TAVIPLLWEAEAGGSLGSRSSRPA
12475	26376	A	12595	301	189	KKIQSQAQWLPPITPALLEAEAGRSLEL KNSRSAWAS
12476	26377	A	12596	209	3	SVKPLFFINYQSQVVLFLFFRGR LKRSG TISAHCNHLPGSRFSC LGLPKCWDYRC APPTLKIDLT KD
12477	26378	A	12597	306	3	NGKKG FYMAPEPPFFHFFFSPLFPTL FFFFIFPLPFCFALSFLVGSSSLSPRL CPMQHYFCDAWNTFDALIVVGSIVDIAI TEVNVSTWRLSLTVRV
12478	26379	A	12598	1	249	NTGAQCPLFESIQLQLLFLGGGEDGVS LLLLRLECN GAISAHCNLRFP GSGDPPA SASRVAGITGACRDHTCEPPRPVPPSS
12479	26380	A	12599	228	404	RLSSLSPVTEFGCLSPD LILKCDPWPG TVTHTCNPSTLGGRGGWITRGQEFKTSF VNM
12480	26381	A	12600	101	580	LSLTKNCALLGEETMMEQEMTRLHRRVS EVEAVLSQKEVELKASETQRS PLEQDLA TYITECSSLKRSL EQARMEVSQEDDKAL QLLDIREQSRKIQEIKEQEQQAQVEEM RLMMNQLEEDLVARRRSDLYESELRES RLAAEEFKRKATECQHKLK
12481	26382	A	12601	464	3	CAIQQTLYEHPMKSSRLGPTQLKIFTCE YCNKVFKFKHSLQAHLRIHTNEKPYKCP QCSYASAIKANLVHLRKHTGKFKADY CSFTCLSKGHLKVHIERVHKKI KQHCRF CKKYSVDVKNLIKHIRDAHPQDMYCGR SRGSARMSRALPS
12482	26383	A	12602	140	1	WIGSFLSSEEDGTVVQKISGVQRSLSLY VYIHTHTHTHTHTHTV
12483	26384	A	12603	112	2	ESLRPGAVANTHNPSTLGGRDGWINKDK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
						EFKMCERV
12484	26385	A	12604	139	1	KKRVKRGPPGGFKGLGGKFFFSPTKTFFF FFFETESCSVAQAGVQWR
12485	26386	A	12605	204	460	SGQNGEICHPRGCTLPKATISSLLIAR VCLKHFNKGVASLSQTANGCFEGFSET ESRSVIQAGGGGDPGSLQPPPGSCLS L
12486	26387	A	12606	317	1	KRPLFKNIFQKPPFKNGAPRKKGPRCIF GPNQKNPLFFPAPLSPPFWETKKGAGFF FWGFPFPPTKIIGGQKVPFPPTFPFPFF FFETESLSVTSLECSGAISAH
12487	26388	A	12607	248	367	TQILSSGSVQSSSLHFFPICFIHTHTHTH THKHKHPHS
12488	26389	A	12608	2	387	QKQQQRAGRETSTCSLRIISAPTMATFV ELSTRAKMPIVGLGTWKSPLGKVKBAVK VAIDAGYRHIDCAYVYQNEHEVGBAIQE KIQEKAVKREDLFIIVSKVQWCINLAFNT IVPKSQWQSLQTPQRC
12489	26390	A	12609	258	23	MWERGIIRPQTQTLTGEPEGLDHGRSIS PNSVMNGIVPHISILTLNGLNAPLKR EGIAEWIRIYQTSMCCLQETGR
12490	26391	A	12610	176	433	DALSSAWGTVLGTQIPSHFTEILMLSP AWGSSSLTQTLFYVPSGAKRTGSYVLAR VGQKYKTLWLGAHAACNPSSLGGRGRW IT
12491	26392	A	12611	312	410	AHMYRTCSRGWVSWLTPGIPALWEAAG GSLEP
12492	26393	A	12612	3	289	VFEFLSRKLSYILRMFWTFKFWLWLERF WLPPTIKWSDLEDHDLVFKPSHLYVT IPYAFLLLIIRRVFEKFPVASPLAKSFGI KETVRKVTPNT
12493	26394	A	12613	294	432	FMKLPFFFFFFERRSCFVAQSGMQGGYN ASLQPLPFGSSNFSGLPL
12494	26395	A	12614	138	375	SPNATCGHADPLPLCCLHICQALKRFT QTFFFEKGKPYLGILLYAVFFFLRLSCS VAQAGVQQPNLSSLETTPPSA
12495	26396	A	12615	232	1	GVPQRAKLRLAGLCPQAMDTFSTKSLAL QAQKLLSKMASKAVVAVLVDDTSSEVL DELYRATREFTSRKEAQKML
12496	26397	A	12616	236	419	LEMENGVWVFPFVNPTLWETEGVRDQ GQHEETLSLKIIFKISRHHGMRLGSQLL RRLRQ
12497	26398	A	12617	197	1	LCHESEGFLSRVSALLFTLLLLVLMESP PSVSQPGVQWPHFSSLQPLLPFRKQFCN TLPSGWDYK
12498	26399	A	12618	132	3	NSFMFHLFTYFEMESCSVAQAGVQWRDP GPLQAPPERVGGRV
12499	26400	A	12619	255	2	MNSLNSFTDIAVPLHYNRILPHFKIIL SYFLKSKFKQVKIGRVRKWLTPVIPTLWE AEVGRSLEPRNCPAHQPGQYKGILLYKK
12500	26401	A	12620	141	2	FHFTYIIISCVCVCVTESRFVARLECSG AISAHCKNHRPGSSNSPA
12501	26402	A	12621	274	421	TYVMEVCCTYYFLAQVLSLAPFNYFIIR PDPRTPRDPDRPDPRPEPRP
12502	26403	A	12622	132	2	NQSTKKKIELQGFQSGGRGKGQVQWLT HIIIPARWEAKVGRSP
12503	26404	A	12623	390	86	IFPFFYQNTNGMAPGNQIPQGFSSRFPF FLRQVLALWPSLEYTGETDQCRLKCSS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SLSLCSSWDNRCAHPPLVNILFYVETGS HYVVHIGLKLHLSRYPG
12504	26405	A	12624	297	396	ITRVRGraqwLTPVIPALWEAKAGGSPG VRKSR
12505	26406	A	12625	303	381	KFHLVPSINTMSGSQELQWMVQPHFL
12506	26407	A	12626	318	152	GDKRRLVSKKKKNLWNFGRIQWVPPVIP ILLEGEGAGGSPEVRSFRPTGQQSMTTF
12507	26408	A	12627	48	388	QLGNGKVRLLYQRHSSSFFFWGEGFPP GPQGGGGPNLGPRESPPPGVKGTPPPS LLEGGEPPGPPPPPGNFWGFWKKGGLPL YPGGPPTSGPKGEAPPTPPKGGGGIKGL P
12508	26409	A	12628	116	3	KVATNQAWLMPVIPALWEAKAGGSSEV RSSRTADAW
12509	26410	A	12629	227	400	VLFLVFFCKEWHVFIFLILFVYSYKRRK KKKKKKKKKKKKKKKKKDSQKKD
12510	26411	A	12630	182	3	TNWLFPFPKFGPVLFFLPPFFFFFFET GSHTVAQAGVCSGAILAHCNLRPLPGSSN TPA
12511	26412	A	12631	134	473	ASTIMDLLFGRRTPKELLRONQRALNR AMRELDRERLKLETOEKKIADIKKMAK QGQMDAVRIMAKDLVTRTRYVRKFVLMR ANIQAVSLKIQTLSNNMSMAQAMKGVTK A
12512	26413	A	12632	100	462	QLLLCCCCRQWTA FNVPASPAPPPAWA HMAPSLLEPPSLVTOICKLSAFSGPSI NAFLLSKKKKKKKKKKKKDRGGAPLKK KK
12513	26414	A	12633	313	441	CWELLKWLVCFLCHITKTNNCWAQWLTP VIPTLWEAEVGGSL
12514	26415	A	12634	129	400	VSQQCWPTPPALYSISRQALAA SPQGRP WDLQPTMPESPLLPAPAPWPKPLRRAL PPAPRCLGPSTAQQLRSAGAWCGTGRHL HLRPQC
12515	26416	A	12635	308	399	EIRGWTQWHVPVIPALWEABAGGLPEVG SS
12516	26417	A	12636	285	390	IFGVLINSTFYFETESRSVV RAGVQWRD LGSLQPP
12517	26418	A	12637	260	2	GQGFFFFGGRGSPKKKPKPLKGFVLVGG KTQFFFPKPKGPFVGFVFFFSQTASRS VTRLECSGMILAHCNLRPLGSSDSPASA SR
12518	26419	A	12638	76	3	ALQVQWLMFPVIPALWEAKAGGSLE
12519	26420	A	12639	219	484	LGLQEPDLDEKPILELPLAQLAQLOTE ELSLESILCSYLKQALKVHQEVNCLMIF LGECEEEELLALKLKKSERGLLYGVPM LKDT
12520	26421	A	12640	33	462	EGLSWG YREHNGPIHWKEFFPIADSDQ SPIBIKTKEVKYDSSLRPLSIKYDPSSA KIISNGHSFNVD FDDTENKSVLRGGPL TGSYRLRQVHLHWSADDDHGSQHIVNGV SYAAELHVHWNDSKYPSFVEAAHEPDG LAG
12521	26422	A	12641	2	414	SGPAAPATPMSIFFELYFNVDNGYLEGL VRGLKAGVLIQADYLNLEQGETLEDLKL HLQSTDYGNFLANEASPLTVSVIDRLK EKMAVEFRHMRNHAYQPLASFLDPTYS YMDNVILLITGTLHORSLAELVPK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12522	26423	A	12642	161	463	KEKARGRPKPLLLPITSATTAMGLTIS SLFSRLFGKKQMRILMAGLDAAGKTTIL YKLLGLGEIVTTIPTIVFNVTVEYNNIC FTVWDDGGQERIRPLWN
12523	26424	A	12643	124	2	TVFGGQAQWLMP IIPALWBAEAGRSPEV TSLRPAPWPRTRG
12524	26425	A	12644	258	454	NRPELCDVQGLREDSKRKGEINQACQF LWPRQKMSSQTKFKDKKEIIAEYEAQIK EIRTQLVEQ
12525	26426	A	12645	636	182	APLERPSMIPPRCSGGQPSDLRSPPAQG TPRPALGDRKGTPIRAEPGGAGRAEAPP PRGSRQRFQPRQNTAHTKRVTRLISA APARHSPAFIACRQVGRPRLSARRSGKK PHLTVWCPSFQDPIDQDTTLQIILLSLL GGDTFSDFFCS
12526	26427	A	12646	199	414	IYHTSRSLDRKLAQRYDELPHYGGMD GVGPASMYGDPHAPGP IIPVHHLNHGP PFHAKQNYGAHAPHN
12527	26428	A	12647	130	3	DRGPLCVHTPLKCKKNTHTHTHTHTH TNTHTHSHTHHTK
12528	26429	A	12648	192	443	LLLCWAQESLGTLGENTASSHTAGLEWE SPLFACWFFWGFCLFVWLFWVFEPKSGS VLTECSSVITAHCSLDLPGSRDPPASA
12529	26430	A	12649	393	179	LHSRVQRSGCFSCSVSNPVTGGMHFTRS SPQSNQEAQGQARWLTPVILALWEAKAG GLPELKSSRPAAWATP
12530	26431	A	12650	263	2	KAPLLVYKWEPNPGGGNFSPGMGTPNTF GVRFGETKPLFFFFFTGSHSVIQAGV QLCNLDSLQPPPPSVKPSQYSWDHRKQS NTK
12531	26432	A	12651	355	111	QDPCFIRLHLPLSFLSVFLECTKISLLD WRMLFPLLGDPPHALSSLVSPINTWNY SFQQLMMFRDVAVDVFSQBEWECLDL
12532	26433	A	12652	271	3	RQLKNILIFFSHKNMLSIKHITYNYTLF LKSAFIFNLETDHLNCFPGSISAKSVFI LFYFFETEPHSVAQAGVQWRDLSTLQPP PPRET
12533	26434	A	12653	333	2	PPSPGVFGNPPSPGDPLGKTTFFPRGPP PRFWGGGFFILAPFPFGGLFPPFPPLPP SQGPPFFPFFFFFFFFFEMESRSVSQAGV QWRDLSSLQPPRARFSDSPLYFLEGR
12534	26435	A	12654	310	444	TYLSNIFYFILFLVETESPSVAQDGVRW CGLGSLGPPPPGFGFRFS
12535	26436	A	12655	336	411	DQPGQHGETPSLLKIQKLVECCGAH
12536	26437	A	12656	114	2	GIFPFFFGLESRSVAQAGVQLCDLNSLQ SPPPGFKQF
12537	26438	A	12657	191	1	KNFILTFSFRGAKNGDVFPFPPGYIQTG ENFFFFFLKWSFTLVAQAGVQWCNLSS LQPPPPR
12538	26439	A	12658	1	445	LRTGSEFSGRDSKGLAAAEPTANFGLLI ASIEDQAGGGGYCGSRDQVRRCLRANL LVLLTEAAGVAGVALGLGVSEAGGALAL GPERLSAFFFPGELLLRLRLMIILPLVG CSLIGGANSLDPGALGRLGAWALLFFLG TTLLASAL
12539	26440	A	12659	2	224	ESTASRIAFEAWQPETLPKGLNYSGASP VVLNAVLPLKKKKKKKKKKKKKKKKKK KKKGGGVFKKKKIKGGGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12540	26441	A	12660	96	1	GLKDRGRGQVQWLTTPVISAPWEAKVGGSP EVMS
12541	26442	A	12661	1	457	CWVHLQKGCHFTLGRHLSGQAEALLTSQ TGRPGRGAPHIPDGAARQRSSHPRRGG QAEALLTSQTGQPRGAPHLPGAAGQR RSSPFRRAAGQRGSSPFRWAAGQRLS SLPRQGGRAEALLTFQTGRPGRGAPHIP DEAAGQRRGGAG
12542	26443	A	12662	175	351	KGIFFFPPSWKAGGAIWFKGTFAPRGKG NPPPNPSGEGGPKKKKPGPQIPRGPPLG PPV
12543	26444	A	12663	247	401	SSNQEPGCKGPCVLTNFFYLGRWWLM PVIPIAWEAGTGGSPVRSWRPT
12544	26445	A	12664	152	251	RENSCCFTKKKKKKKKKKKKKKKKKK KRGAP
12545	26446	A	12665	2	365	APTFRSRLRHASCTACRTVSTDTSSLRR ADPKGRSALLADIQQGTLRKYVQINDR SAPQIESKGTNKEGGGSANTRGASTPP TLGDLFAGGFVPLRPASQRDVAGKEEPI LAPLWTVSP
12546	26447	A	12666	179	1	LELSKSGSHWMRHFLSRSFYSLISPOLN TTVWPTIITPILLTLFLITQLKILNTNY HLP
12547	26448	A	12667	279	35	NQAPFKARFFTTFKNVFLKEIKKRCWS GAPPIIPPPWGGGGGPPWGGNLSPPGP PVSTPFFNGAQKKKKKKDRYGGACL
12548	26449	A	12668	299	399	ISIKKQRKGPPVQWLMFPVLPALWEAKAVG SPEVR
12549	26450	A	12669	1	385	KMQNRGFFFLTFLALLGLTSGAAKKKNK GKKAGPGSKSPNWPWGPPCPSSKDCGGV FRKGTWGAQTHGIRGRGPCNWKKEFEAN CKSKFKNWAGDGGPGTKVRQGTLLKKAP SIARGQETIRVTKPCT
12550	26451	A	12670	357	1	AGKIATCPVSSMQAPTGGFPVGGNDNQ GQAPDGGFQPPLOQNTSSPDSNENSP ATPENEQQGDAPPQLEDEEPAFPHTDL AKLDDMINRPRWVVPVLPKGBLEVLLKK GIDFSKK
12551	26452	A	12671	107	373	TGNYTPLEDCAQEQMRLIAQVHLETRV KQQQVKIKQLLQBNVQFLDKGDENTVV DLGSKRQYADCSETFNDGYKLRGFYKIK PLLNP
12552	26453	A	12672	196	45	YLVFHGSREKRLAKKYYDKLFKECCIAD LSKYKENKVCFFPHYGRFLFK
12553	26454	A	12673	33	448	KEGAERAGAAAPVWSFLDDRDSARTRS GTLGSADMGMKTPDFDLDLAAFDIPD IDANEAIHSGPEENDVPGGPGKPPQPCVG SESEHTASASAGDGGVPAHASDHGLPP PDISVLSVIVKNTGLSRAGWRPWVDV
12554	26455	A	12674	250	29	KKQTNMWQSPYEDYRIFYTISSSLYHLS IYPPYLSIYLSIYLSLYLPLTHLSIITD YVSILEHELRLPLWRIQP
12555	26456	A	12675	377	442	SDRQWCMPIVPATWEAEAGES
12556	26457	A	12676	1	553	RIFPGRFRVKLPSCPDPMGTRLLFWV AFCLLGADHTGAGVSQSPSNKVTEKGD VELRCDPISGHTALYWYRQSLGQGLFL IYFQGNAPDKSGLPSDRFSABRTGGSV STLTIQRTQQEDSAVYLCASSLATAWHS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RLLPAAKPHPSLSLQLLDTLNRGFSLLL PPHGKQVDLDLSLSPG
12557	26458	A	12677	232	3	GWSSDCQQRARVIEEKHSRQKGHIAENP SVHRHHQRPKVDKTTKMGKKQNRKTGNS KTQSASPPPKERSSPATCI
12558	26459	A	12678	134	3	IFIVEFGGKPFSCSISLSQWLWCLFIG IGELLWGQVSTGTLY
12559	26460	A	12679	212	47	NGTHPHGYTLTHKHTHSCAHTHTHTHS LLLVRSKFLPQKNITISFRSCCKLGKP
12560	26461	A	12680	224	2	MKMASFLAFLLLNFRVCLLLQLLMPHS AQFSVLGPGSPILAMVGEDADLPCHLFP PMSAETMELKWVSSSQCI
12561	26462	A	12681	35	397	KPLISQNKIHSVSSSQTGFFFFFFFFFGE KKPPFAPRGGGKGPFPPLPPGGGNRAPP RGEKKGKGPFPKPNPAGFPPOKEKKTGP GGGGKKKTPAPPTPKEVDQPLPRREQRG PGRLPARGA
12562	26463	A	12682	188	514	HTTHLVVYVLSMAAFFFFFEKNFLFAPR VEKRGKDLGSLKLPFGFRHFSGLTLQG SGNNGAPPPSPVIFLVFFEKRGFPLVGR EGLILPPLQAPFCISFRGAINGPS
12563	26464	A	12683	366	3	ISQTQTQWTDWVSLBLQGCCLAHRDTVA IPQTRSFPPFLMISCMTFLSLLQMDRAF PPPPPQTPTITIQGQISTSPATWPLTHLH STPGLSVEYSSNTHKSSLSPTSQWIRVD PMLASPTV
12564	26465	A	12684	99	1	SSCIRFFLEQAYGQQSYGTYGQPTDVS YQACI
12565	26466	A	12685	247	31	FLKEKRNQFYLFIFQRWLDPNKPIRKQL KRGSPYSLNFRVKFPVSDPTKLQEEYTR WVGYIFLENIVKTLI
12566	26467	A	12686	416	253	PSPMTIPVTGAPRDADLWSSHAKMLAQ LKDSDEVFRFLGSSQIFLCWRPSFNL
12567	26468	A	12687	116	3	CLLGRMWLMPVIFALWEAKAGRSLEVR SLRPARPMY
12568	26469	A	12688	380	1	SPESKGLGLWSKHVSPLLCIGVCPFPVS MAELRQVPGGRETPQGLRPEVVEDEV RSPVAEEPGGGSSSEAKLSPREEDL DPRIQEELEHLNQASEEINQVELQLDEA RTTYRRIQESASV
12569	26470	A	12689	157	488	REFVSQGGSHLKAQVRLEALLLTIGTPP WAHLSILHMTAMGQRENKREAASSRIQV LLNHSQAIKQESIILFFEMESGVWPRLO YSRMISASCTLFLSGSNNSPVSAARI
12570	26471	A	12690	514	3	PSIRAGLLCGSAENATPFLCGITMAAGP LYTPENWRAPKALIAAQYSGAQVVRVLS APPHFHFGQTNRTPFLRKFPAGKVPAP EGDDGFCVFESIALAYYSNEGLRGSTP EAAQVQVQVSYADSDIVPPASTWVFST LGMHRNKQATENAKECMRPLRVSSSLV GP
12571	26472	A	12691	304	4	AESLRVAHERLDTRSTSSDIFNFPQTS NLEMNSEILES WANYQSSTSYNTELS LFSKVNKGKSTEFQRMKTLQVKDQAITT RVQVRNLVYTVKINPL
12572	26473	A	12692	221	2	VGPATRDLCFADEPVVGRQKQKQWWWVL CLSPNRLAGRPDTLHITCASAHMRHTT CMHTRHAHAHVHTHCI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12573	26474	A	12693	3	205	YMLCSILSTQEAFCICLGEKFIYLFYTL FRDGVSLLLPRLECNVILAHCNRLRGD RARLHLSKKQK
12574	26475	A	12694	233	3	IMGPAHLFKGNHNGWGLMYKAPFFLF FFKTGSHSVAQAGTIPVHCNLRPLPGSSD SPAPASRVAGNTNVPHTLY
12575	26476	A	12695	408	3	PAREMEKFRVCVRKRLPLGMREVRREIN IITVEDKETLLVHEKKEAVDLTQYILQH VFYFDEVFGEACTNQDVYMKTHPLIQH IFNNGGNATCFAYGQTGAGKTYTMIGTHE NPGLYALAAKDI FROLEVSQPV
12576	26477	A	12696	123	631	REAVQGGKGGGGFGRSRSRSGAVSAA VGDMGDPGSEII ESVPAGPEASESTTD ENEDDIQFVSEGPSRPVLEYIDLVCDD ENPSAYSDILFPKMPKRGDFLHFLNV KKVKTDTENNEVSKNHCRLSKAKEPHFE YIEQPIIEEKPSLSSKKRIDNLGASDCW D
12577	26478	A	12697	429	629	LALLYPLKWVGKPVNFMEEDILGLPLPP LNEEEEEAESEEEEEENPVHKIPDS HEITLKHGTTK
12578	26479	A	12698	158	404	LPILLSVERLVEIYATFIQDLFSASNIP YSSSVFRIEMDQPRTHSGPTTASNAPS STNSSAPSATNSKQERSSSSLSKPS
12579	26480	A	12699	185	3	HRRPISIPSSVIHPAMVRLGLQYSQGLV SGSNARCIALLRALQQVCPILLSLMIQP HLVY
12580	26481	A	12701	181	3	TVWASMFLSALRARAAGLAHWGTHVR HLHKPDMQNGAGGALFVHRDPRENNRDT PCI
12581	26482	A	12702	373	1	ILVQERDSQVRVIRMDKLVSSRDRVGRG VEKQMTDHRVIYSVRKLQKRITPEFFIP SRTTPKLLFLVLP SGKTPGHPVSSRTI PEPPLPTEPLERIEHPVPSGTIPKPPE PPLPIEPHETMY
12582	26483	A	12703	272	508	TKLGKKQNRKTGNSKQASAPPPKERS SPATEQSWMENDFDELREBGFRRSNYSE LREDIQTKGKEVENCEDNLEE
12583	26484	A	12704	341	1	VFQHPHRPLAPPSLGPQSWPLMEGSRPR SSLSLASSASTISSLSLSPKKPTRAVN KIHAFGKRGNALRRDPNLPVHIRGWLHK QDSSGLRLWKRRWFVLSGHCLFYYKDSH V
12584	26485	A	12705	187	365	WEPSCRGPSAFKPTRCQSYDWACMGAE GRSMEQPOEESPEVREEEIEENAHAE GTP
12585	26486	A	12707	238	596	LWLVRVKYSIMSGAALGLEIVFVFFLAL FLLHRYGDFKKQHLVLIIGTLLAWYLCF LIVFILPLDVSTTIYNRCKHAAANSPP ENSNTGLYATANPVPSQHPCKPWSYI PDGIMPI
12586	26487	A	12709	131	2	DRVSLSPRLCSGTILAQPSRLKQSSHL SLTGSWDYTHAAPCI
12587	26488	A	12710	151	2	YRQGLILLPRLECRUMIMALCNFESPG SDPLTSASRVASTTATCHHTC
12588	26489	A	12711	151	1	NFPEDHFTVGCLRAGSSLIHYWWECKL VQSLWKAVWRFIKDLKIDLFY
12589	26490	A	12712	28	411	RVVPARPAGEPREPHVSWMKLNPPQAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LYGDCVVTVLLAEEDKAEDDVVVYLVLFGSTLRHCTSTRKVSSDTLETIAPGHGCC ETMKVQLCAFKEGLPVFDVTEKYFLLPR MYRYRCLYTPSAAV
12590	26491	A	12713	351	675	ENPRHTFIYSLPLGLQKHQVLTVDIGFG GTAIMTVGKSSKMLQHDYRKRWILQDG RIFIGTFKAFDKHMLILCDCDEFKRIK PKNAKQPEREEKRVLGLVLLRGEN
12591	26492	A	12714	326	457	ACSHHQKRSQAPPPAHLWPDPCPHGSLP LLNPSVCNPGREVSPT
12592	26493	A	12715	200	1	TITKVCVFTTRTCGLKGLMAKALFDQRK DRESETECQVWVLTVPVLPALSEAEVGG LLEPRSSRPGV
12593	26494	A	12716	208	405	KKERENKHTNKKGRKMHICQWSSSL HRKFQGIYRKTGTGWAQWLTVPVLPALW EAEVGGPPEV
12594	26495	A	12717	157	3	AKETPTHKGSCKKKFFFFFETESRSVA QAGVQWRGLSGLQAPPPGFTPCI
12595	26496	A	12718	1	472	SPAILERLAILPYLLFDWSGTGRADAHS LWYNFTIHLPRHQQWQCEVQSQVDQKN FLSYDCGSDKVLSMGHLEQLYATDAWG KQLEMLREVQRLRLLELADTELEDFTPS GPLTLQVRMSCECEADGYIRGSWQFSFD GRKFLFDSNNRKWTVV
12596	26497	A	12719	537	1	LHTMNGNESSGADRAGGPVATSVPIGW QRCVREGAVLYISPSGTELSSELTQTSY LLSGDTCKCGLECLNVKVFNFDP LAP VTPGGAGVGPASEEDMTKLCNHRKAVA MATLYRSMETTCSHSSPGEGASPMFHT VSPGPPSARPPCRVPPTPLNGGPGSLP PEPPSVSQACI
12597	26498	A	12720	369	3	AAKIIPATRKASLELELSSPDSTGGT PKATISDTNDALQKNSNPYITPNNRYGH QNGASYAWHFEARKSQILKMECGSSHD TLQELTAHMMVTGHIKVTNSAMKKGK PIVETPVTPV
12598	26499	A	12721	230	3	KFFWVLAGLTGKNSDASASLNQVHISPF LFSRHHFSLGPLSPVLLQGSKRROLL ATTLRALESASLSQHEHPV
12599	26500	A	12722	26	110	REQYAEGNMRGPAPGKKTSGLQKQNEV
12600	26501	A	12723	224	1	WQNDQASDPKYSFTSQCLSFARLAR RYGDVFQIRLGSCPIVVLNGERAILQAM VQGSFAFADRPFAFASFRV
12601	26502	A	12724	120	530	KKVARGSRSRERSRRRRSRPKAIT\NR T*GTRCTPRRWRSTVLGMRSCCTRAR*QR RSGLSRGHTRSAGLCDHGSVRAGSGDGA DGTGGGDRRLGLGRDSLSSSSQSAAFS SSASGSSSFFSATQPLRMLLEYFWL
12602	26503	A	12725	434	222	KEEKSARGEVKEQD*EKREBEVEKSR/ RRRSRRRRRRSEV*YRKGRRRREREDIL VAERSHRSFRNSIPSTL
12603	26504	A	12726	268	370	SNILIHMSMFFFFGTDPISV*KNLPA* KTPGPDGFDKLYITFRGELTTPPHILL H*FTEGAVLFNSPSK\AASITLTPKPNY DIMRKENYSPISSYIWNQCSFFLEQIFP LSFKLNCPLIIP
12604	26505	A	12727	103	636	VCFISMKQPHGSRHPPCS/PFRPGS*VC QQSRLPLGPQPSAFGLA*HRRGLLGLOG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PRSEMQPVPHGGRVSGQTLPKGPTPKRP PGPAPRHGGHSWLLK*LVCAQPPRP*S *ASQAVFTLQVPGKPQVWTPCPVPVRAP TP\PLSNGGLGVSERH*DGH*QAPTSP* PRCQGGAGEGPQ
12605	26506	A	12728	1193	1638	GLGFAMLPRLALNSWPQGDPSVPASRAA GTRGVHRHTQLQVSFNYYKVLAMHSGSQ L*SQHFRKPRSDHLRSGVRDQSGQHGE TPSL/LKNTRISWAWHTPLVPATREAE ARELPE\PGRQKIASERPVKPICTASLG NTCETPPQKK
12606	26507	A	12729	304	101	RHLHWPCPSPLAPTPDISHCPEPPKSQT SP/CPGT*CLGFLKCPSSCHFA*K/PLH PSEFARKSLAPDTCF
12607	26508	A	12730	91	264	SQRSISGLRVKENLIFVMIMFPPIYSSQ TFWSQTFMLMKIVFMGISISICYIL/NT EKNLGQGWLAPIIPALWEAEAGLL*L RVKENLIFVMIMFPPIYSSQTFWSQTFM MLKIVFMGISISICYILKLRKI
12608	26509	A	12731	1026	406	LAHFRSQIFSFSHILVHFERMVLNRYRY LACVRRVVERFLHVLAYPGRIVLKYRYF LVHFRREVFRFRHMLACFRMVLYCYFL VLRKILLIYVTFITLYFRKVFRLRHNFRLG GY*RYKFGYAPRWLSFFLYRCQCFLHYF LFYVLRRLHLQF/CCFVVSFCLEDFDLFL PSAACVFSVLQIAIVMFPFHALQLFFF* VVLCFNSRFRQ
12609	26510	A	12732	1508	157	QDVGGSGFKVDTHPRGRMASIFSLLTG RNASLLFATMGTSVLTITGYLLNRQKVC EVREQPRLFPSPADYPDLRKHNNCMAEC LTPAIYAKLRNKVTPNGYTLDCQCIQTGV DNPGHFFIKTVGMVAGDEESYEVFADLF DPVIKLRHNGY*PQG*LKHTTDLASKI T\QGQFDEHYVLSSRVTRGRSIRGLSLP PACTRAERREVENVAITALEGFKGDLA GRY\YK\LSEMTQDQORLIDHFLF/D KPVSPLLTCAGMARDWP\DARGI\WHNY DKT\FLIWINEED\HTRVISMEKGG\NM KRVILSR\FCRG\LKEVERLI\QERGWE F\MWK*AP*EYILT\CPSNLGT\GLRA\ GVHVRDPQSFSQDPTAFLKILEKPRTPR KRGHKVVWDIAA\VADVVD\ISNIDRIG RSEGEL\VQIVIDGVNLYVDCEKKLGRG QDIK\VPPELPQFGKK
12610	26511	A	12733	261	487	TGSETDCAKQASFLPREVPTVAEMKME LLKNKQFW\RGVVAHACNPSTLGGQGGW IT*GOEFETSLANMAKPHLY
12611	26512	A	12734	382	668	YKRITDIFVDSETVHILNKRQSCRIPG FIQLVQLISHQLAAPRDYTVSHSVAQAG VQW/RNLGSLEPLPPGFKRFLCLS*HAL KNLSSCDTPPQY
12612	26513	A	12735	401	27	GDRAEESAEPRAWSHSDNSHRYTTLFIC LTHTHVHNPVHS\HHTHTHTHTHTHTH TVSHRHTETPPLLLKQTLKIFY*NSRDD TPRSRPGSSGLQRLSSSPVPFPQGTVE ASADFCGHDLTT
12613	26514	A	12736	202	182	KYLPPIFINLITMNLFFFETHSCSVGQA EVH*S*LKPMPFG\SSDSPASAFQVSGI

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12614	26515	A	12738	319	2	TGSPSSSWLIL*FFLKIGFTKKG QNTPPHIYIYIPRVDAFLFLFLEMSYSVY VVAVLSPLYFVNKLALTLHCRLALNSFL HKIQEPS\LGSGSG\PLSCNTII*RLCL RSLHLVFRSLWILPICDSSSVF
12615	26516	A	12739	1363	2000	DRVFVIPGWKCSGTIKVHCSLDLPGSSN PSTSAP*VAC\ATGYPPCPGLNFLYF* MEERGFTQVA\QAGSQNSWGSKPNGTSE ASPKVLGMNKP*NLPNPGRSILN*DGSI RYKDNYP/WEPPKRSYKCLRQKKSIL* SAGPRDYEASQPRKNYPISLLTFCTSS LHFNPTLTCSSQLQKSIRRLKSEESC PPLPACSLKHTQAIKITF*RLHRTA/L FYLLK*NCFRN*S*KYFLLSVSNLKI/ QWVRSSLHPGAPGYTPTV*RPKHKSNVL I*IQS/ITRCLFYILVYMRITFPLQLFL SKHPSTYKEDFA*VLPLSFFFEMESRS AARRSLSSLQPLPRLKRFSRLSLSSW DYRCAPPGLASPSILSS*GSCCSIQFIL RMSTISHAINVLVLKNTYLVLSASEHS LIKKPC
12616	26517	A	12740	1696	743	GCQIMRSGVHDQPDQHGETLSLLKIQKS AGPGGMHL*SQLLRRLRQENRL\NRGCS EPR/SRHCTPAWATEQDSVSKKIKK*KK *NHLESKQQQPALEPPEQAGGQLRKE QLQDGRRELAADMTL*PGHSKRLGALPR PLLSAYYFNKVAARRQAYLETPTGFTS YOREEGEQALILGVEAQASSPTVFHRER RQSQALCSHRKSQEAPVRPAHPPRRVPG LGKPPSQGLSAHLGQDRAPAPRRASWDQ RSQAPISVTFPSVLDKEESVPCGPGFP HAPAPRGIHGATWEGAHSRGYPGHFLAL PQHNSDEQRPN
12617	26518	A	12742	2473	445	RGARRRRRRSRHRRRRHQRPRVRAAPRQ PEQRRRRGAPTHGPQLIMDLPLPPGGL PSQQDMDLIDLWRQDIDLGVSRVDFD SQRRKEYELEKQKLEKERQEQLQKEQE KAFFAQLQLDEETGEFLPIQPAQHIOSE TSGSANYSQVAHIPKSDALYFDDCMQLL AQTFPF\VDDNEVSSATFQSLVPWYSPG HIESPVFIA\TNQA\QSPETSVAQVAPV DLQGMQQDIEQVWEELLSIPELQCLNIE \NDKLIVETTMVPSPEAKLTEVDNYHF\Y SSIPSMKEVGNCS\PHFLNAFEDSFSSK HPLHKNDPNQLTVNSLNSRM/PTVNTDF G*WNFILVF\MAEPSIRQQAWPSPATLS HSL\ELLNGAHGCFDLDFTL/CKAFNQ NHPEGTA\EFHGF\DSGISLNTSP\SA SP\EHS\VESSSYGDTLLGLSDSEVEBL DSAPG\SVKQNGS*NTMYSSSGDM\VQP LSPSQGAHFTCMDAQCEHTRGKDLPV \SPG\HRKNPISQDKHSSPLGGLISQR DEL\RAKAL\HIPIPCRKKSFNLPVG\D FNEMMSKEQFNEAQL\ALIR\DIRREGV RNKS/AAASGICRKKENWENIVELEQDL DHLKDEK\EKLLK\EKGENDKSLH\LLK KQLSTLYL\EVFQHAYRDEDDGKPYSPSE YSLQOTRDGNVFLVPKSKKPDVKKN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12618	26519	A	12743	6	457	RPRNRPGIRVDPVRVRGVGHAPHEGLVPE ERMYRGSPTACETQAAA*ERAFGPSSPT C\RLPIPRMSTSVPOGHTWTQVRKKDDE EEDPLDQLISRSGCAASHFAVQECMAQH QDWRQCQPOVQAQKDCMSEQQARRQEEL QRRQEQAQAGHH
12619	26520	A	12745	297	12	QERPVRMLVLHFGRLRLADHLKLGVRDQ PGQYGETPSLLKIPKLSGM\MMAP*IC
12620	26521	A	12746	98	428	YNTSFNETVLLLTPTITIDCLYTRKDAI APESACGVCPCSLLGVGA*IPKVIRLD LSKKHVTAYGGFMCAKCVLDNRINRAFL IDEH\KIVPKV*KALSQSSKAFCEHET
12621	26522	A	12747	3	638	LWLWSLCWVWAVSLPQFILGSLHPCQG QASWREVDLLHEGSGEASSKPSGSPV GLLLDQEMVTPLLVCICGILLHQEMVSP LLVYTRGILLHQEMVTPHPGLYPWDSPP LDGHSPPGLF\RGAAAPS*GG/PLPVLV YTRGAAPSGDS\PPPPGLYPWDT\PPS GDRHSPPGLYPWDTPPSGDGHSPPALYP WDSPPSGDSHSPGLFPFRG
12622	26523	A	12748	2	333	DMVLLCHPGWSAGSI*KTKKERERMNL HR**IDRERERERERQIQ*KE*KRINEF EGSKERFTQSVKQRNK/ELEKIRTLDT ETIYLSIYRN*SLRRQERRTERERMH
12623	26524	A	12749	30	333	KTSVLLPVQWAAQNDNERYSSTKNTIMA LPLPLPVFPRSPDAERKLDCAAISAH CNLPA\DSPASACRVPAAIAGARRHA*LV FGFFWRRRFAVMAGLVS
12624	26525	A	12750	231	39	INDLL/CLF*FKKLIWGRVW*LMPITIPA RWEAKAGGSFEPRLKIQ*AMITPMYSS MGGREQDPVS
12625	26526	A	12751	49	273	HLQVTEVFVFWVCVFFRRWGGSHCV/AQ AGV*WLTGTGTVPCCSPPELLGSRDPPAS AS*VAGTTGACLAANCGRF
12626	26527	A	12752	505	897	SYLRVQFYSAFSLFFRHEVLPCHTGWNA VV*SQLTTASN/CLGPSNLLKAPHLAN* KKIF*RQGLSMLPRLVLNSWPHMILLP* LPE*LGLQARATAPGSGFTFCLTQDSIL MCSPTVHKLSDSIALETKQ
12627	26528	A	12753	335	542	CCNEFFLSQVWMLMPVVPATR/SAEAGG LPGPGSQRLR*ARSKPVNSHCSAGGRCG IDPISIKQKQNNNR
12628	26529	A	12754	356	72	WHEYVLLMEHTKKCHLS*GLYNGLNN*Q /WCTHPVVPATWEAKAGESLEPRSSRL* CTMITPANSHCPPAWATARSCLNQSNQ SSNNWQGMITGGK
12629	26530	A	12755	340	127	NYLFIFYFRDSITMLPRLECSN*FTGSII VHITLKLGLSSLP/ASASQVAGTTGTRH HVQLSNYFKIKIKPKP
12630	26531	A	12756	290	511	KKNQPGT/CGSRL*SQRFGRRLQADHL DQLGOHGKAPSL/LKNTKISWALWRTFV FPSSQEAEMEELIEPTSSRLQ
12631	26532	A	12757	254	549	YPGAKKQRPGGDSVRGTHLQSRCWCVLL HNCQ*PKSNTQTFP*PKNLRE*NAT*KS TDL/WPGAAHLCPNPSTLEG*GEWIT*G QEFETSLGNIPRPQIY
12632	26533	A	12758	617	451	NKKRRGLTLLSRLKCNVIAHCSLKYP GSSEPPTSFAF*VAGITY\GT*HHAWAY

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12633	26534	A	12759	91	393	KWYTKBCLVLLVSTFSRYLLSIYYREVL AQTLGKLSKTMCPALEETVAVNGLQIK SKK*/WLGVMTHACDPSTLGG*GGWIAW GREFGTSLSMAKPCLC
12634	26535	A	12760	10	221	QSHNTNGCLDLHFQKGPWQSVGETLNL* TIFLCVCVCVCVCVRHVYHM/CYIYSDF ICPSIECEYFSPAHR
12635	26536	A	12761	309	55	IIRYKNYISIKLEGWKRLYHATTHEKKV GVAVLISEKVDFAKN/MYQDKGRFLL *R
12636	26537	A	12762	640	896	TIVLKC�FVLCFRDEVPLCCPGWSAVA /QSQTQLW*TTQPGLKQSSCLSLSSWN *RHVPPHΛMFLKTTFTLLYTCHLETN IC
12637	26538	A	12763	1	357	IVPLHSSLDGRVKPHLLKKKKTCTSLV IRETQIKITRYTYSNG*S*RKNKAGNNK CWHGYTATGTLIAD/CKSKQMLWKT*Q FHIKLNHY*YNSEIQFLGLYPRDKNIA RCGLRL
12638	26539	A	12764	129	320	RWKCVKLKNTGQAWWLIPVLPALWKNQ\ AEGSLEARSRLQ*TLIAPLGYSLP*W SGTSLNKK
12639	26540	A	12765	617	435	GVKGLILPKLQKLLKSIE/I/E*KLPKS FYDASLTMIPLKHKD\RPISHVKIEARI LHKISINII
12640	26541	A	12766	243	5	QKIKKRIKKNQNL*EIWDYVK*PNL*I IGIPERGEKVYNTENIFEGIIQ/ESVFN L/AYLVREVDNQIQEIQTPTVRYTK
12641	26542	A	12767	101	16	RTQLFVSVFVFCFLFCFETGSCSITQVG VQWCHLRSLLQPPPP\GSRDSPPPSSQN RG*TNI
12642	26543	A	12768	362	92	RVPHMDLGEECTSPYMYI*PMTCVFKHG *DGNFCVTFATIIITYYI/YLSVCVSI *I*CYLCVCVYIIYIIYIIYIIYIYKY MKERRL
12643	26544	A	12769	1161	824	QAKDLSTHFTKENM*MG/NKQMKRLSES LVISEMQIKTTMRSHLTTRITIKMTS DKICP*RCG*MRA/LLQC*WKYKIVSPL WKIVWPFLKT\INMNISCNLMILFLGFY PIY
12644	26545	A	12770	241	237	K*RIWA\GVMAHACKPSTLAGCDGWIA* SQEFETNLSNTGRPCLYER
12645	26546	A	12771	326	6	DTVSRKNKSGKIFQLSSRV*YIERSQSG VKVYKCKTFGKAPTQ/HF*AHMRMYTGE KPYKY*ECGKFFILVLLLLMIQKYFHL IKIVRLYLIRKKVSCQPSNKKILQS
12646	26547	A	12772	413	1	KKTFYFFFFFETQAGV**CDHNSPWP*P P\GSDNPLTSAS*MA/GLQSCMHHAQL S*FVFLEAGSHYVAQTDGDSPTSASQSA GITAVSHHTRPILYILIVLSYAISFFSI LYSAYFLQPHLP IHNFLFSYISSSC
12647	26548	A	12773	2	1055	FFFFLRLNLTLPRLE/CVILAHCNLHF PG*SNPASASRVAEITGSRHQARIIFV FLVEMGFHHVSQAGLE/SPDLK*SAHLG LPKC*DYRRDITPGHH*SF**RYFLKTY ISRVL/WCSLLGTFMFMAFDHM*TW*H *QNHFFHLLQIWKLISERLRSAGGQOAL KTVISTFSSKYVCRAFPGWIAILYV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						TF*SLDSRRRTCLVAVSNPFYSTLFLKL RQQVLLTG/PYHLFSARPSSCGSDKKAR ELNLSLSL/CFFFGKRVSGTQAGVQ*H DHSSLQLWPSRLKQCSHLSLLSSWDYRS ITPHLANF/CNFLSGWSRTPGLK
12648	26549	A	12774	315	98	FRCLNSINPLESPHVRKTCAGRAQWLA PVIPPFWEABA/SQMPQVIHSR*LEARS SRPAWPTWQKPCCLKYN
12649	26550	A	12775	275	59	NPSPYKIQKISWAWWYMPVVLATR\RLQ *ARIAPLHSSVGDRAAPCLPKKQKTKNQ TKTSGEFVLVQGPATVC
12650	26551	A	12776	73	381	SLINSELSSI PRPTWESPSTSDSAWPMQ NLASEPLPLP*TTPPDFPALSA/PE/P LPFTPSPRDTLPPPLSPSYKQAPVLSVH PPVMPLKYVPSSPLLSFLYL
12651	26552	A	12777	274	342	LNCVIA*WLMPIISALWEAEVGVSA/P /RSLRPAAWTW
12652	26553	A	12778	2	478	TIYYTKYTTFRVPLNLGLQLLTAFFCVCV CVSLNGFKNAKDYGGSHLKYSVYITGFL LQFSLKFDCLCVCVCVFP*MA*KMPKI M/RGSHLKYSVYMT*FLF*FSLKLYFC DPILRKRI/WPGAMAYTCNPSTLGG*GG QIT*AQEFETSLAKVVKCLY
12653	26554	A	12779	680	453	SETDWRKNKFFPSNFPNSNLTNSWTNSC SKKTFKKH/RVGLGVLAHTCNPSTLGG GGWSP*QGEFENSLTNMNVHFS
12654	26555	A	12780	59	487	SLHKHPERGLQSFQGCWQTQEMLGSSHVQ QRAWELCAPNLTCPGYLSFFLRQDOAL LSKLECSGTIPAHRNPSLPSQLKVSSH LSFPSSWNSRCTTPHQLLLFF*DRIRL FCPSWSAVAQSQPTVT/SSLPSQLKVS SHLSFPSSWNSRCTTPHQLLLFFNFL* RQVFTMLPRLVSNS*VQAILPPWPKVL RLQA
12655	26556	A	12781	109	361	LSPWHHSRNYTLIYPYTLNFWMSAFPTP KEEFFFSFPETRPHSVAQAGAH\AIIA HCGDLLGS\SDPPTSAS*AAGTTAII P G
12656	26557	A	12782	3	204	LIDGSLALSC*LFCGGATIAHCSLELLG LGQ\SPVSATRVAETTGVCHHAQLAFVN LHLRTSRKHCGH
12657	26558	A	12783	2357	6366	LTGS\NSHTILTINI/NMGLNAPI*RH RL\ANWIKSQDPSVCCIQTHTLT\CRDT HRLKIKGWRKIYPSPMGKQKKKAGVAI\ LVSDKTDNFPTKIKRDKEGHYIMVKGSI QQBELTILNIYAP\NTGAPRFIKQVLS LQRDLDSTLI\MGD\FNTPLSTLDRST RQKVNKDTQELNSALHQADL\IDIYRTL HP\KSTYTF\SAHPHTYSQNWTTIVG SKALLSKCKRTEIT\NYLSD\HSA\IK LKLRIKNLTQNHST\WKLNNLLNDY\ WVHNEMKAEIKMFETNE/NKKTPTYQN FWDAFKAVCRGKFI\ALNAHKKQ\RS KIDTLTSQLKKTREAKSKQHSKASRRQE ITKIRA\ELKEIETOKTLOP\LKKISE SRSWFF\ERINKIS\RPLARLIKKKREK NQIDTIKNDKDI\TTDLTBIQTTIREY YKHYLA\NKLENLEGMDKFLDTYVSLPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LNQEEVESLNRP\ITG\SAIVAIINS\LP PTKKSP\GPDGF\TAEF\YQRYKEELVP \FLLKLFQLEKEGILENSPYEASII PKPGRDTIKKENFRPISLMNIDAKILNK ILAKRIQQHIKKLIHHDQVGFIPG\MQG WFNIRKSINVQHINRAKDKNHMIIISID AEKGFDKIQQPFMLKTINKIGIDGT\YY FKIIRRAIYDKPTANIILNGQKLEAFPL KTGTRTGMPSLTSPLLFNIVFCPIVFWA R\AIRQEKEIKGIQLGKEEVKLSLPADD MIVDLENPIVSAQNLLKLI SNFSKVSGY KINAQKSQAFLYTNNRQT/BEAKS*LMS ELMSELPFTIASKRIKYLGLQLTRDVKD LFKENYKL\PLIKEIKED\TNKWNFI PCLWVGRIS\IMKMAIL\PKVIYRFNAI PIKLPMTFFTELEK\TTLKF IWNQKRS\ RIAKSILSQKNRAGGITLSDFKLYYKAT VTKTAWHWYQNSMVLVPKQRYIDQWNRT EPSBIIPIHYTILI\F\DKPILLEKNKQW GK\DSL\FIKW\CW\ENWLA\ICRKLNL \DPF\LPYTKINSRWIKKKDLNVRPKT IKTLEENLGITIQD\GVGKDFMSKTPKA \MATKAKIDKWDLIKLSFC/TICTAKE TTIRVNRQPTKWEKIFATYSSDKGLISR IYNELKQIYKKKKKTTPSKKWK\DMNR HFSKE\DIYAA\KKHMKK\CSS\SLAIR EMQ\IKTT\MRYHLTPVRMAIKK\SGN NRCWRGCGEIGTLLHCWDCCLVQPLWK SLWRFLRDLELEIPVDFVPIPLGIYPED YESCCYKDTCTRMFIAALFTIAKTWNQP KCPTMIDWIKMWHIYTMYYAAIKNDE FMSFVGTWMKLETIILSKLSQEQKTKPR IFSLIGGN
12658	26559	A	12784	787	926	POAIRRPRPPKALG*HNSVDLGWAWWFT PAIPTLWDYTHEPLYLAKIS*CFKKVYK FVLNCIQCPCGPHAAHRS/SGKTS*V*S NYLFFSFCFETKFCSVTQARLQWHDLS LOPPPPGFKRFSCLSLPGGWDYRRLHTR SANFCIFSRNRVSPSWPGWSPTPDLRRS AVLGLPKRWYDRREPPCPAKIYTIMAPQ KVNSHSSQPVSFSL
12659	26560	A	12785	248	285	C*VIF*CVMIYVLIYVEKITSIRLAVY VV/CIITRLFKV*ICSCLLGC*FLFFNV C*LYIFIIFVFFFFFFFFFFFFFFFFFELN ILY
12660	26561	A	12786	243	37	RRSAGHGGGSL*SQYFGRPTRADHKVRS N/RGETLSLVKIQKVSQAWW*EPVVPAT RQAEAGADAWDR
12661	26562	A	12787	75	289	DYRHEPRFFFLYTTFFEMDSHVARAGEH WCDLGSL*PST/*GSSDSSASTSR\QRH HAWLIFGFL*RRGFAC
12662	26563	A	12788	83	256	RKMYVVGLEFVTAQN*K*PKYPSTEE/YI K/RLWYLHTMEYSAIKIEKLGTQAQNR LILY
12663	26564	A	12789	197	499	QSLKSVEETVFRNNKQ/SIPTFQVILMP WWLIPII*ATWEG*GRRSPINPGV*DQP GQHSKTPSLQKTKFS*AWWRVPVVA\ IGEAEVSGIPLSPERSRL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12664	26565	A	12790	394	91	FYNSTKFKWKNIQFLITRCRGDQIQVIR AHAVQLGFHVLVYF/CLSQNLSTIYLYISI YVYTRYIYIHTHMCIIHII*YLYIYTYIVI KH*KEHWIKHCFPTERK
12665	26566	A	12791	735	75	FFFRQEGFLSPPKRGGVPPHTTKYFSP RGSFLWGWGTSRPPPRKCFSPPPPVFL PPPKKKKIIISFSPTKLAPPEYFKSPPP PS\PPPPSSPSPSTFFFFKFPSPSSSF SSPPFFFPSPAWEDPPVQSRRIY*FLPP PF*IPETPR\RVLKKKPGEGRSWGLFPP PKGPKRRVPLGPBFKTRLGHKTKPRFFK KKKKKKRFLISCLWHPAIPSTLGG
12666	26567	A	12792	482	342	MGVVFVFFETGSHSSVTWAGVQ*CNLSL LQP/PASSDPPTSDSRVAGST
12667	26568	A	12793	405	169	FYKKKKTGSGGLALSPRLCSGTTIACHN LELLGSRSLRL\SNPTPLAS*AARTVSV CHQTHLIF*FFVETGSCVVASA
12668	26569	A	12794	270	94	YVCYSYKQIKICSHVKRRE*NTFKIYLL KYIALGLTGHHFPL*TFSKTVTLWPGAV AHACNLSPLGQGRWII/R/QOEIKTIL ANM*IPVFLHVNIFLSVCSYSIHTLDY LFYYSCYILISL
12669	26570	A	12795	284	415	NFIKIIKKKVMGLFYGKTFLNLKKKKR KKK*WPGTVPHA*NPST\LGGLGGWITR GOEFETSTLATN*NPTKSIIRGF
12670	26571	A	12796	1387	32	APSSFAIRSFSSGPMNAFFSSMVWKRPW PNLEVVSMMNLSIFSRARRFVCTSKDLR RVSTRFLVHLTAFLGYKAGMTHIVREVD RPGSKVNKKEVVEAVTIVETPPMVVVG VGYVETPRGLRTFKTVFAEHISDECKRR FYKNWHKSKKKAFTKYCKKWQDEGKKQ LEKDFSSMKKYCQVIRVIAHTQMRLPL RQKKAHLMGDQVERGAPVPEKAD\WAPR EALSSKVLVTQVFWAGIK*SNFIGGDPR AKGYKGGQPVCAWAPRKLPPQRPHPRAL RKGGFVLGAW\HP\ARVA\FSVARRWGR KGLPFHRTIINKKIYKIGQGYLIKDGKL IKNNASTDYDLSDKSINPLGGFVHYGEV TNDFVMLKGCVVGTKKRVLTLRKSLLVQ TKRRALEKIDLKFDITTSKFGHGRFQIM EEKAFMGPLKKDRIAKEGA
12671	26572	A	12797	86	364	EQDNRIFFSFLSLFFFFGETEFGFFAQQ GGQGAILGLPKPPPRGL\SSPPT*GSQE VGTGAPHDIFCFPNKKGETPRLYKKNK NNRGGGATP
12672	26573	A	12798	101	440	HCSRYATGIFEWYSGLVLILLRFGIYE PMNLNIGDPYDSPSRLYKMRLWERMAK SLIEVSLKNSHFWLGMLAHACNPRTLRL IGGRIA*TWGF/KTSLGNIRPHLYLKK I
12673	26574	A	12799	364	195	NPPGDLGEETLLWGGEIMGTTPP*FPPP KEGFLPQDPPGGFNSPPI/QGRSFSFPP PGKFGPPQGGFFKRPPPPFFFLNNNQ
12674	26575	A	12800	86	489	PTAMAEEGIAAGGVMDINAALQELLKTA LIHDGLAHGIRKATKALDKRQAHLCVLA SNGDETIVVVKLVEALCAEHQINLIKVD /NKKLGEVWGLCQIDREGKPRVVGCS IVVKDYKESQAKHVIRENF*CKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12675	26576	A	12801	64	211	GNHKKSNYS LAPWWTTPAT*EAEAGGSLE\L*CAMITPVNSHSSLA
12676	26577	A	12802	300	3	NNVTGSGNTQFHSFPLIRKDICVSIKNDAWNYIKNSNPNGETQVYQ*YSFSN*NLKIWLKGVA\NPSTLGGHGGRIA*A*KPKTSMGNIVTPCLINKQK
12677	26578	A	12803	208	394	SOHFERPRREDCLS\QEGQYSEIPSVQKNVKISWAN*CMPAIPATREAEAGGPLEPRRSRLE
12678	26579	A	12804	183	348	AFILGKGKYEYPYNPCLGWA*WCMPVVLSWEAEAGG\SLEPRSEL*CAMLIGCLH
12679	26580	A	12805	397	238	ETEFFFCPCPGWKWGDLSGQQLPFPGRKFSFCSLPSK\WGO*SLAPVGKCK
12680	26581	A	12806	1	293	PTRPRTSYEKQGYLLLPVFSIVLEVLARAI SQETEI KSVQMGKEVKLSL\FVCVYIYA*ENPVESTKTVDANLFDTRDWFHAIFPQTVGEVGMVLG
12681	26582	A	12807	297	281	AKNPRRQPREIPGGVFPTPGFPYFKA KMPEGFPFGGFFFGKGVWGTPPPFFFFF FFSOTESRFVTR\LQCSGAISHCKLRLPGSCHSPETC**R*G
12682	26583	A	12808	255	59	AGCSGSQLFGRPRGVDHLSPGV*DQSVQHGEILSTKNTKISWVWVSPVVG\EVGRSLEPGR*RLE
12683	26584	A	12809	247	310	PLHSITLGTPTTAPPTPGKELLIRTSILY*KPILSQAWWCAPLVPAQ/EAEARGSL EPRDSRRS*AMIKPVNSHCTPSWALPR LPQPLESHC
12684	26585	A	12810	101	477	IGKEEIKLLFPDNLMEYTVNF*MYKPLELIS*FSKVTEYQVNTK/SNCIYT*QLQIENEIAKTI*FMIASKSIKYLKISLTKCN\KWRDILCICIGRLSIKVLVLPKLM CGGEKIFNPNTGFW
12685	26586	A	12811	1022	696	CFFVLFFKEMGSHYVAQAGVRWCDHGS LYPTP\GSSDPPTSAS*VAGTIGAHHT WLIFKPFVETRSCFLIQAGLKLLASSYP SQPRTSPKCLGFTDVKSLHLAWLCP
12686	26587	A	12812	166	143	RKEERFQINNLGFHVEKLEKEEQI\NPK TNRKKKIKTRV*INEIEYRKTIGK\INKNSWFF*KINKIDKPLAMLDSGRDSN Y*NITKSIEGRRRKEEAGKRKEGRKR RRRWRQRWR
12687	26588	A	12813	163	423	KAFWEFINHKKTGFF*RGPIGVSPGG NLASSI*KG/DPFSPKGPQGS SGGPP PKKEPTGFNLAFGLRGRETGRGPFFLA GLLP
12688	26589	A	12814	2521	2842	INTMYFPP*EMLVGWAWF/RASNPOHF GRLRQADRLRSGVRDQSQGHGETPRLLK NTKISWANWRAPVIPATWEAEAGESLEP GREGCSEPRSCHRTPVVWTRMRLY
12689	26590	A	12815	173	395	LDQPGQQRETLSLLKKKQTNKQTKKNG FKKFL*LDTWVHTY\NPTPLGGRGGGFF *GQDFETLANMGKRGFY
12690	26591	A	12816	43	346	CVYVS/GVCVCVCVCVCLASVCMYVCLH L*VLFGIYFV*DHNICKLRSFCFLFRNT FSHVYF*KIWPVEL*VTVFLFLSSLL HTSCVYEKSYAILIFSAL
12691	26592	A	12817	647	931	SOHFGRPRRADHLRSGVQDQPGHGETP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PLLKI\QKLAGRGA*L*SQLLGRLKQE NRLNPGIRSCSEPGSHHCTPAWATE*DS VLKKKIGADKY
12692	26593	A	12819	392	2	PLFFFFFFFLETESHVSQTQAGVHNPPGP SKPPTSAP*AAGTTGMHYSAHAQ/LIFF L*TELPSCRPGCSAMAVHRHDPFTDQHG SASFLIWASSPLLRTGDSLLGGHHVD AKFSVDTQLALCTKAQNS
12693	26594	A	12820	1183	870	DRVSLLTPLRGVAVARNLAQWKPLPPGF KRFSCLSLPSSWDYKHTPPTPG*FH/RG *FFVFLVETGFRHASQ\AGLNSLPQSDP PTLA/PPKCW\DYR\HDHLAWPRQM
12694	26595	A	12821	172	298	IYLSIYLPYI/YLCIHLSIHPSIYFYLYL SINPSYWVSFSREL*LT*L*YLSIYLPYI IYVSIYLSIHPSIHISYIYLIHPIGFLF LENFD
12695	26596	A	12822	51	254	YDFLKKHLLSSYRAKDLESFLHLHLIF SGN*SVSYICVCVCVCVICVCVYICIL IKSWCS*S/CGVL*AIAGVGWC*LIFG VL
12696	26597	A	12823	199	668	QPLPAPSPSAQKGRAHPTSPAPQAE/ SLPSQSLGTRTRPPLGRPP*SPPWGQVD LWGWLGPSPTLPAPESLSPASLSTEVVL CGTRYLVWGRSGAGQA
12697	26598	A	12824	33	442	GRGKLLKKSQKQRKNALLKYDSKTRVGT LFHWTSVPVTRPLL*INIRLIKLDVIK CSIHKIFHSEFLFFKQHSGL/CI*LSK* LCS*KIHQSGLGTVAHVCNPSALGGQDR RIT*QGEFETN*VMVGPCLYPPLPP
12698	26599	A	12826	363	75	HWEPRPAGPTLPSAPGSPSGRCPPHTT SG/PPPPNTHTPMSRSPWSWEGSDQRPQ PPHTDTGSPFN*GSLRHERPPWGRERQ RPPPTTLVRPLHSH
12699	26600	A	12827	76	486	CTVNLFIYFEMESCSVVQTVGVQWCDLSS LQPLIWFSCVPTQISS*IPMCCGRDLVE GP*MMGAINSFLLCCSYDSK*VS/ARSDL FFFFFFF
12700	26601	A	12828	345	672	KMKCTADLSLLEKDT*IKLEENR*QERI MLRAEVNEIENKIENINKTGGSSSEKY. KIDNPLTRSIRRKVN\KITSIRNEKGSV TTNPTEIKRTVKEYIMKNFMPINLTT
12701	26602	A	12829	208	1	PSNSTPIFKRNENICPHKDPCTMLMAA LFVMSKK*KQLKCSNDE\KLWYIHMME *YIAIKRNKLLI
12702	26603	A	12830	649	172	FPLKYSLSSTTSVMAPSFTSCGGSQQVLL APLSRLLAWPNV/HPPPPQHRHPAPHSFL SPPRSPPNYSP*SSQGPLLPQSKHVRP LPQANARLPSAKNPARGPPGAAQAPDR PPA/VCPLPPHSPLRHERAPRLFLPLP ATEFAALHAVHPGRRQERT
12703	26604	A	12831	1068	667	KLSWFFCSRLRLHFGSIFKVPSTL/PVPK LLLPISLCPSLPLQLQPAQPVFNTAT WLCFC*/P*RV*PAPGVQRVGHNFPP QLNFIPILQ*HLGF*KSASLSSSSSPK KVSLSCHPGCSAVVRSACNLKLLIS*SA CLGLPKC*DYRLQSPRP/PTIFKVTRM CLLKSLTGSVSF
12704	26605	A	12832	268	1	KCFLLALNWPEFILDYFILNW*NSLRT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						VTEKFLFMTLFLTY*NMNRPGMVAHACN PS/TLGGSGGRIT*AQES*TS LGNIVIP CLYQKL
12705	26606	A	12833	654	321	LVGIRFLKVYFNIFPHLLAIIISPSLE VFNLQHFYIYFLLFYIP*ETRSCSVA\R LECSGVIIIVHCSLKLGGSSNPALASQV AGTITAHHCAQOHFCILEKSNLCTYFPL
12706	26607	A	12834	867	201	RQMSPTLRTKSRDVASRSSFSAWAWGKL FTFWDFSMSLVSLQGGPFHSPQP*TQ GR*VENNQEPATPFPGPERSLPQPRRL EPAHSGKRRGLPLEIRPPVNVSDIHGDP SGAQWLVRGVEAGPWAVGGQAP*SEGPS PSPPLDVSPDPGSSSLPRSSSP*MDLRA* LSLTF*TFQKSGN/DPASSPA\GKPG* EWRKI KGPPQGLLLGPEMWGSQARVLS
12707	26608	A	12835	328	1365	YAFCLMMLDKKQI*AVFLFEFKMVHKA AKTTQNIISNTFGPGTANKHTVQWLKKF CKEESLEDEERDMGHGKVDNDPI*BP\Y *TT*KITEELSVDYSTVIRVVQHSKQIG KVKKLDKWPHELSGNQNYRFEV*SSFM LRNNNPFLNRIVTCNEK*ILYN/RPAQW LGPRGQLQSQFPKPNLAPKKRSLVHW/ SPVGLLAPILDPTYSFLNP/GGETITSE KLCSGKLGKMHGKLYLLPALVNRKGP I \LLHDNT/RDCVFAQPVQLKELG\YK VLPHPFPYSPDLSPSDYHFC*HLDNFLQG KH/SQHGAENAFQEFVKS*STDFYATGI NK/LFSHWQKVCDCNGSCFD
12708	26609	A	12836	7	328	RRERERERERERERERERERERERERER ERERERERERERERERERERERERERER ERERERERERERERERERERARV*EKST RYKSPPPRIPLRR/RRV*RKHPHARAL SFFLYKKCTGGERAPSPVCVGGKFTW
12709	26610	A	12837	219	350	PFNHTYATWSIIISNVQVCFMRAQDIYL LIYLF EAGSCSVA\RLCSMDIMLHCSL DLPGSNNPPISAT*I
12710	26611	A	12838	189	359	LGLDGMVRVGPCRALGPS*EEKSSRVQW LTPVIPA/LLEAEAGGSPEVRSRPAWP TW
12711	26612	A	12839	368	77	KNPNFLKFGSKPMGPPIYSPP\LEG*AG GFINPGF*TPPGYMGKPPFLKYSNLPG LAAPGCSPPFGGLGRKISFTPEMEVSI NPGSPLSLPGEQN
12712	26613	A	12840	16	173	KTDVHSKCTKLF TAALFLIVKKWKHLK PP*VD/EINKMWYNHIVEYYLAIS
12713	26614	A	12841	425	45	NSFVFFFLFENRVLTVPAPRLE\CTGV IL/APHCTLPALPEFKRFLVPSALLSSW DYRPVPMVPLNFCIFVETGFH\HVAQS VLKLVSLKL/PSPTWDVPKC*DFRYSVR CCGLFF
12714	26615	A	12842	237	375	LLLVVVYILKKLW\LGVAHACNPSTLG GQGGWIL*GREFETSQVNM
12715	26616	A	12843	21	325	TSFFFLSYSAQAG\QWCDPGSLQPPQ PG/SQ/DNPPTSQ*VAVTG/MHHARL IFVFFCRDGILLYCPGRSKIIFSSCIRE LFFKISDFFLLTMLIFCNSNKG
12716	26617	A	12844	369	58	PISPLQFMFLPNQSPYGPFFWKKKNF PPFLLGGAVLKTPGF*NFLFKKIQRGFP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PPFKKKKPRERPKPCPPKFG/SPFFFFFY PGFPPPKKGPFFFFFFFFFF
12717	26618	A	12845	211	409	NALKPKIHFFFGGGLKGIWVGNLTLLDI GLHKTFFF*GDFYAL*I*AENALFGG GGDCAPHLQVK
12718	26619	A	12846	200	33	QKTNNKCKWQGWGATGTLIHFG*GEFTRV QSHWKIVWKFL*/SLNILP/PSSSSSSS SSSSSSSVKNLCLHKACTWMLAALLLL AKTWKQP*CE
12719	26620	A	12847	416	125	KIPTRPKGKGGPPLYPRPFRGLNKQIGLT PEFGTPLGNKGKSPFFQKNKN\NWPRG GGPIGPPSPGG*VGGTLTKGEVSTKLD PPAPPPGGQKWPLP
12720	26621	A	12848	85	397	KIHFFIFLVSLLKGLSFLLTFSKN*VF /SFIDFLILCVCVCIEFYCFILILFHYF CLFGPCLFLMFVS*QSLDFYFNSF/YI F*YKIQCYKF/CILIF
12721	26622	A	12849	1	246	RPRRHLVASLVLTLQNGSSPLPIKISW AWWLMFVPTFWAEVGGLLBPRSSRQ* *AMT\SPCPPAWAT
12722	26623	A	12850	161	1	NKTTSSQIW*EMPTVSTT*EAEVGGSLR PRS/L/KLKCAMISPVNSHCTPTWTTK
12723	26624	A	12851	65	244	STYVLHSLPFLDISYKWNHTTC\SRVFM GALFLIAIK*KQPKRPSADEQI*T/IMW YIYTLEYDLAKRNEILHAATWMNLKN IMLSKRSQTQKT\HVV*FHL
12724	26625	A	12852	235	34	TTIAVSVLILKELMEP*TLQPDPLG/WS LITESVDHVQWHPVIPALWEGEVEGLL EPRSLRPAWATW
12725	26626	A	12853	168	453	CQLRGASGTQGPGLSESQCCQPCP/PEC RPSKERPCGCRISPARTSPQPSAASM ALPTNERTPPPAKW*PK/CPKQSPQSA KSKSEPVKSTERTAK
12726	26627	A	12854	244	3	ELQVYMHY*YI/C*SIYTKANIYIKYM HMCVYIYTHTHVCIHLYLLRHGFG CWLMLGKVRGCEGMAGLMKAQQGWG
12727	26628	A	12855	376	428	KWEPGGHTSFFFFKGLVLNFGRGVLQKT RP*GGGQGGKFNPNFSGPREPPPP/PPP GGGKKGPPPPPGVFVFLEKGGSPILPR GVLNPGAPKGVYTQRGGIKSGNQGATPL SFFLKVWF
12728	26629	A	12856	129	395	APPNTHPFLSEAPQSLSLRPPSPAPSN SSSR/PPVWRASQTHPPQDWSSHCSPW GAPPQI*PFSDSLAHPQDWSSHCSPW GAPPQI*PFSDSLAHPQDWSSHCSPW GAPPQI
12729	26630	A	12857	363	97	GLATLRLVSNQAQVIRPPQPPEVLSL PKC*DYRPRPPASLIHVNSRQT*KVAP /CSKPLAAAHQGSFGATETTRCPSR CGPIF
12730	26631	A	12858	322	361	KSEKQS*VMLAVCTLDMMKMT\FISVVF LPKTHN/LMSNYKKNTRQIPMEGHSTIY LTRIPQNCQGHQKQ*KSEKQSQGESKKK
12731	26632	A	12859	88	417	HFTFFFFFFFFFFKRGGFFSPRLKRLGKN FFFLDPPPPG*RDSPSPFKEGGF*KP/ SPPLVFFFFFF*KKGFFPLGAGGF*TSG PGETPPLYSPEVWFFYGGTPTGPTFFF
12732	26633	A	12860	217	2	LILINKLANMHCFLVFETSLT*AGVQW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						HDL/GLLLRLAPPRFKQFFCLILPSSWD YRCALLHPATREDEA
12733	26634	A	12861	375	145	LSFFFFF*KEGSCSVAQAGVQWHAHSSL QLQTP/GFSDSLNSAFSVPVRVHCHT RPLSPFNICWRARPQKQVFL
12734	26635	A	12862	525	852	NLLSIYFFETESRSVAQAGVQWCHLGLS LQPLPRF*IKKPSNTALFM*NLLSIYFF ETESRSVA\RLSCSGAILAHCNLCPLG S SDSPASTSRVAGVHHSHLSWDYSCAP PCLANFFVFF*VETGFHYVSQDGL/DTS *PQVICPSRPPKVLGLQA
12735	26636	A	12863	3093	204	EPDKTGPVLWVKVGGARVPGMAETLSGL GDSCGAAGAAALSSASSETGTRRLSDLRV IDLRAELRKRNVDSSGNKSVLMERLKK A IEDEGGNPDEIRITSEGNNKTSKRSSKG RKPREEGVEDNGLEENSGDQEDVETSL ENLQDIDIMDISVLDEAID\NGSVADC VEDD\ADNLQESLSDSREL\EGEMKE \LPEQLQ\EHAIEDKETINNLDTSSEDF TILQEIEEPSLEP\ENEKILDIL\GET* RSEPVN*ESSELEQFFAQDTSSVGPDRK LAEEEDLFDSAHP\EGDL\DLASEST\ AHAQSSKADSLAVVKREPAPQPGDGER TDCEPVGLEPAVEQS/SVAASELAEASS EELAEAPTEAPSPPEAROSKEDGRKDFD A\CNEVPPAPKESSTSEGAD\QKMSSPE DSDTKRLSKKEKGRSSCG\RKFLGLVG LSSTTRATDLK\NLFRQIWGRVGGAPRL WTNARSPGSFAVYGFVTMSTAEATKCI NHLHKTLEHGKMISVEKAKNEPVVKKTS \PKRGSDGKKEKSSNSDRSTNLKR\DDK CDRDDAKRCDESVESK\DKNDQK\ P GPSESRATKSRKSRGPKRTVV\MDKSK \GVPVISVKTSGSKERA\SKSQ\DR\KS ASREKRSVVSFDKVKEPRKSRDS\ESH S RVSESREREQR\MQA\QWEREBERLEI ARERLAF\QRQLERE\RMERERLERER MHVEHERREREQER\HRE\REELRRQBE LRYEQERRPAVRRPYDLDRDDAYWPEA \KRAALDERYHSDFNROERFDFDHRDR GRYPDHSV\DRREGSRMMG/SIREGQH YLERH\SDPEPH\QDLSL*LGWGYEL* Q*RLS\EGRGLPSFPPGAGRDWGD TWLE DEDDPVMGKGTAERGPMMDR\DHK\RWQ \GGERMSGHSGPGHMMNRGGMSGRG SF APGGASRGHP\PEGGMQGGFGGQSRGSR PSDARFTRRY
12736	26637	A	12864	2	456	IHLGSGSEGDGSSGGLGRGNSNTRSFSS SSWARGDNVPRPPPAVCSWISSEGDVQN PGLGEAGAGSSTPGDGGELRY/WPGLLG A*GRGIGGDDDLRTLGLAGVQCGKG/ RRGPRGPRGQEPRRPRDLGLRGPRAQ GAA/SATAAPPP
12737	26638	A	12865	388	1	LIKMTKVKKTATK*RGWGRGTGAFIHC SWECKMIQPLWQTVWQLLKKLNLYL\WK QPKCPLM/VKWKIKLYISMDSYSAVKK ETLMYTTA*MTLEVALLSERSQTRKGER GHILWDSIYINFQKMQTNL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12738	26639	A	12866	198	3	KKQKQTKNPPKIS*ALWCVPVVPATWGA KVEGSPE\PRRSRLQ*AMITPLHSSLCN RVTRGRTRG
12739	26640	A	12867	415	973	NPVNCAQFSLLPTEYMGHRVEGATGHG TCPSVPPNTHLHTGWCLQHHRSCRAWG RGGSHTHRCQRPVDPGEHP*IIYIAVHGE PP/ESPPQPSPLSCPPQGNIALREPP QGLPLPGTLPSPHPPFWHICKTHSSSR HPFPFGFCGLELEKGVDFIIHPLTLPL KPLPNPLKPEPTPTPQTHI
12740	26641	A	12869	715	893	PCVAPHISIREERFRLTSESTNQKVLWWG ID*T/VILILTGNWQKRHLKSFFLGQKP GGMAP
12741	26642	A	12870	342	58	KKKKPKENEQSIWDMWDFNRTSDI*TTG VLBEQFRE*GRKII FKEIVRENSNLTK /QINLLTQEV*TTT/HKNMNSTPIHII IKLMKTTTKEKI
12742	26643	A	12871	110	401	SFYSVMILKASRIVICLPT*LYAYIHTL YIYTLCIYAYYVNIYICTHI\NIHIII HVYTYIYVYASIIYSMYSAWYNIKVS RQTYENIALITY
12743	26644	A	12872	439	256	SYPMRFGGDKISKLYQFILSRRWKQSTC PSMDEWINKMWH/ITIMEYYSAK*RNEY SYMRHE
12744	26645	A	12873	356	43	GTPERHSHSHSQSPFIIGAFMGIRASV YSLLSCVLLMLSPQRVLFYFSAFKQQQS \WSGKVAQAYNSNTYKAGSIT*GQEFK TILGNIARPCFYKKKFLANS
12745	26646	A	12874	341	205	REIKKMVLNKKFSLQFLGKKKNFWEFF LKKKKKVKFAPPVQF*VPIF/CSF*KK KVFGFFFGPKIFFFFFFFFFETESTSV TQBFNGTILAHCNLGLQSSSSPASAF* VAVSQDCAIELLGDGRRLCLEKKKKKK KKNFGGKKSKNLFFLKRRKMG
12746	26647	A	12875	474	206	PIRANGPVFSPPPPPAPGTCPHPLVIM LSRHLRQSHPHTTVP*TSGLLPSPPA* LSLETQHFKTAHFIFP*H*SSGLGPGWG SPVGEQPG/HPKLCQPAAAAEAWPPRE GTKARRHEGLPPAPCANGPAPRDAGSRL EFFTLPTIPVSQSPGR*HGAGGRPSCLR AFVPSRGGQASAAAAGCRQSFGDLALLP LGSPILGQGNFSARGR
12747	26648	A	12876	257	467	YRVFTLLRLEYIMAHCNLDLGSSDP/P QVAGTTLK*LSRASRVAGTTGVHHHSWL IFK/YFL*RRWRFFSL
12748	26649	A	12877	867	1409	GPTVLVGGQDWSVLQOPRAHSFTPRGG AGGLGGGYVLHKEIPFSQELLAGFPQK QYRVPPPLEAQLLRQARSPAFIY*AAVL CQAQGPSPPSPMVSPPRPSGRAPHIGA APQSGQKALASTSSPDAEPV/SVG*WCP SNPALQGGQNGAEPRVSIITSGALSLYD CFLDGWWEGRSLGP
12749	26650	A	12878	1416	740	IRNPRWQLDVFAAAPMGRSSPLFLLLF SFLKTVLRGSMIPSTVPS/FHKGPOACL YSLSLRS*SQAAPSAPSSSLTPSPHFG LTQPGRRRKADIS/CSHSAFYVP/SL PHLPWACPLSLPQPVLSILPCFVLP*D GVLLCHPG\WSAMARSWAHCNLHLPQFK

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						QFSCSLPSSW\DYRCMPF\GLG*FLEF *VEDGGFTILVRLIWN*PQVIHLPPPP KVLGLQA
12750	26651	A	12879	961	31	PSPVRDSCVWAGERRGLGGSGVWRSH ARGPGLMRGLPASEPAPCVLGSRPCFRV AFETPWTSPASCMFERCPLWRPPALVAA GLDPFLLSSTLTAVCPDRDLIRSWKKGC DVCDNRNCWSTHSRPACRDAILAPILAG RGECIGLWG/AAAACTRV/TPVSGLT STVDFSSARG/V*GGLPRSTGGPRVRG PGQPVPLPGLPAGVALAPLEGRPQBPAP ALSHSLTGSFLGAWLCCGTRHGRAPVL LEVSIVACGQLCRAAPQIFIQPGLQLP TPSATSPAYLWVDVLLTLPSTVIRKQKRV SFLTKE
12751	26652	A	12880	232	28	PALWVPVAREFDGMEETGQNHWSKEKAW PGAVAHTCNPTLGG*GGH/MT*GQEF TSLANMAKPRIP
12752	26653	A	12881	331	1	KNGPFFKPNPPEFFPPPKWGVPPNPTPYF PWPEPI*LTGPGLKKQKIPFQ\KGEIL GWGGKMGNPLPFWKGGPPRESKSSPRF YKTPPIFKKKKKGGSSRSRTSPRV
12753	26654	A	12882	370	287	VSILAGCCGVAMIDNTVLVHKEVKILRK *IIKK*CI**FRGHSK/HNFSG*AWWLM PVIQHFRPR*GSLEARSRLPAWATWQD PHLYEK
12754	26655	A	12883	656	1168	EPSPRGVWPHEDARINGSKKKKSKDKKRR REDEETQLD/IVGIW*TVTNFGEISGTI AIEVDEGTIHALNGLFTLGAPHK/ER IALKPGYGKYLINSDELVV/GRSDAIG PREQWEPVFQNEVRNGGPAEMGEEKRN GTKWRETDHTSFPLFPSTGGQPKAHSN WRKVCH
12755	26656	A	12884	205	452	ASGSAHRFRFTSPETGRVLDKPSQTDHT NRKRGGPNVK*SFL/WLGAAAHACNPNT LGGRGRTA*AEFRTSLGNTVRPCLY
12756	26657	A	12885	112	290	KYNI IQNIVFSCHDPLVSFNLFFFFFF GKGGFPLSPRLKARGRVWGYLNPPLPGK RNFWAPPQGFEEKLGLPPP*SPFPGGVG QAKNLGPGFQPPAPMGKTPFF*KQNN PNWGGQPLNFKTLGGGGPKISF/PPGGG GLNNPKPSGPSTWKGGNPLSQKKKK KD
12757	26658	A	12886	406	190	TRSLARGGFRPLQKPYWNEQSFIKAKK \YEQKCPWTDKWNKMWISLTVG*YAA MKRRDVLTCATITCR
12758	26659	A	12887	440	160	RVCVCVCVCVCVGVFCFALWLSLIYN *VYLFVHNLGRVSFSYFLNLI*FFEH VNHV/HNYVQMIQNTKLYLKSYLETFH/ CPC*FPPIILH
12759	26660	A	12888	201	411	HIWDVILIRHALGNFLTSSICYIVKIWL DAVAHTCNPTLGGGG/WIT*SQEFKI ILGNIGDPLSTKKNK
12760	26661	A	12889	138	464	SCTMNPSEMORKAPFWRWRHRS*APSTH KMNRVMSEQMKLPSTKKAEPPTWAQLK KLTELA/TKKKSLENTRGTTQTSKNMLFA ALMIVSTGCAGVPSSSKETATIEDKP
12761	26662	A	12890	146	366	FSVSMKYFV*IH*FYHL/KLLLMVYL*Y

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						GFLAINTSONISCSQKIMKHL*GRGVV AHACNPGTGG*GEWMA*AEFNTGLSN TAKPYLDF
12762	26663	A	12891	368	50	KGRQSGVSSFPVGTVTNYTNLVAHNNRY LFPSPGCGTSEVKVLA\GCSLLKASRG EGFFPLPGSGGSKCPLAYGCITPISASS CDLLWVCVFSSYLAY*DTCHWI
12763	26664	A	12892	227	456	KLTTLLKLFKE\IEDRTLKSKSFYEVST *IPSSSSSSSSP/ISLINTDAKKINKIP RNRQQCIKKIIFHKFSTGIYS
12764	26665	A	12893	461	89	IYQNLRSRKPNDIKW*RCTEIQTILHC W*QCKIMQLLWKIIWQFL*/ELNTEVPY DSIPLLDY/PKKTTC/YTSTQTLIYCM NPIEYSAIKRDKVLIHATTWMNLENI/ ISKRRSQSKSTYCMPLI
12765	26666	A	12894	222	185	RIVMQYLHLNLGACVCVCFVCD/CVCL CV*MCVHIHIYISTHTYIHIYVCM*ICR LS**CEFYS
12766	26667	A	12895	186	166	IFFFFFEMGSHSVTQARVQWHNHSSKQH PPP/GASDPPTSAY*VAKINIFFF
12767	26668	A	12896	55	485	TCWDCRDEPPRPALLESVFLTSFLEDEFS IEIADLVPHPTPCSHPLQPPP**VIYFC S\KPLVTGSSPPRKPFPSLHEPKSASL *PPSSTIQVRSSPKG*PSPPLA*VQFP KGMTIPTLCLSPVLPVPSTIPLNVSKP LPFY
12768	26669	A	12897	923	312	VDVIRKVOIEITLRCHLIHVRIAIKKT RANKCW*GCGEAGALVHC*WEC/NYILV QPLWKTWVRFSLKLELYDDAIPLLG ISPKGNEII/CCTPKFLAAQFTIVKIQT QPRCSSMGKWKLL/W/HIERSIDR*LE YYLAFKKKAVLSFAKTWIDLEDIMLNEI SQTQKEKYCVISLIGIRKKKVKYIEIE NKTVITKVRIRWK
12769	26670	A	12898	320	3	ESWRWGRIVRPHSVPGETWLCVPVPPGP NAPDGSFPLAICPVPPSCRS/CPP/DD CLASAGV*GGFPLRTEASPHHSWACPQ EQWPPQCKLKVGA PNSTALSEGS
12770	26671	A	12899	138	447	IFVFHYKTONIYNEDTLHVIIINLWCYP GSYIKSTGRLRPEVERGLGPTTMC**FS SIKNIFYF*KLKSYRKL/WLGTVAHAYN PSTLGG*GRWIT*GQKFNRD
12771	26672	A	12900	279	1	INQSIHNNIKSTYISQCKLIQP*WKIIV RFIR/NLKIellyVPATPPVGV*LKELK SAC*RDNCTT/M/FTAALFCIGYGSNLG NSTALIGSRVLP
12772	26673	A	12901	235	183	IINVGSGPPEKKKKGGKKIPLIFYKKIK KFLWPKKKLFGGAKNPV*AHHIFTV* IDVTRADFTSATI\IIAIPTVGVFS* LATLHGSNMK*SAAVL*ALGFI
12773	26674	A	12902	180	19	LFTYLFYLFICIRCHFVTOAGLQW/L IIASCSFALLGSSDPPTSAS*VKGI
12774	26675	A	12903	406	949	APVPGHGFVSVF/CGENGVSLYCPGRS* TPGLKLCCL\CLPESWDYR/R*APVPG \LGFVFLTL*KPPFFKDYMKSLFQFLK YLIQG*CTLV*GVRYRSSFIFFFFLRR SLA/SVTQAGVQWRDLGSLQSPPPGTFP FSRLSLLSSWDYRRPPPCANFAFVFLV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspon ding to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EMGF\TVLTRMVWIS*PCDPPASASQSA GITGVSHRARPKFVLYFKDNGEPLGGVL HRSHIAVHWM
12775	26676	A	12904	265	385	GNGSPSLRWIGVLRGRSPTLELRH*PIF LTAASRRSLDRVSVPWMTPLSEPLSIE GLVSRYLTTNNLMERIPILYRN/PFNNET M/PESLCYRVLIIFLSKGYPRVKGRLDTC YSPVRRSPAKKASFLPDAPRLACVKPVA SVHPEPGSNRTRG
12776	26677	A	12905	363	137	APGMQA*WCM/HCI PGAQAEAEAGWTEP RSSRLWCTVIMPMSHCTPAWATW
12777	26678	A	12906	315	565	TPVDHGWLECSGAIMAHCSLKFLGSRDP PASASRVAGTTGVCHHSQILFLFFVGTR SNFVAQAGIELLG*VILLPQSPKVLGL
12778	26679	A	12907	376	412	DAWPTWRNL*FGVYVMTDR*EPROMLTY LTA\PLKYFKSGVMAHSCN\PTSLGGQG RWIT*QOEFET\LANMEKPCLY
12779	26680	A	12908	215	2	NIHINGQKLPL/WLGVVAHTYNISTLGG RGGKIS*TOEFETSLANTVRPHLHKQK IALPLPLPLPLPTVR
12780	26681	A	12909	307	379	KR*KQPQYPLTEEWINKMRHV/LQYYSI LKKKEIL
12781	26682	A	12910	279	123	KMILSWARWLMSIIPAAWEAEAGGSVEL RS*\LRLE*AMTVPLRHFTPAWARE
12782	26683	A	12911	1	194	AKQHIPLLARLECI/GLFTNTVTAHCSL ELLASSHPPASAS*VARMTECVHRAWLE WIFLVCVIL
12783	26684	A	12912	206	388	IELSKQGPVYKWKYVRITPPYFPFFFFFF ETGSCSVT\RLACS/GTITAHCSNLDPD LSYSPTAAS*VAW
12784	26685	A	12913	238	426	TPLLPSQQLKESLWLGVRVHACNPST LKG*GGRDS\RGQ*PETS LGNIARPLI REKFLKI
12785	26686	A	12914	115	1436	AKDRHFTFV*IANQMKRCSTSLGMRBM QSKIVRYHLSE*/R*LFFFGGNCWQG/ CKK/IQDLIHCWECKMVQPLWNIW\RF L*NHTCICHASGIALLSIYPREMKTCVH TKTCIRMFIALLFVMVETWRQPIYPSLG G
12786	26687	A	12915	282	21	IKFPPPCPSTWGTKKKLFPPKKKEVMKML CFHFNLLVQNIIP*YRLGNEISDKAG\PV AHAWNPSNLGS*GELIT*QOEFDTSLAT IVKL
12787	26688	A	12916	254	150	TLPGRSSDFSLPEV/YLKKNNH/WLGVV AHSCNPSTLGGKGGWIT*GPPHMLKVSF LPTDPTSRVKQLYNWVPHSTVLIALFPT KNPG
12788	26689	A	12917	181	24	AQWCDGIPVSKGNL/WLGMVAHACNLST LGGPGRWIT*QOEFETSLANEFHRTD
12789	26690	A	12918	75	298	LPILFTS*VD*MRPTHIKENNL/LAQST NPNVHLIQ/KHPRHSQNRVWPNVWAPH G/QSSCHIKMTIMARPSGSQSL
12790	26691	A	12919	251	9	KFMFLARCGSRL*SQLSGRPRRADHLR PGVQNPQGHSQSQYLPKSTNFCRVWWC TPVVPATREAEA\GESTEPGRQLQ
12791	26692	A	12920	198	211	RFCSVGDEREKRA/RENRETERKKQ TEDTETQREERDRDRK\ERETDERER PREERHTEREKK*KAAFPQTLGCRAQD

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						FEKQLFESRGWGVGPMIVLL
12792	26693	A	12921	438	127	RVVMERIFVRPHIKDSMWVVRSTLLGRG DALNDLFLYCWEKEDPRYKERP\REERER ERERERERDRCWEK*APGWRERPVSQSLR ACHPPWHRFALAGPVPSAQ
12793	26694	A	12922	158	460	EARVELLSRCKPRAVITAETQPAVYR LQLEIENFPGLSPRLCSGAIHAHCSLD LLG*SDPPNSASR\AGTTGMCHAQIVNS CKADWLVLSSRGLTHR
12794	26695	A	12923	33	484	GIQAACIPGLRLSPADAHCHRHPSP PSSTAPRDDVGPMQITPDNFPQDPFL\ TPPSQSLLPHRAP*PQGSSVDLPGLLFK LPQMPQTPGPEEVDTCVQIHKTSKARED VQMRKTPMAREGRHRAHRWIGALGKAP QSQRRLRHITVG
12795	26696	A	12924	335	332	RIKVYVRGHAK*LRPGP/VAHTCNCHT LGGQGMRIITQAQEFETSLGDIGRPHLYK KKKKKGGPF
12796	26697	A	12925	302	407	AQWLMAIIPAPWEAEAGGLLEPRS*\AW VTW
12797	26698	A	12926	766	244	RVPRLPPAL*LEFSPSGLRLARSHSFQ LRSSPPVSPST/PFSPHRSPLSLLS LSVPS/PPLHHSFFSQRAHILPPPLI FPSSPPAPPPPPSSSSSSSSSSPPPP /PPINWGTPRFFPPPPFFKNPPPEINFGG PKKKKIFSPRA*KPVFLKGPPPPFFFFF FFFFLGINLL
12798	26699	A	12927	127	720	WGGLLESTELQSLPGLVSVIFGKIF YISGLGICCTKIFPSALPSAQAASLPL PARSALGIVFPLHFC*IE/CNYKKLP HHI*LIKTFSYGLT*LEFFFFKTKSLIF SPRLNCRGPFLVN*NLCLRG*GNSPA*P FGGAGIEGAPHKAGLIFGGGGGAFLLKT G\LHHVAPGGASNSGTGNISHPPLNPPK GAGE
12799	26700	A	12928	308	49	KEHW*AVGHFNICVTGGP*GERKKGTER VFKEIITPNFPNLIQTIKPKTQETQHTP SRNTKI/TPRYIIKFLKTSNKEKILT TAR
12800	26701	A	12929	375	2	GCMLSLKTINILEVLANVLAQKKIKRRK LND\BQADTTFTI*PCVRQTKKSTDKL VKLI/ERFYKVATYMINFLKKSNSFHTP ATINC*KQIPFIMATKTIKYLINPRKK CVRFGKKLTFPER
12801	26702	A	12930	202	379	SSENFSGKTVNLCCGLRLHRMISWLHTV AHACNPIT\GWIT*QGEFETSLADMVVKP CLY
12802	26703	A	12931	209	376	TVGEKMYLKVKRI\WLGVAHASNPNTL GGQGGWIT*QGEFETSLGNMAKPHLYKK
12803	26704	A	12932	280	31	ISCKVTKKVTLFELKYIWNKFYIYERVS IVGTTEDAACEVTSNVITGPGAVAHACN PST/RGRWIT*GRELKTSPANIAPRLY
12804	26705	A	12933	1	189	QMYTESEP*CKLWTLGDYNNV*M*FIS*/ IQCTTQAGNVNIRE/RLCMCSGGEYMRN LCAFLSILL
12805	26706	A	12934	108	409	HHSLLKLPNVWFSFCHFIVTVFLSL*R VFFVY*IFLSSSHFLFSFCFCPIPMIM FPFKFILSCNIVFI*NIIFFL/VHV*G

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						*STLVSLFVFFFLQF
12806	26707	A	12935	225	11	ILLCMEPSFLFWFGFTCFVKTGSHYIAQ VEVLWLFSGMIKVHCSL/KLLHSSNPPT SAS*VAGNTGSSYCTW
12807	26708	A	12936	74	12	GTTHASAGVINILVFIILSVFLLTHSLCI HISKYMFVYICVCICTRTDFYTFKSF TFCFFGSSFFLEKKFPLVAGLEEQKGD LG*LKPPPPRLKKFSCLTLP/AWE*RT NG
12808	26709	A	12937	166	311	PHS*WECQMVRAPELENWQFLTTFKIRGL PL\DAALPLHM/CHRSCTQLFIALLI VAKKCNHKKNL*ANEWINKM*YIHTTDY PLAIKQNEILIHATTWMNVTL
12809	26710	A	12938	51	296	LCMYTLHTLYMHTCIYAYICYTCKYIHR Y/LHT*IPEDANSVKHKYTHTHIYVHTL VYPHTTYLMCSYIYSWVCVCVYIYT
12810	26711	A	12939	426	28	KGFNLVNPRVFPSPRF*TPAPVFYFCGP IKKIFFFKAGGVKFDLSKRAPLFFFLK TGSCFVP\RVECNIGITAHCNLCIPRSN DPPPSDLQVTGVKPPP\AKLFFFLW*M GFHHILDYQGETCLSQLLGWR
12811	26712	A	12940	11	213	ATAPGLFSFFETGFCSDQAGVQ*HDHG SLQP*PP\GSSDPPALASQSARITGVSH CKGPBHTSLLT
12812	26713	A	12941	416	38	WLNNHSRLGFFPNCWDYICKLPRLGPDVA SLLIHNSS\GTWYGATKLESNWYFSIPI YKDHQK*FAFTWQQQYTFVLPQDYVS SAL*HNTVHRDLDDLNDPNITLVHYS DTMLDLMSRKYQAL
12813	26714	A	12942	361	74	IIHPSFSVSSRNIIHKNAYPAALGGYSVY GVAILLFHYFINKLAFTLHCGLA/LNSF LR*IQEPPLG\SGSGPFCNVFLAPTEG TIVQKPDPMATFG
12814	26715	A	12943	125	401	SSFEPRGIPLNPRVAMQKESVNILCSPR SQEFLESRIKIKVLTDLTQDEL*GOAQ* LTPIIIPS\IWEAKAGGFLEPRSLRLRSC HCTPAWVTE
12815	26716	A	12944	92	306	KRTNSPWGCSAY/GVAILLFL*IL/KL LAFTLLHGLPSNSFLRKIQEPSLG\SGS GPIFGNKLVAFGGLMIVVS
12816	26717	A	12945	322	24	NFKKNINLNPFLRGYFLFLKGGFGLTFK KVGEPLKKKKKLNQQFYSYFLSTYTVK* NN*/WLGAVARTYNPSTLGGRGWIT*G QEFGTSLANMVKKILAK
12817	26718	A	12946	2	448	GGAPMKRHGSLDRNRYVDITRPSQLFLF QLYHNYLKFAYEATKEYMHRKETCLPC PAIQSFPPKSNLCYRGYLCMRCTAHTQM *MYRYIYTYVMHIYICM/YRAICTYTYT FE*KYILQKICILLCIFLFLQYLYKVS LNRHHFLIAA
12818	26719	A	12947	155	415	LLETGGNAGCSSWMHVLLGKIHRYGMGS RPISLMAG*\GPPWLRVAGLRGRPATL GLRYGPDYGRQQW\EYCTMGASLMQRR RVRD
12819	26720	A	12948	247	250	KYVYKYIHIYKCVYIFTHVYGYTYLYT DVYKYTYLYTDV*ICICIYKCIYLYWYI YIHLINMYIYIHLINMYIHIHV*IYI HIYI/HVYIYIYIFLYTVYK*IHIEVC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EYIYTLWKLL
12820	26721	A	12949	25	407	EALSLLLLVLVGLLLGIARKMYQQMNL VQYCLLVLP*P*NL*EQKRFEREVLGDR EP*FHVLCIHSKSESRFWSW*EL*IRK LTLVA\GGVAHTYNPNTLGHRRRIT*G QEFETSLGNVVRPLFL
12821	26722	A	12950	370	106	ILYLETLKSFISIRSFSAVDSHFEEKSS TVGKMLPNSITCTDPI\FNKKKSQMLMWQ SSLLPFSQKLQSPQSPVSPSPSRQGS IPATR*QLA*GSVQVMLFGSILPTVELF SKWESTAEKLLILINDFSKVSRYKIYV
12822	26723	A	12951	280	319	DQPGQHGKTLF*VSH*KKKKGWM/PGVY AYNPRLGGRGGWIT*GQGFETSLANMG KPCFY
12823	26724	A	12952	337	113	YQLAISLLGICPRDLNVTCS\SDTCTQ MFLSVLLMVAKR*KQPKYLQIDEWINKM QCIHMESYLVSKGRKYLCKL
12824	26725	A	12953	9	186	DPTVCCLODTHFTYKDTNKLKVMGWTKY /CHANGNQKRAGVVIQIEYP*SKSLKSE IVQN
12825	26726	A	12954	46	381	NENTYSYKKNQMFIAALFVVTNPNWKQP TCPS/SGEWINKLL\YHLMVYSAVKTN /ILVYVATSVNLRILILGKQPDKKRVLT V*PHLYRKYKLISDRKQIHGRLEVENK GK
12826	26727	A	12955	19	250	CSDMVLKACIKKLMYSKMGHIQAMDYY TAL/NKEL/LMYATI*ANLEDIMLSKIR QTQKDNCLMVDCIYIRYAEQSSL
12827	26728	A	12956	173	163	GAHSAAGTGWIRKDFTRPGAVAHACNP STLGG*GGWLSRSEFETSLTNMVKL/CL YKSI CCTRCLLGCFQALSKAID
12828	26729	A	12957	301	79	EKDNQPLLTNRNPNVLHAIKESENHRIT ELKVTLRPDVAHTCNPSLGGRRSG/WI A*GQEFETSLAKKVKPCLY
12829	26730	A	12958	314	126	KHHHFKKHNFRLVCVCVCVCVCYKHF YLFSLSFSQ*P/CICC*CVCCSFLCCF *SATYLKII
12830	26731	A	12959	529	1697	VPFMGHISNFFSPFLRQKYLALLPRLG VQWQ*SRAHCNLRFPQ\SSNSHASASRV AGITGACHHGWLFFVFLVETWPHHVG/Q AGLKT*PQV\SACFSLPKCCDRRCEPL CPATSSILNL*TMDRL/PGEKPNQ*NLL VSFMCVAFYREGQGHVYFQSLWCKREF IVRSPWAINLEKGGRLRMGAV*IRIMLNL TLT*GFCTEDEKTVNSRVNQKLTPT*LG DE*DVKREKNINDEIKLLTCNSBYTKSY RLGR*IKLGAFCCFM\VPMGTGRNGQL KVQV*TGTVAHVCNPSTLGG*DRRITRV QEFETNLGDHSESSLQKIKLARHGAAR L*SLSL*VSWDYRCSPPWP\SNFCIFK\ RDGVSPYWPKA/WS*TPDLQSAHFSLE KVLG
12831	26732	A	12960	1	395	GTREFRILSEKFKKIDFFFFFKQSSP PPGPKKQTL/C*KQTTPTKPKQTNLGP KFGGQPKPKFKISHPQIGPPKKKNYNP* GQPVWNPPGEKKEGPTPPKFKDPGANLK VMGLKGGVKRRKGGKTFPQRA
12832	26733	A	12961	90	436	LWRLTSPKSAGWAGNLETQESMLQPKS

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						EGHR/PAESPLA*SSVLFSLSTDWMPRLI/MEGDLLYSKPIHFNVKISSKNITYRN IWNVWPHV*TL*PSQSD/CLK*TITPI VLLTCTH
12833	26734	A	12962	415	463	LRAKDQVLPKILVC*TLFPFCAQIKKKK K/WPGAVAHAYNPSTLEGQGGWIT*GQE FKTSLGNMVKPSGIPPHWI
12834	26735	A	12963	774	316	SISPTCSGKIGGKLNHRHFSKEDKTG\RY MNKCFISLVISECYLKP*EDTH*TP\LR MAKIKRADH/DKC*QRYKMTGTLIQC*R ERKMVQPLWKT*V*QFLKRLNIHLPPDSI PLLG\IY*RKMKACVHTNTIIMPIASL LVKAK\AKKQPKCPSR
12835	26736	A	12964	44	395	MYFTLVWGSILGPKPLGGHQPLOGGQPF L HFLKAL**FFPQTPGNGGGTPPAKTFF PFPTPLSSSPCPSPAEGGSRPSLSTP /SCLHLYIGGAASNPPSPPLPPPQCSG LGYPVC
12836	26737	A	12965	424	50	MAFFPLSCAPDAINNKKCCREINNEE PPNEPLKWRHIMIFFEABSHSFAR\LE CSDAISAHCKLCLPGSRHSPASAYRCP RHLANFSAFLVQTGPPRVSDGKDLQTS *SALLMPPLDPAIP
12837	26738	A	12966	245	44	QSKELGNYPLPSPSPSPSPAFHGLPPP SSPSPAFHGLPLLP\SWTVQPQ*RLTAT SLPDPPASPRPG
12838	26739	A	12967	205	30	QEGASLSRIKRGPGVGAWLGMVAHACNP STLGGQG/SWIT*AQEFETSLGNPHLYQ KYKN
12839	26740	A	12968	114	465	DPVSNPETTKPEPPPKTTES*P/EPKSL LWLPS\P*NSS*CANREQPPSPQHLP HPLPTSLQVHRLP**SLPPNLFTHLYD /SPSPSLLPVIQFPA*TSPP*PPVYSSP PSPTCPLH
12840	26741	A	12969	1618	1038	VHMVQDKDINLNNQFLSGTMLLFFKETS HR*DRGPGDF*SCLYSAPIPTQPLLF*Y LPQNFIEG*PS*NSRIKGTSLKTYISRV PSFFFSFL*DGVS\TVPQAGVQWHDLGS LQPPPPGFKRFSCLSLSSWDYRHPFLC PANFLDF**RRGFTMLARLVNS*PCDL PASASQIAGITRMSHTLPHVFFPLNV
12841	26742	A	12970	197	411	EQALRSTVCYCLNPLPPAPLRPRQDC\G PCRFRWMPGGRTRWLPVITL*EAEAQ VWLEARSRLRQAWATW
12842	26743	A	12971	616	777	MGIHGVHRHNAQLNFVFFVEDGGEWQLTC TGAGDSSWVLGEP*VFAC/PKNVLFYLH P*LFG*I*YQLKITF*NYEGMV/FVF RFLFETRSLSPQLECSGTITTHCSLEL VGSINSSISAS*LDGNT\GVRHNAQLNF VFFVEDGGEWQLCTGAGDSSWVLGEPL RYKRLIKWYL
12843	26744	A	12972	222	389	VITEALGSDELEGRQLNW*IKIHSQVQW LIPVIPAL/LEAKAGGLLEAKTSRPAWE T
12844	26745	A	12973	425	145	QIIFFLFQIKNQFNKASFKKMTLEQM TSRQKNSAQISVFKKKNSKWITDLNVTH *TIQLTGKN\NIGKNLQDQGLKEILNL TLKAQSTKG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12845	26746	A	12974	322	411	NNKKIFMSTS*KFFYCFIVQLIFETILS VRVLESIIILINYL*YCIICIFPFL* T*EIRKVTKFTSFQIEEK*KCRR/WLGT VAHTYNPSTLGG*GGRIA*AHEFETSLG NTGRLPSVQKIL
12846	26747	A	12975	428	1	SRKSSSQFRLSFFPSSHFLDLGAKGAVSQ DRAIALQPPGPRSR*S*RPSPRPRCFRR PRPSRSRSNKERAGEKRRPRSLQPRPP HIAGP/VPRRQGPSAGPEAPLATDEPP PQRRSGIRGGSANIRSKQTSSLRPRVRG RVG
12847	26748	A	12976	60	294	NHCTETVLFQ*LTCVCVCVCVCVCVCVT ERI/CFFKFLIGKGTGCIYLPKTFIL IFIYILYSPRGRSILKKKFFFLT
12848	26749	A	12977	6	341	DSLTLPLGLECSGATSAHCSLCLSG/FK QFSCFSLPSSWGFTG/VPPRMPQLIFPY FSVKTGFH\HVG*AGLKLIPASASP CWDYRREPPRPGDLWNF*PTGFKLRFPQ FPL
12849	26750	A	12978	296	42	SQPASLGFKSVLDLPLAVCPLGKITLTL WDFSFIIYIKQE*WPRAGIFMPY\NPST LGGRGGRIS*AQEFKTSLGNIKPHYLV K
12850	26751	A	12979	20	373	KLYGGIWFFFFRGLNSATQAEMQGHN LG*LKSPPPG*RNFPASASGEPGITS HHKAGIVFYIKKKPGLKFTLTKPTPPP SFRHWHQPA PMGVYSEILGEKSLTNGWD PQTKKG
12851	26752	A	12980	380	96	PVFPFPWRAQKGGSIGREIRPPRGNOGK PGPP*KKKNYPGGGGPPSPFFPEG*\n PKKWHNPGGGTTP*TEFPWPSTRGGEK KPPSKKKKKEK
12852	26753	A	12981	331	71	ELLTYSWVWCTPVVPATW*GRELVGRI T\KSRRLRLQ*AKIVPLHSSLDVRVPC PPPTKKKLANLCPWTEGSLSFYLLLEQ FHSC
12853	26754	A	12982	383	189	RRALKSCAHS TPAGPKNAALSQAQWLTP VIPTL*EAEAGGSLELRSPRL*AMIEP \CTPAWVTE
12854	26755	A	12983	144	6	ILAQ*KTWLSVVAHTL*S/TLGGQDGRI TGAQEFKTS LGNTRRPCLYK
12855	26756	A	12984	341	509	ETLYTME*YTAIEKNEIMSFAGTWLELE A\VIL\SNLV*EQKTKMLPCSPLMGWBL K
12856	26757	A	12985	387	125	DLPTTPPKLEPRTCSVAQVEVWCL/GSL QPQPPGP\SDPPA*AS*TAGTTGRHHA *EMFFF*VYFVQTSEHILGINPPGRHTK VAWEV
12857	26758	A	12986	151	350	GRGGF*PLP*IFPPQEREGFTPPKAPP PLGFFFPG/RFFFLRRSLALSPRKWRD LGPLQPPPPPTPGY
12858	26759	A	12987	251	1	RMSLLEKRNSNN*EARV/CGRVIYVATE VIKIMIGISMVAHAYNPSTLGGQGRRIA SAQBFETSLGNMTNPCLYKKYTHKKSRA
12859	26760	A	12988	320	3	TPWGVKDFSPPPPPGEGVFPGRAPPPR* KFFGNFWKRGFPNWRGVLFKFWG\KNF FPPNLPKSLGLRFKPPGPP*KAPPPFPL FFFFFEMEFLCCPGWSAVAQS

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12860	26761	A	12989	353	183	EYGHILTAAIFSLAKWAHR*GSLTDEWVRKNSSLQSM EYY\SAIKKNEVLLHAA P
12861	26762	A	12990	377	2	LSIILINFRFSLQRGKYPGPPPPKKNP POKTTPRAPKKKKPFFFFFSPFKKNP PFFFFKGQSKGGFFGPP*PLIFRPF\NPP PPPQKIGFKAWVFSTPPPIWGFFFFF FLRWSLALLPRLEC
12862	26763	A	12991	134	298	PPNSYCDGSTITLPKSDKNITRKEKYL/ P/IYLMTIDAKVFNKVLNRIQQ*IKRI I
12863	26764	A	12992	892	171	QT*SH/SLSRLEYSDTIIAHCSLKL MGS SDPPASASQVAKPTGHCTTMPQPHTEGF
12864	26765	A	12993	269	2	GLWCFVQQLKLTETCPHFVAPQFPLGIS KIPISILPFFKLLL/WPGTVAHTCNPST LGGRGGWT*GQEFGLMFHWPSPKFHGG QHGET
12865	26766	A	12994	324	4	SLYPLLFQAEIYFLVTIHRSSMESCIYF FSVVPLDSLVIQHVKI/HIKGIGML*V N*QNCFKINISE*L*YIWPSTVADTLGC QGEITRAQGFKTSLSNMTKPHLY
12866	26767	A	12995	106	531	WLLNLFALNDKGLVPMNRSRIFSQQK VKQRSFEGCSSFNDVGSCYVQTAGEQWL FTGVIGTL*PGTPG/SSDPPASASQAAG TTGS*HHIQLNLILYSSG*QTI*LL*TT DSTHLIFASLYAKEQLITFYFQATSLQP CT
12867	26768	A	12996	1	367	NTEPFLNIFFKDKVS/CSIAQAGGQWRL YSRCSLKLGGSSNSPTSASLVAGSKGRH HYTRL*LFFYVSRPQDYLWSPVFFFSF FLSFFFWKGSFFLPPSWKARAPIWVNGS LPPRVKPIFLA
12868	26769	A	12997	3	379	YRPSPSETKAVLVFFSFFSFFFLGTPGG KGPPKGAPNPTLTWRGKENFFI*KKKKP /RLI*KKGPPPKMGFKRERFWLKP KGP QFGKGEKG/SPNYPHPRGDPKAPSLWKK PQFFGGGGGAPKKAS
12869	26770	A	12998	230	409	SCRPKLLAFLKSSTEISQRWKQPIYI/ PSTDE*INKMWHHTMEYYSALKRTRKVL IHATT
12870	26771	A	12999	310	343	DPVCTII*IICTIINL*IECSKVW*SLKF YKILILFNVCVWPSVGNCHKWLCDCVV* KQW/LWPGMVAHTCNPSTVRGGGGRIV* GQEFETSLGNIIVRPSLYNNKSCI
12871	26772	A	13000	390	289	IKLCQPRGVKLDSEFKRAPPFFFFFETRS CFVS*AGVQWCN/LGSLQPQTS GPNNPA TSA*LSLIFMCSNSYVCIVK
12872	26773	A	13001	1	289	GILRQISVNYLPVGRSLAQAGVQRCDLG SL*PLPPKVKQFSCVAGTRGCHHAWLI FIFSREG\GHPVKGASSDSPTFGFSKAG ITRLSPRALACT
12873	26774	A	13002	359	105	KQKKNPSPPPGGGGQKPG/PPKPPFN SRDPPKNQSPFFPKLKKKFFNFY*KAK NP*KPNPPLKKGKPKGFFSPPPLK KP PNV
12874	26775	A	13003	243	293	MNSQFLKRL\RIESPYGSVISLLGTYST EK*KACPKCTCTQMFTSALYIIAKKN\N KCPSTVRW/IKLWHINTMEFFCQ*KKFH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CIDMPQFVHLTVEGHLSPFCYYI
12875	26776	A	13004	465	307	SEACFILKLFMFCG*CCLFVC\SILLVFYFVFCFVLFCEAYMQFFNQCLFG
12876	26777	A	13005	207	3	DGSLTMLPKLEC/RWLFVTGVI MAHCHLE/RLGSNDPPASASRVAGTTGVCHHA*LI FIFVKMRSHYPTRP
12877	26778	A	13006	2	56	DLALLFRL*CNGMITAHCNLK/RPG*LL GSRDPPTMVS*STGITGMSHEAHRPSPS CDF*RSCSVVQAVVQWHDYSSL
12878	26779	A	13007	402	74	FGASLLKRHFLFFLSKPLVYNKKIPRPL VFLKKT\PPPPGRATPFYCCFFHKEGP GFGVKKEG*PKG/SPPPQQRSTPPFFL GAFKKPKVTTPFFKKNPPKTLKGPPFF
12879	26780	A	13008	356	145	RPPPPFFFFFETVSHPV AHAGVQWHDHSS LQL*TP\SSREPPASAS*VAGTTGVHYL PGSQLP LELHSPRR
12880	26781	A	13009	227	353	GWSELT*/SN*AQWLTVPVILAL*EAEAG GSSEPRSLRS AWATW
12881	26782	A	13010	249	32	NPDSHSAWNCASVVPQTQKARVGGSL ESRSLRLR*AMIVP\CTPAWVAQEPLSLK KPPTIETLFFSPQDPSQ
12882	26783	A	13011	247	403	TPGGGGKYFFFWGPQKKNRGGGFKNGGG GKTRGPP*KQPASSSPFAPPPFWGAPG FSPPPRF\KPPPPVFFLGPKKKIFPPP PGGLFFFFLGGPPSPFFFFFLLGGGPL FFPGLGAMGPMAGFRSLAPPGNSLSKKK KSEGLGEGGNSVLT RVLLISSYQIPGNP R
12883	26784	A	13012	206	386	TREAQTFWFPLYS*KAL/WLGTVAHT*N PSTLGGQGRITSSQESSETSLANMVKPH LLEI
12884	26785	A	13013	354	31	YKMNWDI IHI*HT\YIPVVPKGKERKR KKLEEYL/QDIMTKNFLNLMKNMNIYFQ EVQQTSPRINSQTSTPRHII I KLSKYKT GREQWILSVMLALWEAEVVGPPPEVRS
12885	26786	A	13014	1	419	EETSFGKARCLPGYPGFHPRRLRSRSP LLS*MPLSHPOGSPQPPAGSMSSSPATT STCSCSPPAAGCTRGRTTGRPFWTASGP AELD WASGSSV/EALTSGLPARGLWGQY AGLGVPPRLGPMTSCCMLPFPSPARP
12886	26787	A	13015	109	426	TSLGNIRPH*QTHMATIRSVPPPSWKD ST*LRLHPPPHMCF/PD*SLKSN*Y*H YLVNP\IWPMLTLLFVCLFVCFRDRVSL CCPGWSAVVPSRLTAAS TLWVQVILPP\ RLAN*IFFLRWGLAMLPRLV*NSWAGDI LPP*PPKVLGLQA
12887	26788	A	13016	149	422	LKRIFFLKVVFTHDTAPGDPDMCPYSC F*NQI I KSLGFFFKKPHL/WLGE GAYPC NPILLGGQGRIT*FQEFETTPANMAKP LLYKKYKN
12888	26789	A	13018	162	377	QSPGYPERVSKLPTITQRGMWMMHQP SFV CTSL*NV*TGWAQWLTVPVAP*ED\AL AGGLEVKNL RPAST
12889	26790	A	13019	205	427	IQTGGPPARPFLWPAPGKK*RVPPEGG PPKKKKKTPPHPGGEREGS/PFSKKK KKTPKKRAGVFFPGGPRPKEGPGWGPPR LDSKPVGAPPEPGR LGNGPGKIFFGPGP FFPLQPKGRP*PGGEGGSFFFLGVPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						LGEPSTFCLDLPENA
12890	26791	A	13020	248	358	SRCGGEAQWLLPV/I/PAF*BAEAGGSF EPKSLRPAAWAT
12891	26792	A	13021	2	434	ITEAGSDTQBIHHTLYTHLCVYWRPFTK KAQVKKKVWHM*PQLLGRLEMGGSLEP RSLRLQGAMTLPVTSTT\QAWAT
12892	26793	A	13022	162	410	LTQKTAASQIILSFSSSTLEKIPISSES GGGGSVSVTQAAEQWRYHSLLP*TPGD KRSSHGIPHP\SSWDYRISKDWMPV
12893	26794	A	13023	250	40	LILKLNIFSCSLAIWTSSCMTSLFKYFAH FSFF*IDFYSSYYILDTNPFNRN/GITN ILSSSVTCSFILFVV
12894	26795	A	13025	264	1	VSSTKHGKRLLEPEY*CFIHH*EEKVFE SYFEY/PCQTFLRKETVRPGAVAYACNP STLGGQCRWII*EQEFETSLTCLAAALR VTLR
12895	26796	A	13026	110	523	CIDSSSWTQTDRCEDRLCPGTTGTGAP GLLFLSAPPLGPF*PSQAHPSFHVSLSG PSPGLRPQLDIPHPSTSIAPRPLPGPA S\LPRLEPHPSLPSPTGACFLLPCLGE QRHWPLPTSLWLGLDGHCLATPSVS
12896	26797	A	13027	52	53	CPTLLQLTLC/LPPQASAMVDAPP*ARP LPPSSILACCTSGEQGSVVVGLAEFVKF YNLLVCRLLRPLEKCGIWAIVSRFSLYS LSWLPLARKG\NPLTACASWVR
12897	26798	A	13028	262	381	HFGRLRQVDRSLSPGVRDSLCKNVKP*QI IYTF*FSVSLSVINTYLGKPSVHTYN PSTSGG*GKWIA*AQEF/TSCLKNVKP CLY
12898	26799	A	13030	1	846	FRPIQAGRAPWALTLP CMGFTEGSPALL SHSSRCDIQMGCNTHAVDDSTGEGPFHK GRMRESCWLRTPRCGLYTKGVGGPGMEG RERRSRSRQHMPGRGHSTMASWSLRQC MRLKLQWASDLLSQLEMQIPSLPPGESG SLGLTGPRSLH/CEQTIGLSPTPGESWS EELG\GGIVGGGRGTVAGRGGHREAGNK PSGTWGRQCCASGDKAMSI*LTSLY\AR RGEPPGPRPVKWLRESSQNRI GGEGR WE*GQRRSREGRECPVGWGRKKPLRWG LMWS
12899	26800	A	13032	308	1	KHYHDFWCWIIALSDAQSLDHTCV\CV CVCVCVCVCLRDQGSLSCL*CEG*LVP HFVPGPVLCCLSPVIYVCFICSLTCKVE SLSNFFKKLNKALLRHCI
12900	26801	A	13033	763	244	FLGPRIIGLRHEISVETQDHKSAVRGNN THDNYENVEAGPPKAKGKTDKELYENTG QSNFEEHYGNETSSDYNFQKPRPSEV PQDEDIYILPDSY*L/CQNI DFCYWMIN IHCNFTAKTRNQT KC*STVDWIKKMWY TYTIEYYAAVKK/DTKLTWEQIKYHIF SLKSGS
12901	26802	A	13034	326	58	EHYKCNQCQKIFQKL*/HL*SKKHVYAE DKYKYKDGVVPLLVSQLIYTFYTRGK P*SSCSNFVQNQIIYIGQSKCKNKFGN TFFKKP
12902	26803	A	13035	199	3	RFIYNHKVCITTFPLPHFYF*KLVL/WLG TVAHAWNTSTLGG*GGRIT*GQELTGL DNTARPHLHTV

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12903	26804	A	13036	94	448	GSCATSMAPKDTTRKTAVEPGVHVHIGIRI KPLEKVCADLITGKFKNL/KVKGVPVCM PTKTLKITTTRKTPCGESSKA\WDGFQMR IQK*LTNLHSPSKIVKQIISISGAPGID SEVTNADG
12904	26805	A	13038	964	1717	HKLSCVKDLKDFMRQAGE\VTFA\DAHR PK\INEGVVEFASYGDLKNAIEKLSGK\ EINGKNINLIKGSK\RFSRSRSSSDPG TQKSPLGPRSRSPSPVVRKP*QPVQEAR SRBPGARSQVPVPVK*GPPPCPEKEBPQK \RGSLSQSKILSPSTLWIRPEVSGPRSK VPRSVDSGN
12905	26806	A	13039	2	725	SLLFSPVLPFLPLPLAYILQNLKPLQF SPDLKSKHLIFFCNAA*PQYKLDSSK* PENGTLNFSILQDLNNSCRKIGKWSEVP EVQAF\SHQSLPSLCAQCNS/CPNLPS FPP\VPSPVPTPSVTSF*SSFSTDPSD LSLPPQALLARPS*VPILPQPPLLHP ILLSPPLLTTPRPAYSFIP*L/CPPPPAQ QFTLKKVAGAKGIVKNAPFSLSQIR*H LGSFSSNIKIQPSWLVWQQP
12906	26807	A	13040	1131	2	DGVSLSPRLECSGTISAHCNLHLLCLN DSPASAS*VAGITGPATTPPLIFVYFFF LVETGFHHVGSGLLELPTD\SDEPPASD SQSVRITGVSH/AYLACSQF/CTRC*FP II*EQCVNMNINSSK*IFILISYLYRWM NKDPI/VIIERLLVRMPEGQSHAAN*NK TNKQT*ILELVLSVTSCGVSVRPNLSIP *VFPSTK*EGWMRCVNPSTLT*FIPQVA *TCQEHGLMKIQT*NPGLDPSIVSDHQT Q*EPSVKQVLDISHDKLPMSEELYHCR HTLASGKQISGVPRTIFLNHFHGFYFIY /CIFEMESCSV/SQAG/VQWRDLSSLQA RS/PGSR/RFSCLS/LPVQHPPPGPANF \CIFSGDGVSPC*PGWSQSPDLVIR
12907	26808	A	13041	97	626	ICFTQVKVLNESQVQWCMPPVVPATWEAG AGGVLEPGS*EL*/CPVNSHCPPAWAT
12908	26809	A	13042	2	431	HDPDTHSQIKVIKLMQSEFCWGWAN*LT PVIPALWEAE/AGGSPEVRSS
12909	26810	A	13043	405	1319	RYRKKLQNKPLWLH/CLLLPNSATR*T LQK*SK*ISPLESSA**KEPPFLSVLSV TSVKT/SAIPMPPHWENVNTQVPYQLIP LHNQTHEYNEVANLFGKTMDRNRKRIQ RIONLDLWEEFFCRKKAQLKKRGVPQIN EQMLFHGTSSEFVEAICIHNFWDWIRINGI HGAVFGKGTYFARDAAYSSRFCKDDIKH GNTFQIHGVSLLQQRHLFRYKSMFLARV LIGDYINGDSKYMPPSKDGSYVNLIDS CVDDTWNPKIPVVFANQIYPEYLIDFH *FHFQISVVKEALFFAGRFALQSSSH
12910	26811	A	13044	23	450	RSRAAAIQLGQRLRLFGPDSPRLTGRQL EPGTGRGSRARGPCSIFFRRETTPPQR EGGEALGATSRQAPPCCPPRPWELDAS AKAAAVAPPKKVGFKAVERDPRAEALGG KGSP\GGKGSLLKGVHR*GGLGPL*GAP EAI
12911	26812	A	13045	172	16	AHVSPEVDRTKFW\LGPVAHICNSSTLG GRGGQIT/R/QEFETNLNMEKPHLY

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12912	26813	A	13046	181	9	YKWGPAMLPRLLKCRAT\IGSNMAHCRLD LPGSSDPPSSASQVAGTTGTCHLGARGG MV
12913	26814	A	13048	2	3507	YVRVSLPPPPPAAGRFGAAVADDAREEE EEAAPPPPPPPPRLLAAARPPGSQPRPP AAGEAQAAADNMHQQQQQKAGEQQLS EPEDMEMEAGDTDDPRITQNFVINGNV ALSDGHNTAEEDMEDDTSWRSEATFQFT VERFSRLSESVLSPPCFVRNLPWKIMVM PRFYPDRPHQK\SVGFFLQ\CNAESDST SWSCHAQAVLKI INYRDEKSFSSRRISH LFFHKENDWGFSNFMWSEVTDPEKGF DDDKVTFFVQADAPHGVANDSKKHTG YVGLKNQGATCYMNSLLQTLFFTNQLRK AVYMPTEGDDSSKSVPLALQRFYELQ HSDKPVGTKKLTKSFGWETLDSFMQHDV QELCRVLLDNVENKMKGTCEGTIPKLF RGKMVSIIQCKEVDYRSDRREDYDIQL SIKGGKNI FEFVDYVAVEQLDGDNKYD AGEHGLQEAEGVKFLTLPPVLHLQLMR FMYDPQTDQNIKINDRFEFPEQLPLDEF LQKTDPKDPANYILHAVLVHSGDNHGGH YVVYLNPKGDGKCKFDDDVVSRCCTKEE AIEHNYGGHDDLSVRHCTNAYMLVYIR ESKLSEVLQAVTDHDIPOQLVERLQEEK RIEAQKRKEQEAHLYMQVQIVAEQFC GHQGNMYDEEKVKYTVFKVLKNSSLA FVQSLSQTMGFPQDQIRLWPMQARSNGT KRPAMLDNEADGNKTMIELSDNENPWTI FLETVDPELAASGATLPKFDKDHVMLF LKMYDPKTRSLNYCGHIYTPISCKIRDL LPVMCDRAGFIQDTSLIYEEVKPNLTE RIQDYDVSLDKALDELMDGDIIVFQKDD PENDNSELTAKEYFRDLYHRVDVIFCD KTI PNDPGFVVTLNRMNYFQVAKTVAQ RLNTDPMLLQFFKSGGYRDGPGNPLRHN YEGTLRDLQFFKPRQPKLYYQQLKMK ITDFENRRSFKCIWLSQFREEEITLYP DKHGCVRDLLLEECKAVELGEKASGKLR LLEIVSYKIIGVHQEDELLECLSPATSR TFRIEEIPLDQVIDKENEMLVTVAFH KEVFGTFGIPFLRIHQGEHFREVMKRI QSLLDIQEKEFEKFKFAIVMMGRHQYIN EDEYEVNLKDFEPQPGNMSPRPWLGLD HFNKAPKRSRYTYLEKAIKIH
12914	26815	A	13049	30	477	VRAEHCAVWERNFEETVRWTSVKFLMTS PEIASLSWGQMKVKGSNITTYKDCKVWPG GSRTWDWRETGTGTEHSPGVQPAAC\DVKE VVEKGVQTLVIGRGMSEALKVPSSTVEY LKKHGDIMRVLQTEQAVKEYNALVAQGV RVGGVPHSTC
12915	26816	A	13050	179	389	NIETIQSMFPI/DNEMKLEINLKKAIWG IHKYASQVLWFMPIFPTLWEAKVGEFLE PRSSRSVWETWRDPI
12916	26817	A	13052	466	1489	PGKGMRTSPSPLAIVPRPQASRPLL CAVSPMASASGATAKHEQILVLDPPIDL KFKGPFPTDVTTNLKLRNPSDRKVCVKV KITVPHRYCVRPNSGIIDPGSTVTVSVM

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						LQPFDDYDPEKSKHKFMV/QIFAPLNTS DMEAVWNEAKPHELMDSKWR/CPNENDK LNDMEPSKAVPLNASKQDGPPTQPHSAS LHDTETRKLTTECKRLQGEMMKLSEENQ HLRDEGLRLRKVAYS DKPGSTSTASPRD VTSLLPSLLVVI AAI FTGFLFFFWRRSL TLVAQAGVQRDLGSLQPPSPGFKQFSH LSLPSSWDYRRPPPHANFCIFSREGVS PCWPGWS
12917	26818	A	13053	892	189	SYDPGALGCRPAPRSGRGKSGATRDMH PMSRERAKFVKSL/YCKTTRMLHAR CCLNQKGTILGLDLQNCLEDPGPNFHQ AHTTVIIDLQANPLKGD LANTFRGFTQL QTLILPQHVNCPGGINAWNTITSYIDNQ ICQSQKNCNNTGDPENCPENGSCVPDG PGLLQCVCADGFH/GIQVYAPGLVLTAY VLRDSGSHHSIRLSALGDPAPKSQDFM NYIGLTIDLRSI
12918	26819	A	13054	423	12	SFNQKNPLRQKCSLRPTRPASQSLATWP GQSTRFWEQALPWALWDPSKRAE/MQL EPPHAHTWTHAHTCGHTGA/FCSAHTEV YVHLHSPVHAHTHAHTSPPVHTCGCRL HAHTH/PQTPSPPGLLSLLA VARPQS
12919	26820	A	13055	16	349	RRSGKNDPWTQSPRAAASHTRCPHPAV AAAAMPKRKTEGDAKGD KAKVKDESQKT S/ARMSSKSAASKAYAKPIKAPAMNGEN VPNGIQRKLEAFYDLQACRHLTRLIDFA
12920	26821	C	13056	716	594	MMQTETGVMPPQARQCLEPPGAGTGRKD SPLYPSEQSWPL*
12921	26822	A	13057	353	2	IGNPGKTTFNKPPPPKKFIFSKFFMFLF FLVKTRSCYVAQAGLQTPG/SSDPSASA NQSAGITGVSHHTQSEILKYTVFCLTFQ TPEYTIPTWSIPCCSHFSCYLCLFAC FLRQSF
12922	26823	A	13058	864	529	EVSTSKTAGCRGCALVISM LCIYFPQGL FTRALLRTCSALLHADWPEISFVVVVVF FKTESCSVAQDGVQWCDLRSLKPPPP/G SSDSPASASPVAKITGMHHHARHGLKS
12923	26824	A	13059	2714	1376	GRYDGLVEQLGGRATPAVGFMGLERLV LLVQAVNPEFKADPVVDIYLVASGADTQ SAAMALAERLRDELPGVKLMTNHGGGNF KKQPARADKWGARVAVVLGESEVANGTA VVKDLRSALAVGVILGVGALIGWRYWNS HQVDSARSASLAYQNAVTA VSEGKPSI PAEKFAENKNTYGALASLELAQQFVD KNELEKAAALQOGLADTSDENLKAVIN LRLARVQVQLQADAALKTLD/TPIKGE GWAATVADLRGEALLSKGDKQGLLSVTL LSGCSLFPNSEEDVVKMSPLPTVENQFTP TTAWSTSDGSGIGNFYSNLEPALADNVV YAADRAGLVKALNADDGKEIWSVSLTEK DGWFSKEPALLSCRVT SVVPPNNQTEKFN KQRTGEPVAEPEQAGVRRHYLYPFTGG YRRRRAACQAEPAARCATEEHGSRN
12924	26825	A	13060	99	254	RNHHLVAFKELSA LKVKRVWDAPWLMFV IPAF/LEAKVGRSLEPRSSRPANAT
12925	26826	A	13062	127	386	FSYYYFFFLFFLCVFVIPGEPFLMKKL GKPKTITMLKEKKGESYSELFETDQME

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						WL/TPVIPTLWEAEVGGSEHRSSR
12926	26827	A	13063	1	209	GKYILLKVFCCFLRQGLCHLAHCSRL PGSSDSRASQVAG/ISITGVHMHARL NFVFCFFFLVCFCE
12927	26828	A	13064	132	1	SHAMCCNYLKRFGWARWMLPV/TPALWE ABAGRSPEVRSSRSAL
12928	26829	A	13065	269	134	TLWSVFASS/WAWNLTPVILAPWEAKAG GSPEVRSRLRICKQKVL
12929	26830	A	13066	853	461	RLWRSVSQFLCACVHMCVPSVCVGLAH AGTYAVSTCVH/MCVVCVMCARITLAKI CSETSGNLLFRKIISLLDLFTLNFSIKY KVQLVLKSRSLAWWGRIKLLTLSPFPD VNTFERINYWLINDISIIR
12930	26831	A	13067	57	2066	AQPTGRQTSTVAPTATARSRGGRVPIF PCPHAPITLLSTSRVVTASPAAMKAL RLSASALFCLLLINGLAAPPGRPEAQP PPLSSEHKPEVAGDAVPGPKDGSAPVR GARNSEPQDEGELFQGVDPRALAAVLLQ ALDRPASPPAPSGSQGGPEEEAARALLT ETVRSQTHSLPAAGEP/EPAAPPRPQTP ENGPEASDPSEEEALASLLQELRDFSP SSAKRQQTAAETETRTHTLTRVNLES PGPERVWRASWGEFQARVERAPLPFPPA PSQFQARMPDSGPLPETHKFGEGVSSPK THLGEALAPLSKAYQGVAAFPKARRPE SALLGGSEAGERLLQQGLAQVEAGRRQA EATRQAAAQEERLADLADLLQLYLLQG GARQRLGGRGLQEAABERESAREEEEA EQERRGGEERVGEDEBAEAEEAEADE AERARONALLFAEEEDGEAGAEDKRSQE ETPGHRRKBAEGTEEGGEEDDEMDPQ TIDSLIELSTKLHLPAADVSIIEVEE KRNRRKKAPPEVPVPPRAAPATHVRSP QPPPPAPAPARDELDWNEVLPPWDREE DEVYPPGPYHPFPNYIRPTLQPPSALR RRHYHALPPSRHYPGREAQARHAQEE AAAEERRLOEQEELENYIEHVLLRRP
12931	26832	A	13068	282	53	PGFPQGGKFRFKKILPQDYPFGAPNSK ARPGQGVPPGIPA/LWRVKKGGPLRSGG GPPGAKGGTPFLPINTKKS
12932	26833	A	13069	177	2	VSLCRPGWMECSGVISAHCNRLPGSSN S/PALASRVAGITGARHHALLNSLFKVL SRA
12933	26834	A	13070	789	302	PHPEFYYSFYFYFYFFISFHFRHFIVH YFISSHFISCHLASSSSSSSSSSSSSS SSPPAFHYSFHHFISFHLAIHY/HFIIS FHLFHLFSSPHSISFRDRDLLYCPGWSV PPHAFHYSFHH/VHVMRHFILRQTRS IAQAGIQWRDLCSLOPEVGSSRSA
12934	26835	A	13071	193	2	PPYLKSHSQVDLSPGVQDQPGQHRETPS /LTKN/TKVSWVWVCTPVIARWEVEVR ESLEPRCSTRA
12935	26836	A	13072	122	1495	LLSDFFFFETE/SRSIAQACMQWCYLSS LQSLPPGFKRFSLSLPSSWDDRCPPPC LANYCIFSRDRVLPWCPGWSRTPDLR
12936	26837	A	13073	178	347	CCLCNDNSVLLCMYLLVCMHACMHALY IKTNK/MQLGAVSHACNPSTLGGQGEWI T

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12937	26838	A	13074	165	34	FILSFPFETVSYFVAQAGVQW/LTIAHCSLDLPRSSDSPTSAP
12938	26839	A	13075	205	105	GGWVQWFMSIIP/ALWEAKAGGLLEPRN SRPVWAT
12939	26840	A	13076	3	357	HEREYTOAEKRKFIAFFFFKMGSCSVIQ ARVQRHDLSSLQPP/RVAGTTGTHYHTW LIFVFSRTDSRLPSSPSPLTSVISLII PLSLIPTTYLTTPSRPSSTSPSHPSFR APLTSDP
12940	26841	A	13077	3	477	STPALTARGLSGGSRASVAAMVLESEQ FLTELTRLFQKCRITSGSVYITLKKYDGR TKPIPKKGTVEGFEPADNCKLLRATDGR KKISTVSSKEVNKFQMAYSNLLRANMD GLKKRDKNKTKTKKAGSNSS/ATTAAP AAAATAATTAATTAATAAQ
12941	26842	A	13078	1077	1566	RQVTSLDPLKTFPRTSLEFTSPTGQLDS GATAFTVWVPSGAPTGRGRESAAHQGN/ YPVGQRS/RMAGLSRSPFCWVVSFSR/ SHSC/ICWVQLGKSAVLQQSRGPGAHE GSRRRGGSSPPCPPLQTQLVFSPOELSM SAPIHRLSVTLQGDICISTGGAPSRCLRA
12942	26843	A	13079	3	396	HERGRKMVSVT\RLIQLRNWASGHDLQ GKQLRLYQEI SKRTQPTTKLPEGPSHKL FNNYY\CTRDGRRESVPPPIIMSSHKAL VSRMPAYSFAEAATDKKAVTPAPSIYRG EQSSDHPYLRHCTLTVTRELL
12943	26844	A	13080	467	109	SLVPVVSPLKEPSCRYLIENVMLVPKE QEFWSKEAGSLFSPVPVFCWTPSIVFS SSFFFLFRVCVFFFFFCFFFFF\LLF FGTKKALYLLRARGCKQYKQKLIWYLT FLSLLVK
12944	26845	A	13081	458	51	VSLFCTVAPLLLLPEGIFFSCSLLEVKA PMRDVSGVFLTLFLYSVLFFPLGVFFFL FFFLILPPPKIFFFFFCVVALFFSPAF GAVFLF\SLWSSVLPGVGFFTACSFFFF FFFFFFLLRQSFALVAQARMQWR
12945	26846	A	13082	23	327	RSDSEGGRRGHKYIFIPYTHHTYIPI YTIYICLHIYACLS/LICHTIPISIVI HTYIYISYAHYLYIHTHIYLIHTHT YIYIYLHIHIYSSWVCKGS
12946	26847	A	13083	352	153	KKLVEYYSATKNSVLH/VSTMRLKN ITLSLKTQSQRHLYIIPSVRNVQNRQV HKYRSRLVDSER
12947	26848	A	13084	121	417	DYDYCYVYPKIYLTLLLYFY\VGNYIY THYVRHVYICETMPVYTHIYIYIY IYIWKETTWFSCGISKTYRTHDLAYTY LVFCLTHVTFHVSST
12948	26849	A	13085	242	12	LSSRLPMLLETKEITSKILFSRKL/LPY GWCFSFKITWVSQIRNRL/AQWLTTVI PQLWEA\SGLLKPRSRPAAWTTW
12949	26850	A	13086	274	340	GGEKTPGGFLEKKSFFGGGIFGPPP/P TKRGVFPSPKFFFPKTKNFGRGGGP KIPPPKDDFFSKNPPGVFFSPP/YKKKK IIFPPPVKLGPPKDFLKSPPPPFFFFFYF FFFFFSSQEVNLKALSSTSEIIFFFYLV
12950	26851	A	13087	241	405	PPPSKIHNFRKMSDVKNATGWAWMLT PVIPARWEAEAG/VSLRPNRSRPAAWA
12951	26852	A	13088	537	375	KHSITLSLRLECRGTILAHCS/L/CTSL

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						LGSSDLSLPQQIAGTTGACHHTLEKIF
12952	26853	A	13089	448	186	GALVFPSSQAPPCPKMEQSFFFFFLL ETGSRSVSKAGVQLHHGSLQPPPPGFER SSHFSVTTI/TYLYHRLALHVFELHIN GIMHR
12953	26854	A	13090	365	191	GOERERERERERKRQKKREVE/REEBKE RVRDLSESNNRALERERSALVDRAPLSR PG
12954	26855	A	13091	148	316	DKMESCSLAQTGVQWHD\LG\YLQPSPL GFKRFCLSLSSWDYRWETSTEPQQA VF
12955	26856	A	13092	712	229	FVAWVKMAEYLASIFGTEKDKVNCSEYF KIGVCRHGDRCRLHNKPTFSQEVFTL QEKYGEIEEMNVCDNLGDHLVGNVYVKF RREEDGERAVAELSNRWFGQAVH/GBC TRGGFCNFMHLRPISQNLQRLYGRGPR RRSPPRFHTGHHPRERNHRVFP
12956	26857	A	13093	835	405	ELIERLGPKNQPPILMWKMPSPSNMKA SAALLCLLLTAAAFSPQGLAQPVGINTS TTCCYRFINKKIPKQRLSYRRTTSSHC PREAVIFKTKLDK\EICADPTQKWVQDF MKHLDKKTQ\TPKLLNIHDWNLENQAMT LRKPN
12957	26858	A	13094	1137	424	LCPSHFAPTTLTQGAHKMCCIKSRFK RDLGLCRTCLVNKMTSSILGKSHRSL VSINQGNALWKAAG\PLSWKAGYC/QG FSPCDSLKYG\SWDEKDLTVPPDTHKG SVLRWISKRGKPLAVEIEGRATGLPGLA PWGTE\CLGYKTPIV\HLPNSEMG\ENR PYGGEARHVCNSAALLFFTPLRCLGGEK HKSGLRHPVIVLSLELNYDIDSFAHMF FADLLIIITLLSCYIPFC
12958	26859	A	13095	1	324	ARGERERERERERERERERERERERE RERERERERERERERERERERERERE RERERP/RPRVLFFVRGREGSHPEKCBN KKERAPFSRALRKISIEIRGGVSITTEA CVFVIGAHVRCSVYIYI
12959	26860	A	13096	508	840	DGVSICRPGRATADCSGAISAHCKLRFP SRQSPGLSLPSSWDYRRLKPMRPAFFFF CIFF\VKTFHLVSQ/AMGLDLLNS/SI PPRLGLPKCW\DYRREATAPGQELLNR TGM
12960	26861	A	13097	53	254	WPQTASCLVAQAGVQWSDHSSLQRTPG \SSHPPASASQVARITGMHCAWLHLII LLRAHGSSPLC
12961	26862	A	13098	329	67	GPGAPLLKGEKLLPKEPPRISPIVSAP FAWGPPPGYCFLKKGPPFF\VFPPSFFG KKKNSPPPPHINGGAKTFNPPLLFSSF FFF
12962	26863	A	13099	253	444	EGAFSLGTIFYFIFFVLVLSNTFLLSIRNQ QIWNKKTW\PSPFLPTLIALTLLLP SPFILL
12963	26864	A	13100	341	590	PMASQICIGRIPFLYLKWFPGKVV HTCNPKTLGGRGALITQGQKFENSLAN\ MAKPHLY
12964	26865	A	13101	55	184	RLREPTPLYSE/HAPTKYYRMAHHNYPH SPPIQPFRHYRVLL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12965	26866	A	13102	433	762	RNLNCKRGLERKGCASWPAVPLFLQR RVWFRPTAELNEACMLAQHONCONVKME YFQLSFTKRQEI/WLGVVAHACNPSTLG G/QGGGIACSQEFKTIPTSSKVRPCFYLK
12966	26867	A	13103	349	250	DLFPSTKPPPPPPPPKNLGGP/GPFGPP FQEG
12967	26868	A	13104	3	236	YPOHYPSCTPTQYTLTKNHNFLIPFEV GSCSVVQARVQWCHHGSLLQPP/NSSDPP ASAPQVAGTPEGVSHRAPPKNQNF
12968	26869	A	13106	154	4	KKVKNTVHYNGKYFLKSNQSTFLKEIL /WLGGVAHTCNPSTLGGRSGRIT
12969	26870	A	13107	391	150	RPPKKPNKKYSQITSGIKMVYTRKYLT QKKKAMSQALWY/V/HAVPATQAEVGG SCEPGSSRPRCTMIMPMNTHCAPAWAT
12970	26871	A	13108	90	252	KVGDGGRCLVFCFYFKRQGFVQAQGVQ W/ATIAHCSLKLGGSSDPQNYEDSWG
12971	26872	A	13109	197	414	LYEFIKITVLLGLGCLGRYGCNQRPF SLEMEFHTVAVARVQWHDLDLSLQPLPPR PNRPSCLR/YPQSSWDYR
12972	26873	A	13110	2	317	GRVGANVHKGHRQRTYGSVIPHLPLHV LKKTFSLRDFHFSVSLKK/NLVLTCLEH FL/GVRTPRNDPFVSMMLLFTAFDRPS TILGTGLLYTEGLTVALRLAYLR
12973	26874	A	13111	413	162	LILLPQPAECLQLQASATLDCGLPFR RDCRRSLVHSLVNGAQAGVQWRDLGSLQ PPPS/TCLGLPKYRDCSLCPAATPSGK
12974	26875	A	13112	40	296	ESRLSALYIYHICVVCVYNREHLLYGIHM /SIHTYTHTHTHTHIYIHMRAFALEDKF ICSLLCRQDNAPILVSVKLQRKNYFLT RR
12975	26876	A	13113	2	288	FEPRCKNSARGKVPGRGFSNLPHTVET PEGSKTGFELES/RRHRQIHSSAQCP TAVPGAGDAIPEDASGHTWLP/LHAQNC FLLYIQAPEQPPA
12976	26877	A	13114	685	340	LSPPRAGSARPTGPPTDAPGQRSTWTCG ALKFRRRALRDAENLFQELQEHFQALT ATLNLRMEEGMNRIEDLQK/NVNDL/MV QAGIENSIKEQMLKTVTANMSVFGDGAS YRSH
12977	26878	A	13115	65	3021	GVLTMGDEKDSWKVKTLDLILQEKRR KEQEKAEIKRLKNSDDRSKRSLEEG ELRDHCMEITIRNSPYRREDSMEDRGE DDSLAIKPPQMSWKEKVHHRDEKRRK KCRHSHSAEGGKHARVKEREHERRKRH REEQDKARREWERQKREMAREHSRRER DRLEQLERKRERERKMRQKQREQK RERRAEERRKEREAREVSAHRTMRED YSDKVKASHWSRPPRPRERFELGDR KPVKEEKMEERDLSDLQDISDSERKTS SAESSAESGSGSEEEEEEEEEEEEGS TSESEEEEEEEEEEEETGSNSEEASR QSAAEVSEEMSEDERENENHLLVGKN LPGDRVPVPESRFDSDGSESEAEAEV EGTPQ/SSALTEGDYVPDSLPLSPIELK QELPKYLPALQGCRRSVDEFQCLNRIE TYGVVYRAKDKKTDEIVALKRLKMEKEK EGFPITSLEINTILKAQHPNIVTVREI VVGSNMDKIYVMNYVEHDLKSLMETMK

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						QPFLPGEVKTLMIQLLRGVKKHLHDNWIL HRDLKTSNLLLSHAGILKVGDFGLAREY GSPLKAYTPVVVTQWYRAPELLLGAKEY STAVDMWSVGCIFGELLTQKPLFGNSE IDQINKVKELGTPSEKIWPYSELPPV KKMTFSEHPYNNLRKRFGALLSDQGFDL MNKFLTYFPGRRI SAEDGLKHEYFRETP LPIDPSMFPTWPAKSEQQRV\KRGTSR PP\EGGLGYSQGLGDDDLKETG\FHLTT NPGGLPRGPGFSLRVAEVELDPVIGR NSAGDHRRGYLPWNCDGTRNSSSYFVL PCFVFVFLVCKLSRIKSFSLWRKELCF LRDLPRAEVRGIFRGAHVQHKPHHPL PLSTRTGLGWAIVKGTGSSRVDCLIFG AGDLFLCWDERCPLAPTHSSRPALSTTS PRPPTTQPQLLPAGLEQVFFYKVVGVVLK CIKIFFEE
12978	26879	A	13116	469	202	MTIIVGLCEYTKSAVLVQHSDDLPPAPG VFPLAVLDVVDIKIVVHPVFCFLVCLYE MESCPVAQAGVQWRDLGSLQPPP\PGSS TSCF
12979	26880	A	13117	193	383	AARMASTFFVFWFSTF\SLYSICVCV CVCVCVCVCRMHTVQLYFPQVGCQCSSL LNPLFPMN
12980	26881	A	13118	146	350	HYLVKFLLLAHPGSKAPPLNTLQPPPLA TREQPLTVIFHYPPTSYKMAP\PYLPS LTLFGLSPAPR
12981	26882	A	13119	124	254	HALLQTLRDLQANWHALVIPATW\BAE AGGSLEPRSSRPAT
12982	26883	A	13120	150	45	SLPRLECSFTVLAH/C/NLHLGSSDSP ASASQVVGGI
12983	26884	A	13121	336	446	IPLKISSWAQWLTPV/IMPAVWEAEAGG SLEVRSSGPA
12984	26885	A	13122	181	39	QNLTAQDGVQWCDLGSLOPP\LPSSWDY RRESLCPSSFFIFWKRWGFT
12985	26886	A	13123	463	2	GPAVPSGLYLKGPMMRLCASHSPESH HDKGQGTLPRIPO/PLLGSGSR/PLAW GAVAGLPSNRPRIVPLPAPTRSGTRVRP HTGHQPGMSFGCGCESKWPSSAAWPEA YPHFLLPFPTQGCVELGPLYTADPWVI CVSLLPSCPNSTAVDVO
12986	26887	A	13124	429	263	DHFSFLCVTGSQSVAQGVQW\LYIAHC SLKLLASSDPPASVFQSTRITGPFLSFT
12987	26888	A	13125	310	486	NKKTTRGESSKQRQPRVSHHPGWGTVP SGFTAASAS\RARVILLRPPE
12988	26889	A	13126	124	461	GSPLQLLPSPLAALTRDCSEAPMGSCSV AQDGVQWRDLGSLQRLPPGFEPFSCLS TPAP\FPSGWDR
12989	26890	A	13127	2	337	RGAAPAAAMAVTALAARTWLGWGVRTMQ ARGFGSDQSENVDRGAGSIREAGGAFGK REQAEERYFRAQSREQLAALKK\HDE EIVHHKKEIERLQKEIERHKQKIKMLKP
12990	26891	A	13128	681	422	CRSDRWAKEHRGKRGQDSSKDVMRLME APKQTAQYFFIFYFFETKSYSVTQAGVQ WLDLGSLLQRPFP\SSDSPASASCAWPQ TAH
12991	26892	A	13129	299	579	LVMFCKVTKIERLNLWRPGTVAHVLSQ HFGRPRWAVHVGWVRDP/RLTQHGTEP

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						SLLE\NRNISQAWCMFVVPATREAR ESLEPGGQRLQ
12992	26893	A	13130	268	438	KVDKSMKMRKNRPKNAENSKNKKASSPP NDCNSSPARVQ/SWTENEFDKLTEVGF RW
12993	26894	A	13132	1108	1529	KIHSSFVLLNAKLVAAPKTPKFYKKT DLPQTYHSAQTAVPEIPVSAHSTFIRSF IHSFIFETESYSVAQAGIQWDLPS\PP GS\SDSP\ASVSRVAGTIGVCQQAFLFF V\FLVET\GSFPHLSPLTMIRNKQLFK RGH
12994	26895	A	13133	497	370	RPSTVSPRLECSGLILAHCS\LDPPASA SQTAEITYGHHAS
12995	26896	A	13134	217	373	CNHTETIYVNNKKHRPGTVAH\SLYNPS TLGGQGGLITQAQEFDTSLGNMTLS
12996	26897	A	13135	257	507	PVSPGFPP\CPVPHTPHLCPPCRYPES PGQPAQHCGAPRQPPNPRACSSRGFL RCPPACHHAPSCLLCVCPPLPQCCRVQ G
12997	26898	A	13136	137	309	PSFPTHQFCFLFCFLFVFETE/SSIVA QAEVQWCDLGSPDQSSASPPSASSLPL SIW
12998	26899	A	13137	297	419	GGSVYIWEIVQVLWLMFVIPT\WEAY AGGLEPRSSRA
12999	26900	A	13138	213	492	QVGINYQPPTVVPVGD LAKVQRAVCMLS NTTAITEAWGLPGAISSAKCALVHW\YV GEGMAVGGEFSEAREDLAALRDYETCGPW NPVTEAERR
13000	26901	A	13139	246	534	DRVLPLLPRLECSAILGHCP/APASQV TGTTGTHHTQLIFLLYCWLCPPPLASE ASAESPPLLPRGFLCFSSTTSSITAIPA TTRDYVDVSRSGS
13001	26902	A	13140	1	206	SLEWFFFFSFSETGSHSFTQAIQWCNH SSL\SPTSASQIAGTTGVHNAQL/VFV FCFAFMSPQLNSC
13002	26903	A	13141	164	582	GLVLVNLVLRSLMVFIYINSRLQVTD ASRRERENESSWFCRSVCRM/PPVGGP SCVHPCSPRGSIPTPHCPLKTTOAPA \PPRPLRVGPGPHLDQSCCVAARPLYD PILVAHSSWPAPPSPVPVQEDTEHGA G
13003	26904	A	13142	235	367	LALNTFCWLGVAHACNPSTLGGQGEWV TRQGE\QANMAKTCLY
13004	26905	A	13143	91	403	GALQPATAPWEPLSGLAEGAI SPCLQG G/SGRGASENRGCTRPGRVPGGRRINR PRAWSSWPAPPAGSERPSAINCPRAEE CGRRVWDWQAALPAAPAWVFV
13005	26906	A	13144	558	147	GHSPQNWLLGCPLQLQRHLLHPPDASEE CGSPFWTPLRPHIHP SAGPHGSTHK\HA GGCLFPLRPSPTHP CGFPVPLPWSQ/QA PLCPHPIHSPHDWECDPKKSALIPPPA AQSPSRLIKHAANEPECSFRNRPGIP
13006	26907	A	13145	321	421	GCAQWLTPV/IPALWEAKAGESLLFRSL RPAWAI
13007	26908	A	13146	3	398	IELLQSHDKTLTDKLLLLDEQRKWFLE MESTPGEDVNNVELTTKDEYHINLDD\ KAGFERIDSNFERVSAVG/KMLSNSIAC YREIFHERSVKVAFTVAILQPHKLSV TINLIQQPSTLRQDILLAKR

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13008	26909	A	13147	228	261	SKTQRSSEYYSLSVCVCVCVRVCIYIYI FFFFETEFLS\APQAGVQRCDSLRLP PP\GSSDSPFSTSQSAWYRREPQPTS LHYFVQLKHNLRVKKRDLRNTTR
13009	26910	A	13148	3	275	KHLSDLQILRLGLSSKTRKTRYSHFAQG RSIFLLRPSVDWIKPACMDGNLLFSKF TNLNVNI\TKKHPRNVQNNVWPNVWAP WPKEVDI
13010	26911	A	13149	218	382	AWDHIKLESFYTAKETT/RMKRQPTWE KIFANYPDSDEGLVTRMYKELKQLYRKKI
13011	26912	A	13150	391	29	FCFLFLFMFLFFEMQDGVQWNCNLSSPQ PPPPG\SSHSPASASQVVEAENCLNPGG GGCSLGDRLRLPQKRERERETERKRKR ERASCAFCGAIITFVNMWQCKHHTCNHLP WLVFETNKL
13012	26913	A	13151	351	157	FGYSRFLCVYINFRNLSTIYNYICIYIN LYL\NIHTYTLIYTYVHTYTHIHIFYIY IGILTGIT
13013	26914	A	13152	402	111	TFFGGGKPPFTLRPGPPRREGGGGPPGP REGGFFRVPLGAFGPSRPK/RPEKSGPV WAPQIFLWGGKSRRAIKESGKGFFFSRIT LLVFATEKKKKTTLF
13014	26915	A	13153	310	141	REHEKQKPLSQVRWCTPLVQAAQAEAG GELEPRSSRLQCSMT\TPVNSHRPPARV T
13015	26916	A	13154	153	21	LNKCVISWLGAVAHACN/PSTLEGRWIT QQQEFKTSLSGLAKPHLY
13016	26917	A	13155	429	275	SVDIPLEKTLINKDVFKAEAPCKVS/R QARVKFKKRYKPKVTKKWFQKLWF
13017	26918	A	13156	303	42	YRERAPVYPIIINIAFGPHKQ\TRAH THTHTRMHAHHTHPAIIIPAFKNGLT FHHKGRTYNDKVKPRLSCAAIPSNLKS REFR
13018	26919	A	13157	198	13	SHGVAILLFFHFLNKRAFT\YSPAMNSS LCBIQBP SLG\SGSGPLSGNRMSGKGHR KYFAKI
13019	26920	A	13158	192	2	ISNSHRDKIDPEVLLIEQKYILSGMQ WLTVPVIAL/V/EAEAGRSLEFRSLRPA WATDRDSVSK
13020	26921	A	13159	40	190	RVDPRVRESRSVAQAGMQWRDLGSLQAP P\PGSRHSPASASQVALFLNRK
13021	26922	A	13160	1	178	PTMVLSPADKTNVKA/ANGKVGAGHAGEY GAEALERMFLSFPTTKTYFPHFDLSHGV SSYL
13022	26923	A	13161	411	41	ESLQICVGLHAKPSWDACRPWLGOAWFR YLLTFLGPLVFLLVFWFSKIYFLYHLK NPSLSSCYNLD\ENTQVLKYCKKKRLG AVAYACNPSILGSQGGIRITRGQEFETRL GNMAKPDWVDP
13023	26924	A	13162	372	218	FWKRSWISKGLFKRGVSLSLSL/CDT HTHTHTHTHTHAHSGYLCVLRKVK
13024	26925	A	13163	247	89	QGLVLSPLWLCRGGITAHCGLLGSSHPT TSA\QVAGTTGTQHAQLKFFILIL
13025	26926	A	13164	122	409	FPSTAIANS/CSSPQGCAYGVAIRLF LRSSNKLAL/LYGLAL/NSFFCNFQEPS \LGLSLGPLSDNKSNNLCCFKSPSSWLF ATAVLGNYSNLTVRSGRDDPGTPNACS
13026	26927	A	13165	69	313	PSVSLFFPPNHNIVIHMLLLKINSIFGE

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						GLALSSRMESVTTTVHCGLDLLGSGGP PSAAS/RVAVTAGTCHHSWLMFLSFV
13027	26928	A	13166	310	26	IKSMTPLPALNVSLSYLLPFLRPCRERG MVQDRFFCFLLCCCFIFSETGSHSAAQ AVSQNKKTGWAWLTPVIPATHEAAG \ESLERGRQLQ
13028	26929	A	13167	296	68	KNGPLNLATKSLILLTMKCLGVVLGGKP NCSKLLKNKIKTKKKGWAPWLTPLPA/ LLEAEAGRSLEARNLRPVWT
13029	26930	A	13168	2	235	GATPCPREPSLFFLAGWAPLSCWAPP CTQGTTPPGLMGTG\APIAIIIGNARSP PMPFLPLSGTRRALSQAECPTF
13030	26931	A	13169	248	406	TERCGFDLLSLGQVQWLTSPVPALE/EA EAGELLESRSWRPAWATWQNLISLKK
13031	26932	A	13170	33	308	NSLQGAEMAAQSSLSFASSEGVRGERGR GRGRGRPGRG/RSEGRDGRGRGRPGRG RKVLLLRICVWRRVRLRLWNRGRIGVGG VTYLMESI
13032	26933	A	13171	294	56	ICKRNYLFFIYFLREGLTLLPRLECSGA ITAQCSL\GSSDPPTSASTVSGITGACQ CALSSRDALISLCYPGWQAAPGLK
13033	26934	A	13172	71	476	DSLNYDNHIYQMPLIYINMGLAVTISLL G\ILVYRSHLISLLCLEGIILSLPIIA TLITLNTHSLLSNIVPIAILVFAACEAA VGWEECGFRSRPTALILBGPLRSCQPR CVRFPACTRRGPAFVGKNRHSIGG
13034	26935	A	13173	86	318	NNCNVVCVCVCVCVCVCVCIHICIYV/YV YICITYKYICYTYKYICYICVYIHVYM YMCVYVYICYCMCVYICIDSKGR
13035	26936	A	13174	466	726	NCMKFGAVTRIG\DLPEINPLSSCSLL REKDPPTTSGPQTDQPKHLTNFKSGKR PLFTLFSNLFHPSTSFSPQSWRHTSIS PFS
13036	26937	A	13175	128	325	FLRVILICHKMYGCVVCVM/YACICNGM CIYMCVCVSKWKLKPELKCLCISDEVGW VLTQWAGREEN
13037	26938	A	13176	134	311	INSNSEKMGSHYVAQDGVH/WQGLFTGH GIAHCNLLKLGSSNFSASISQAGTTGI VANG
13038	26939	A	13177	577	1052	SPTSTRTGSGVAMWLSQPMGRT\CRSKV ASKSRLHGPLIWAHPPIVRCPLMRHHY\ KAQAGRGLSLEE\LRVAGIYKKVAQTIG IS\EDARRRQST\QALQAKVQRLK\ED RSSLLLPFRK\PLAPKKGDSABELELD TQLTGPEMPIGNVYKEKARVIAD
13039	26940	A	13178	496	678	TLNFVWAQGLKITRPWKNAPVFPVIW\R LRRKNLLTLKGEICSDPKWPYCLPPWKT KKNLV
13040	26941	A	13179	192	421	GIYTFFLSFFLFLRQSLTSLPRAGVQWC NLCLPGSSDSPASASRVPG\ATGT\CHH GSANFLYFLVGDRVFGYVGPR
13041	26942	A	13180	144	5	LQLAIKLLKMRGLGVVAHCNPS/TLGGW G\GRSQGQEFETSLANIVKP
13042	26943	A	13181	351	51	KKKKKIFFGTKRRFFFLKGVWGPPPPK VSPPPPKISPNNPKNNPLLA/IKSPQ NWLFFFPPPSCKFFPPFLNPKNSPWEN PPSGGEFSPPKKKKKSAI
13043	26944	A	13182	2	218	IHFGCFVFLFFETEFCSCHPGCRAGVQW

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						RD\LAHNSLLPPLG\SSDPPTSASQSA EITGMSHHACPIFKKHS
13044	26945	A	13183	33	304	EKHGIFRAVKILCMILQRTYATHLSRP TGYTAPRVNPKLWTLGDNDVSM/SGSLI VTNTALGWGLLIRRSSACMGQGDMLNC TFLSILL
13045	26946	A	13184	277	13	FSFFLIVEMGSCYIAQAGLELLGSSNPP SSASQSAGITGMSHHPAWLATLKRAFVS D\NSLSFPSSENAHLSILAGHFCLMGFF FFQ
13046	26947	A	13185	140	361	ITCCCVCIYTHIHTYVYVYVYIYTHTYI RVCV/YIHTHTYIHIYIYHVIYIYIYIY FMHTYIYIPYVCMVLLQLTL
13047	26948	A	13186	64	759	CLSAESAPTSTMPMTLGYWDIRGLAHAI RLLEYTDSSYVEKKYTLGDADPYDRSQ WLNEKFKLGLDFPNLPYLIDGAHKITQS NAILRYIARKHNLGGETEEKIRVDILE NQVMDNHMELVRLCYDPDEKLPKPKYLE ELPEKALKALTS\EFSGGKRPF/SQGDK ITFVDFLAYDVLDMKRIFFPKCLDAFLN LKDFISRFEGLKKISAYMKSSQFLRGLL FGKSATWNSK
13048	26949	A	13187	41	426	LFFFFFFESGFCWVTQAGRR/WNDHGS LQPGFPGKLGSPCLTLRRSWNYRPGMCRH TQLVFAFFFFFFPREKKFLGAPTGFKTRG LRGFSRFGFQKGGNKGQBPFPRAKGLIF LEPERGQAFGFGVFGPTQ
13049	26950	A	13188	39	197	FFFLFKTRSCSFIQAGVQWCEHSSLQPO TPG\SSAAPASASCAGTTEAALKL
13050	26951	A	13189	221	396	GIQLQGAEGLDVNTNSPFCWRLYDQKTV YHECRMWANSHP\PPKGLLRDITPRCW AP
13051	26952	A	13190	2	826	PGSTISSRRRGACGSRGGHFPSPRGSG VASLERAESWSTEPAKAIKPIDRKSVMQ ICSGQVVLSSLSTAVKKIVENSLDAGATN IDLKLDYGMDLIEVSGNGCGVEENFK GL\TSLALKHHTSKIQEFADLTRVETFG FRGEALSSLCALSDVTISTCHVSAKVG TLVFDHDKIIQRTPYPHRGTTVSVKQ LFSTLPVRHKEFQRIKKRACFPFAFC RDCQFLEGSPAMLPVQP\AKLTPTSTPP HPCSLEDNVITVFSSVKNPGGSSR
13052	26953	A	13191	235	1	SPCARQCCPENPAGQEPRRRLERGPGKW WPRSIFPLPAV/RARFPLPSAPLRQL VSGRVGGRVGRPGKAVQVSGGLN
13053	26954	A	13192	2	386	VIYLLFFETESCCVAQARDGVSPCWPG WFQTPG\SSDLPASAPK/VAGITSVSHR TRPDVRGFKKC/GLQLEMSHLALL/TT SHREWFVLLFSFVSKGFFIFPFFLFF FFLGKGGFFFPFGGGGQI
13054	26955	A	13193	749	506	GQTKAFVLSYCGASPSIKQ/PCPQARDH PLEPSMHPEGTQLQSCSTMLGPRQLSSE KQILLPPRSHLKSPPMLRACKGLTS
13055	26956	A	13194	73	297	RMPGFGALGSPFSCQRIECPC\AGAGSC TYASFCKCKEYKCTSCCKSECGAFPGNQ GAGQSQRREPRAQQAGAGQ
13056	26957	A	13195	670	390	PRETYIKPFARSGCQPPKTIHPTSRRP STRPPARPHARPPVHTP/APSVHMSDRP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						STCPSI H\ RPPSTDVSRPOYSLSPTS LALPGQSC LGR
13057	26958	A	13196	2	438	LSFTSIEFCHLLFLNQLICNYVIFTRSS TISCEALGRLLVVYPWTQRFFESFGDLS TPDAVMGNPKVKAHGKKVLGAFSDGLAH L\ PPLKPTFATVSELHCAKLVDPENFT LLGNVLVCV/MKHNFGK
13058	26959	A	13197	57	499	SPSWPRSSARPCSGHCLLPGLWDHGKAP CLRAARHSQGHGFRKGRKGCGLWAAGW TKNPVPTWRAG/SRRGPGVTSPPPVPSV QNPP\ PQRHGGSQATREPVLFPTPPKH MEGPNAPILGDQRITAPPPBILYRPPRA ATCDALRRG
13059	26960	A	13198	34	465	GILPYSFVLRAPNSKRVRKCGCTTPRH L/CKATRKCGCTTPRAPLNETRKCGCTT PRHLSRQLGNAGALPRGHLNETRKCGCT TPRAPLNATRKCGCTTPRHLSRQLGNAG ALPRGHPLKETRKCGGATPADAFYETTK IGGGL
13060	26961	A	13200	177	1075	PTSSSMAPFKKQLQGLVAATITPMTENG EINFSVIGQYVDYLVKEQGVNIFVNGT TGEGLSLSVSERRQVAEEWVTGKDKLD QVIHVGALSLKESQELAQHAETGADG IAVIAPFFLKPWTKDILINFLKEVAAAA PALPFYYVHIPALTGVKIRAEELLDGIL DKIPTFQGLKFSDDLDFGQCVDQNRQ QQFAFLFGVDEQLLSALVMGATGAVGST YNYLGKKTNQIV\ EAFBQKDFSLALNYQ FCIQRFINFVVLGFGVSTKAIMTLVS GDSNGPTPASTCRKPPGEFT
13061	26962	A	13201	35	464	VQEFKTS LGNVAKPCLYKKKKKSP LGG GVPPPPKKTWVGGLTSPQKIRPAGPLIF PPPLERGOQGEPLSPIKGGGGGSS\ YP PPPPCLTGRA/PPSPISAKSSPSPPP CQYVYHPLLPLFFFLHALRRATAPLFL FLVRA
13062	26963	A	13202	1153	259	AGGVLR LGVVTGSRMASDSGNQGLCTL EFAVQMTQSCVDVAVRKS LQGVAGVDV EVHLEDQMLVHTTLPSQEVQALL\ EGT GRQPV LKGMG\ TQGFSESGGQPV AIPGG GLGTVQGVVRFLQLTPERCLIEGTI\ PG LEPGLHGLHVHQYDGLTNNCNSCGNHFN PDGAS\ HGGPQDSDRH\ RGD LG\ NVGAN AAGGAFFRMEDEQLKVDVIGRSL\ IID EG\ EDDPGAREGQSLYPKITRELPGSRL SCGI\ IAKSAGLFPEPQSKICSDGLT\ IWEERGRPIAGKG\ RKESAQPPAHL
13063	26964	A	13203	281	420	VDGSKKYNEMPVIPALWEAKAGGLL\ EP RKSR TAWATREDSVSTKN
13064	26965	A	13204	3	1125	SDSPQTPRMRVMA PRTLILLLSGALALT ETWACSHSMRYFYTAVSRPGRGEPRFIA VG YVDDTQFVRFDSDAASPRGEPRAP\ W VEQEGPEYWDRETQKYKRQAQTDVSLR NLRGYNQSEAGSHTLQWYGCGLGPDG RLLRGYDQSA YDGKDYIALNEHLRSCTA ADTAAQITQRKWEAARAEQWRAYLEGT CWEWLRRYLENGKETLQRAEHPKTHVTH HPVSDHEATLRWALGFYPAEITLTWQR

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						DGEDQTQDTELVBETRPAGDGTQKAAV VVPSEGEQRYTCHVQHEGLPEPLTLRWE PSSQPTIPIVGIVAGLAVLAVLAVLGAV MAVVMCRRKSSGGKGGSCSQAASSNSAQ GSDESLIACKA
13065	26966	A	13205	417	13	GHPRVMLQCHMGASLSIMTPPPIRSYQ PALTRSSATKPA\TSAPSIPTMPTVTAN IS/VWPTANTTTTKLSNPTSS/STLSTP IWHPSILPAPPSTPAPLTITVNTSATTST ICFHVQLFQAHHCHCIAAALEYTS
13066	26967	A	13206	1139	559	GLSELSIHPSVARVQEGHGATPERSIFW PGGKPRRGGRGTGLREWGGSHRSLGQT KKKGAKAKRDHCAHGPIAFAQGPFRAT QLLSPCHGCSWKENQPP*GPPGHACTAW EKTVTHGSCRVPVTKPSDPGFVGOAPGT KGNPAPGMDGCAGFRISCHPVPITKPLS NTGICVLLCYEFGFLIAIVGCWGFK
13067	26968	A	13207	306	332	ENGEIRIYIYICLYLIKHWEEAGCGSV HL*SQHLKRLKWEDYLRPGVDPQPGHR ETPSQKLNK*INND
13068	26969	A	13208	48	233	GKQNHKLKCLWCRLLFLLSAVISRNVYIL T*LSLSLQCVCVCVCVCVCVCVCVAIL ENYPR
13069	26970	A	13209	250	2	YCEGDLGSSSRPGVSKCREFSPPRDKRIM PWPGAVTYAYNPSTLGGRDGWAIA*A*EF ETSLGNIVKPHLYTHTHTHTHTHTHTH
13070	26971	A	13210	615	120	SVFWPLLGGVSWSGYTEVRGPLEKAVCP LSELEYCAGRSAALFRAIRLFDALSL KLCQPPFPPLGAPLSP*EALVCVPLHV STCLS*WCPTPCPPERSWCVLFPSPMYPR VCPDGLLPVPLRGPVCVPLHVSMCL LSLFNSLLRLRTCGVWVSPVPLVC
13071	26972	A	13211	239	429	FILLRNKLQPGTVACGCNFTLGSQGW IA*AQGFTSLDNMVKPCFYLPQLKKKK KIKNLGV
13072	26973	A	13212	954	503	VQLPLCLGRDLYLFAFNLPYRCWQHFL SKRAPILAGGSDRWPCPCPFWLP*WC HVSAAHAPQFPCKAPEAPLPVGCPCSPA PSLEAALLILRAGLVVLRAPFCFSAHLL SCHSQCCQFPCEKRSCLGGRDRHAASN PLSAVWPPGE
13073	26974	A	13213	1844	1147	LHSQIYSTAKKASLSMKGSRDKTRAASS RPVPSVLGVPPWSTLLQHPQNMWPGPAQ QQGQPSGRQAWCTPGEAPGAEAAPQ*QP HPEEDHSGGPQASAAALPSPSPSQRDV QGETGMQGRSAPRSASSACCACRWSRL PCPQLLQRHPGLRLVSPAHSRPPGPAPS SSSGSGLVPGYLPQKGLAGLSAGAVLCP PGLLRVAHGAGYGPSAQMHLHRLSSSSL RGKRFLRF
13074	26975	A	13214	413	60	LCCKSCHGFSAMDCETLLTFPRLFPYPL HMPTVPGQALPVHTFPL*KLPLLPGIP SCHSPLFLD*AQESPPPGGLFGHPPGSG VLCLWFHSLKHPVLSGSSVSTPGSASPS RSRAL
13075	26976	A	13215	67	196	GLSLSSPKVTHNATLMGCIFQN*KAFVY HSMKQKKIILLFNMA*P*YPLDFGEQWP LHGSHAYSTIL*LDLFCCKEER*DEIPY

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						V*CFMLLWKSTTM*KKILLFNMA
13076	26977	A	13216	161	2	SVFFLFIDRRLYLIKSVAAYNSSTLGG RGRRT*AEFKTSLGNKARPRVQ
13077	26978	A	13217	57	184	CLTVCKDKVSLCYPGWSPV*SYLTAAS NSWSKAILPPQPE
13078	26979	A	13218	292	400	LKVKQGRGHLDLNQPLDL*SNLPLSH TPSHRTV
13079	26980	A	13219	186	394	YLVLSFLFYFLFIFLSRVSLPIFFILEI *LGIVAYTCNPSTLGSQGGRIA*AEFD TSLGNIVRPPLI
13080	26981	A	13220	315	448	KTKDLGVVDHVYNPSTFGG*GGRIT*GQ KFETSLDNRRASC LYK
13081	26982	A	13221	3	13	LRPLRSFVSVERLWASCCLGSELVVDKT KKRRELSEEHKQEI KDAFELFTDKD EVIDYHELVAMIALGFDVKKADVLNIL KDYDR*VIGKISFGHSIEIVTDFQL*R
13082	26983	A	13222	1	715	VDMHSRGSPELTHASTHASGKMAAPWAS LRLVAPMWNGRIRGIHRLGAAPVPEGNQ KKRTILQFLTNYFYDVEALRDYLLQRE MYKVHEKNRSYTWLEKQHGPGYAGAFFI LKQGGAVKFRDKEWIRPDKYGHFSQEFW NFCEVPVEAVDAGDCDINYEGLDNLRL KELQSLSLQRCCHVDWCLSRLYPLADF VAGAFRWAGCPRI FRTGAKHGFHHLQ*D LSSGWATCGTSPT
13083	26984	A	13223	1019	1238	LTGAEYKKS DGLTESVTANLEPEAPKVF SRLDDEAPVTVLPARLPLPAP*HTARPD PPQRRRSMQLAPARPFL
13084	26985	A	13224	1534	1181	RWNSEPDYSAGGPPRAGRARLLPVPKSP GGGAVAPGPGTPLRAERTAVRLSISS* NSSTAPADPGAAPLHPQPAEAGTWVSA FLRVIFCFPSLGFPGWEKKIAFVFPPPT DEKCL
13085	26986	A	13225	328	22	CLESFDRDPFGGPAFPKHPPLAFLSQ PGKVQYFFESNCKSLSSQBIKNSRSVPT SPPAPSPPPPPFLYFSLTAEAGEV*KET LDSRAPPSSREAPICQV
13086	26987	A	13226	180	5	NSIDYKINVKNSNRPGAVAHTCNPSTLG SQGRIT*AKEFETSLGNIVLLIYTIY YI
13087	26988	A	13227	237	528	VGLCQDPLLLTLTDSFCSVLWGGSHLAF HKNLYVVHIDLVMYFSRISFYFTLSAAI CLSLYLGSHILSPFL*LFYCAITTLYLCL LITLFFLIPKV
13088	26989	A	13228	140	366	NATCLWHPMSPYAPTY*C*LSPGLLRWV LAITPIVLMILISSYNHVSISYGGTFRS NFFLDQIILTLIYELHIV
13089	26990	A	13229	257	25	LPAHSLGRDLQAQPYSMRPGGELRAEG QSSLCVARSSL*LHVCVCVCVCVCART CVNVFACVLLSTKVCCLHPLPE
13090	26991	A	13230	561	52	WPSCSSSGSPMLLPVPFPGSLG*SFSP LPAAALPAPCAAPRAPLRPCGPAPT AAPAPAPAAASLSAARAAGSPGSR PSARGARRRPSGCPAPPEPRLGPRAPSS APRTRTPS*GRARSGGSAGNAPSARRTP QGPPRAACSLARSWIPAGRGGSCGRAL GA
13091	26992	A	13231	335	103	CQKYSTSYCNKWLATLVIICSRKI*DGL

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						KGOAWLWLPVPIPMLWKAEBVGLPEARSLSSPCNMAPALKKIFLIGQV
13092	26993	A	13232	452	712	VGLEGED*PFFSPAQSLSLSCWPDSCSPSWPPDQRPGERPQPPDPESHGABEEGLPERPSDA*ARPQPSLHPGVFPQNAS TQ
13093	26994	A	13233	480	2	SCFSEDWNPLKFKLQLSTLSYRKSHTLHCAHFRGQCHSD*AFLVFSLTCLQVGLSLRFTAGDVSPSYPEKLRVL*EGRVADFHV MARKGQQAALAILLQNARTGYVWVLT FVIPALWKAKASGSVKPRSLRQTWQNGE TRLLDRGESASQSAGMTGM
13094	26995	A	13234	692	824	QIMALEFPSPFPVPLVM*CKGGKIPPPP SKNPRTCVGNTVIIKA
13095	26996	A	13235	657	872	BRGPRLDVLVACEPQLITCLELGTPLKV RFWLEVVDHTYNPSTLGDQGGRTA*GQE FKTSVGNSTLSLKKK
13096	26997	A	13236	168	365	QESLCILQTCTCAHQNLK*KFGGKSRLG AVAHACNPSTLGGQGGRII*GQEPETSM VMVKPYLY
13097	26998	A	13237	31	338	WYIVYICVCVCVCYIYIYIYIYI*YI* YIYIKHTVQ*H*HLAFSTFLLCNCHHC PSLELFHYPTLTHT*ITPHCSSC*Y QPLFYFHLVFDYSRYLV
13098	26999	A	13238	714	1001	SSGVSCINRAGWITGVNHHIHSVLKKR EK*TONIITEVCLMFLLLPHLAIEATVT WPGMVAHACNPSTLGSQGRRSV*AREFE FSLDNIARPL
13099	27000	A	13239	250	406	NLA*HGGVHMWSSASQVAGITGTRCHAQ LIFIFLVKMGFHHVGDGLNLLTL
13100	27001	A	13240	256	193	WINFISLPLSSLT*TLSLCVCACVYVCV CVCLRPCVHIVGGLKRYIVFARSVTLG CKFTHLHISLIINNDT
13101	27002	A	13241	1	257	GMDLWQMCHSLSLPLIFFFFFFSEKTRS NFVPQAGFQLRALRDPPA*ASREAGITG LTHVVRPGQIFKKIGTLKPTILLELLPR K
13102	27003	A	13242	319	406	KRGWT*WLMVPIPTLWEAEAGGSPDVRS L
13103	27004	A	13243	228	56	KGAPPVLKPGYPKAAKNPTPFKPPGSKV GENPPLP*NPCPGGPNPFTFFFTFFFFF F
13104	27005	A	13244	1687	612	ILGNQCKKFDAYNALANESTMISIKLNE *VREREREKEKEKERVREKEREKKKL TSSKGTGSTATPHV
13105	27006	A	13245	220	1	TKDPSSTMPQPNNLLSFKSQFIFLIFL FIKKYVGWQWLLPVIPAL*EAEAGGSL QPRSSRPATWRNP I F
13106	27007	A	13246	204	375	ASWPPGLQYELRIIKCLLHCWTRAMIFR ERERERERERERERERERERER*VHLKRKG A
13107	27008	A	13247	158	2	IWVFKETFFQNFFFFGKNNFNNGFFF FFFFFFFF*DRVSLTLHPSLGYR
13108	27009	A	13248	221	3	NPSQGFLLKIFFFFLRLWSLALSRLE* NSI*KN*KI*KISWANWRTPVVPGAWEA EPGESLEPGRQLQNE
13109	27010	A	13249	81	341	GELNDTIHVKYLK*YIKVL*RNRTNRVC VCVVCVCVCVYACTQKDLP*GTGSCNC

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						GALVRPKSARQASRLKTQKTVVIRSLKAVC
13110	27011	A	13250	299	1	ATARLRFLHGAWWYASVVPPTQAEARG FLDPRSSRME*AMILPRTCPASVTDKIP SLASQIHRPSRVACVILLSSHAPTEAPS RWPPPSPLCPAGSRA
13111	27012	A	13251	106	146	LCVLKQVKQATWTKYSSSQIFAILDCMT TLSSHPALKYCNYVLISNQSPNHLRL*C SGMISAHCNLCCLPG*SNPSPASASRVAVC FKASQASYLD
13112	27013	A	13252	217	158	LFEIFCIPFFFFFFFNFETRSHSVSQA GVQWCKQGSLLQP*IPINFFWGKEGVIDK LILISYGNAGGFKVAVTPVCTTALQPGR QSETLSQKRN
13113	27014	A	13253	150	56	TILILLLYETESQSVADGVQWCDLGS IQSPPRSSCHSPA*AGVNRLRQENGMSF EAEIVLSPDRTTALHPGLQIETLSHII IILILSTISFHQLLH
13114	27015	A	13254	174	145	PCLKMTTYDFKSALEIAFFCFTAILRYK LLIKVTHFKWLRVAHDCNPNTLGSGGG RITWGHEFKTSLANMA*PTTRYSQRVG IMGITIPDEVWSRTQPSHIRSGPSKVYP
13115	27016	A	13255	179	273	GQWLTPTVISAL*EVEVGGLLETRSLKQAWAT
13116	27017	A	13256	264	382	GLKIGKGCSSWFTFVIPTL*EVKARGLL EPRSLKSAWAK
13117	27018	A	13257	1199	1563	YLVVGPVAVPPLDLEPGQAGATCGPVSHY KIFAKLWAVGSIIDLMGPGE*GSFLSVF TSLCFIYGVITYPFHSEQPHPASPSASGL LLLKGRAANLVSTLCIGSPAPMLTGIFP HKVYNQLFI
13118	27019	A	13258	194	242	ILYVETGSHYVAQAGLELLGSGNPPAST SEIAGIEA*ADEFIYVGVSQWQDECIKSM KQVAHASIPAISEVEAGGLPEPRSSRPA
13119	27020	A	13259	322	120	GPTEVLDAFOKCLSFSTGGQADGIIIPA FPIRKQGGTQWPKPVIPTLWEAKAGRFL *PRSFPAWAT
13120	27021	A	13260	237	1	TSKKISLGNWKGQIGPWEG*AKRPF PGKPRVQWTOVPALDFSLGGKARLCLKK KKKKQKQKTLKCLTHSRITYSRA
13121	27022	A	13261	52	318	SAVGIRHRCDDGSH*P*TPCHKQLSFLSL PSSWDYRGITRELFQRFPIPLQLITAV ISSESTVLKNLELAAVRGSHVRVIMMAV PINPF
13122	27023	A	13262	274	1	KKKKNSPVWWTFVPIGSPG*AGELLEP WRQKVLAQVVPPLAKVVPQTKVVQGCPL ALQPGEHQGIFVSQKKKNPKTKRYWAL FCSLPSC
13123	27024	A	13263	717	877	NSTKEMAHWPVGVAHTCNPSTEGG*GGW IT*AHEFETSLPNMVKPHLYKKYKK
13124	27025	A	13264	288	131	SLYIWHSKRLITITNNKISGVWVCLPVV SSTWEVEAGGSLEPRR*RPWATK
13125	27026	A	13265	80	287	FMNGEAS*KTSILSQAWWCAPIVPAQ* NEAGELLEPRSEWLWATRALRISRL RFRFLRRTSTR
13126	27027	A	13266	3	241	VGLFLFFETESCSVTQAGVQWCGLS*L *PPPPGIRDSPASASQVAGTTGTHHHTW LIFLYF**SSGFHYVGLGRSSNS

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13127	27028	A	13267	103	359	ICVVVYVCIYVYEMRATSKDFLNQVWFS FLRTVAVLFEEYLIVL*MWLSFHIHIYI HTHIHIFIYVYTHVLIYVYIHTYSYMC HIYI
13128	27029	A	13268	172	12	SARSSQAIQIQKSVTSQGVKQW*QS*P TPFLPTLIALTTLLLPISFFILIL
13129	27030	A	13269	2	203	RIENIRSYKNLAALFMTAKRMGTIQMPH NFEWINKMWYIHTLEH*SDKKKKKKV RAEIPKLIQK
13130	27031	A	13270	236	365	KIYRQGAHAHTCNPTLGGQDGNIT*GQ KFETRLANMVKPHLY
13131	27032	A	13271	371	15	QNQINFALILIIINTLLALLLIITF*LP QLNGYIEKSTPYECGDPISPARVPSI KFFLVAITFLFDLEIALLLPL*ALQT TNLPLIVMSLLLIILALSLAVE*LQK GLD*AE
13132	27033	A	13272	2	16	PRVRTSSRSRAALELIFFFLGPPNLPV YNGPLGRTPGTGELDTGSPILCVGQG RHPYWKGGAKPLAPFGKGGP*GTRPLA GPVPPKAGLQSEMPGMAFFCGSFG*PT RPD
13133	27034	A	13273	329	290	SSALVPRLECKGIFSAHCNLCMGSSNS PTSASRVAGITGVAGQATDKTPQTL* SQPSHMDPVRVVS
13134	27035	A	13274	175	13	APCDHRPCPPENNPL*L*FSITFPNPIK RPHPLPLTLFSDSAHLHPGEIQR
13135	27036	A	13275	355	861	PLITTPAAPRAPCPPSRISGQPLTGPT GSRRLSPNISEQGEPLALTGVHPLST QPGPTVPSELEPIQGPRG*GDCPTPSQS A*GGVLSCTPESHTFKPPPTGGRRWA RLGLNGAT*GREBPLQTRLPAEYPGPGP IDPLQPPPISTASMATAFSDFLLRDP A
13136	27037	A	13276	865	667	KFLCILLDLFFIF*EMRSQHRLECSA IIAHCCLKLASTDPPTSAS*IAGFTGM CHCAQLFTF
13137	27038	A	13277	103	375	WSRRLPWRRGLGYIELFQGLBIRHFLP GPHYLRRTQCQGPVIPSLEDGQWDYMS PGV*DQPGQHDETPSLQKI*KTSSAWWH APVVPAT
13138	27039	A	13278	177	3	QQTEGSRASHNSHRRPGAVVHASNPNTL GGRGG*NI*SQKFKTSLVMVKPCLYGR V
13139	27040	A	13279	379	372	SR*WVCMVAHACDPSILGGQGGRT*AQ EFETSLRNMVRPCLCLGNTNIYIYIHTH TYIFIQN
13140	27041	A	13280	83	1184	PPAHAARASPPSYTWLCYEVKIKRGRSN LLWDTGVFRGPVLPKRQSNHRQEVSSWE CRKHISKMSGGLSTVYFFHRRFQITWF VSWNPCLPCVVKVTKFLAEHPNVTLLIS AARLYYYRDRWRVLLRLHKAGARVKI MDYEGERCQGSGMTGRNSLRDGIWICNA INVASLHRTLKEILR*GSPSGLIVSLLS PPAHPPEDSPGNESWLCFTMEVTKHSA VFRKRGVFRNQVAPKSYLHPK*ELSSWE RRKHNT*HTNYEVTWYTSWSPCECAGE VAEFLARHSNVNLTIFTARLCYFWDTDY QEGLCSLSQEGASVKIMGYKDFVSCWKN

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						FVYSDDEPFKPKWGLQTNFRLLKRRRLRE ILQ
13141	27042	A	13282	1558	1824	SFPYLASFPPCLGLEPLETLFHPGL*KD *SDTHTHTHTHTHSHTHAHFPPFPDP LFQSSPFPSSGFIDEYKYPHLWPMVSVTC CRFCV
13142	27043	A	13283	1	519	PHFFLPQGFWGFSPFPL*KSSSPKLKAL IFLGGFSPFFPPPKRFFSKI PRGVFFP PPKGGKFFFPFG*IWPPQGFLLKGGPS SSSSSSSSSSSSSSSSSSSSSS
13143	27044	A	13284	349	159	CPLEPKKNYPFCFF*ETGSCYVA*AGL VLVASSNPASASQIAGIQGTSRHAQPC RIFLSKT
13144	27045	A	13285	748	869	WLGVAHACNPSSLGGRGGQIV*PQEFET TSRGNMARPQSL
13145	27046	A	13286	315	410	VQWFTPVNSALWESEAGGLEIRS*RTT WAT
13146	27047	A	13287	355	499	ARCGMHLYSQIFGRLRWEHCLR*KVLS QVWWHAPVFADIWEVEVGALLERSRL *CAMLPLVNSHGPPTWAMQ
13147	27048	A	13288	880	701	KSYFSSHLHFEGKKCVSSILD*SILVLM CSWLMNYTHHTYIYIYTRTHICVHVYV HNF
13148	27049	A	13289	379	434	KRGFPFPPKKRGCFSEKFF*GPPKTPFF FFFPKKKKKKKKKKKKKKKKGGRSRS RLADAWADAW
13149	27050	A	13290	253	344	GLFYNLQKIKIFYVKNLFFFSNSITRA GVQWPNLQSLQPPPSGNSDSPA*RV V
13150	27051	A	13291	561	745	AWEPSLVGETNVNSFNQYINWPGAVAH TYNAGTLGGQGGWIT*GQEFETLANMV KPSPY
13151	27052	A	13292	289	2	TLPQGEDFNKFVFGSIKQLQYNL*NTD FIGNVFQSWAQYTTPVPPSWVAEVEGS LAARSSRPCTIITPLNSHCSLAWATQQ DPAGRVGRPRV
13152	27053	A	13293	281	229	LKNKNVNKEKLRQGVVAHACNP SILGR GGWIT*GEM
13153	27054	A	13294	276	441	GLFFKFLIQKINQNPDAVVHAYNPSTL GVQGRWIT*GQ*FKTSLANRGRKSENK
13154	27055	A	13295	258	389	NMVEKRLGAHAYNLSTLRQGERIT*A WEFETSLGNVVRPCI
13155	27056	A	13296	358	353	SFLAFFNGAFLPLRGFFWKTFFFGVCW RRPPL*RKKKKKKKKKKKKKKKKKK MFERNIGGEERGGG
13156	27057	A	13297	196	1	LMGKAPFLGGFIPPAFFFLKRRKGGPG AVAYTCNLSTLGGGRGWIT*GQEFETSL ANIAKPCSC
13157	27058	A	13298	182	436	GVTLNVHRHRKVTLYRDLKKVRKCP KLHGNLRKVFAEGIASSTLKGHVWWL MPVIPAL*EAKMEGLLEARSLSAWATQ
13158	27059	A	13299	334	440	RHYWLN*AFYHSSLAPAPQGGGHWPFP GITPLNSLHVPLNTSA*LASGV*LT*A HHRLVPNNRALIIQALRITRILGLYSTL LPA*KNFEAPFTISDGVYGSAPF*ATGC HGLNVIIGSTFTLTCFIRQLIPHCTSKQ *LWLEPPAWDW
13159	27060	A	13300	359	372	KKKKICGGKKNPNKKKVKPRGEKTPK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GV*PFFCLEGFFSPHKFFFFFIFSPNIC SPKKSFFLKFPALFFFNLPFLKNIPSP PFLKKASF*EIFFCGPPPPFFQNTLF FFPPFFFFFFFFFFFLLDKFAVY
13160	27061	A	13301	233	406	VTVEGMEEVLGSSSEGMGSRPTS*V*FL KYLGAHAHAHKPSTLGGRGGRIT*AQE LKTSLSKNKVRPRLYKINK
13161	27062	A	13302	92	429	GSHFNSELIEMKFYIIRNIFITLNCFY LIKQHFHYTKFLLVSVINKF*LATVAH AYNLNTLGGQGRSA*THEFKTSLGNTV RSCLYKNLKMSSVWWTATWEAEVRGLP
13162	27063	A	13303	302	140	GGAVNSVQSAWVWMPVVPVWEAETGL LKPRSLSL*CPMIVHVNSHCTPAWAT
13163	27064	A	13304	115	312	LRSPSFVLSPRLKCGGTIMVHCSFDLLG *RNPPALPSKVETIGLHHALLRLLI FF*KWVVLFF
13164	27065	A	13305	90	246	PGVVAHACNPSTLGGRGGRIT*GQEFKS SLCKIAPPPERKEGRKEGKKKERG
13165	27066	A	13306	19	310	DSSFSFIMCFGMSVNTGLWLGGKKKKK KKKGGPP*KKPLGGPNLPGGKKKFFP *RGAKKNPPGDFWKKTLFGGEKLGPPP PQK*NPFFGGGKIGPTPPPKIKPFGEKK KF
13166	27067	A	13307	179	56	WVLVYKKQSILG*AQWVMSVISALWEAE AGGSLVSTSLRLA
13167	27068	A	13308	425	290	KKNIYLAPPGYFWPPQRFLLSPPPPNV VIFFFLFFFLFFFLFFLIQYABGIG VMRGRGEGKMGR*W*KFFGRRVLNIRSI LLANFKHVVPY
13168	27069	A	13309	214	371	IYF**RWISQAWWLMVPVIXLWEAAGG *LEPMSLPGQYNETSPL
13169	27070	A	13310	975	572	AWGMVVGKHSLSVLSIGIECQASTALS LDKSGWNEAARREDVLCBDRCLLCHV PAGVRGSLKPELGSRKNGQQSGSKPS VPSLGRPRQPGNPALSGTRPN*AICF LCQTPADHSAKQAPHTLPIR
13170	27071	A	13311	270	10	TPNKSIL*RLQFSNLIKLANLGLGTMAHS CNLNTLGGQGARITSGBFKTGLGNIDP IPIESKVIKTLAGMVSPDAWDAIKRTG TSG
13171	27072	A	13312	103	290	LTEVVSGVIL*NCIYLLPQYTSTRVHAY IHTYIHTHTHTSGLSSTSVGSTNHKSKI FGGKKG
13172	27073	A	13313	136	1	SNTSSSLVTQAGGQWCELGSL*PLPPKF KRFSCLSLPSSWDYRRL
13173	27074	A	13314	88	183	RVSTLLKSCFFFFFFFFFFF FFFFSSQKCNLKNKKR*KKSCFFFFF FFFFFFFFFFF
13174	27075	A	13315	481	517	LLSF*RPKGKPKGKRRKPNLKEKKIGEA RGGKERQRTQRTGKQKRRKYRRIGR RNYR
13175	27076	A	13316	307	196	GMHLYLPRTW*WVRVIPGSREIEVHAPL EPGQRLLVAEMTPMHSSLDNMNKSFPF QPPKTEKQTKNPPKPHIIA
13176	27077	A	13317	2	209	PARALDLKGSFYMESCSDAQAGVQDSIY GDHL*LRAPAV**GQTVFVASPSKVGGI TGASHHPGLFFLF
13177	27078	A	13318	3	178	SFCFSVLREIIGQSLIMKTL*ITHTHT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						HTHTHTHTHTQREIERERDRERGESQVLGC
13178	27079	A	13319	40	382	DSVPSLLLLKLLMETGPHHVQASTTTPS *FFILEGFHHVAHAGLKLPSSSRPPhLA SQSAGIYGCEPLRSARLIINYIGSRLWG LRNICLSQDHEBCLLCFILQAISMYPFC LG
13179	27080	A	13320	107	1	PPLIMANSQWAOQLTPVVPVLWEAKAGG *SEVRSS
13180	27081	A	13321	111	382	ASSQLELELAIQVFPFGIWIPTTKQKGV SGKTLVTSKIIAGLKMPKDSRSPRTVA HTYNSSTLRGQDRRIT*AQEFKTSLGKI GRPCLF
13181	27082	A	13322	49	108	CGLY*FFF*ATRSWHVAQAGLEFLGLSS FPASASSVAGTTGMCCHHTQLEY*F*V
13182	27083	A	13323	1	257	ARGRERERERERERERERERERERERE RERERERERERERERERERERERERE RERARERE*ECV*EGETVSDRERDFERA PFRVLGAVALYIEVVCLASLIQ
13183	27084	A	13324	1	248	EFQYILCSALIFGRSKILK*ATKEVKKS KHIPRISQDTRKYNWSAKAKRRNTTGT GRMRHLKIVYRRFRHGLHEENLFLKH
13184	27085	A	13326	375	1	PPKRRGKTHCSPPKVFPFPQNN*TTPPP QLIICYL*RGGVFFSLPLII*APPAPFF FFQFFFFFFFFFFFFFFFFLQGYWQFRDT DAEGHLASSRPSGAVFPSPQMHTTGSTR RWGQCVFPFPTRP
13185	27086	A	13327	382	15	NWPKNCPLHFQNWFLRKTPQIFFCLKNF FFFFPKKVFPYPPKPKFLEKPPVPLN*K KPPPPFFFGWGPQGYCPFKKAPPLFI RGKERFPLWKGDFQIPCPGGLKKKK RAAADLGTS
13186	27087	A	13328	2	220	GRVGSRRARAVALLFFFFFFFFCFFFFFF QNPPLKRGKKKNTPLKKRPLRGGFK KQKEC*EKKKLSGPK
13187	27088	A	13329	427	289	IQLWSSL*K*LHTHTHTHTHTNTCPL TVMKELSTHGNK
13188	27089	A	13330	203	269	INFGPPREPFGFNQKPQFSPAGFEPWN PPQGPKP*KKKRKKPKFWAPGGGSKV QNPGLRETGVFG
13189	27090	A	13331	216	418	DVPVHYCRLYKPTLRLHSIYKKQILLW PGAVAHACNPTTLGGRGLWIT*QGEFEA SLANVVKPHLY
13190	27091	A	13332	160	325	WERQLFKIAQSGLARWLTPVIPALWEAE EGGLFEYTSLR*LWATQDDPISTKMFK
13191	27092	A	13333	339	62	GMLPLFVPPQKRGSPPPYPCYGVNSPPL KKQRFSSSLGIVLPPIVFITPPPPAFF FFFCFFFFFFFFFFFFFLI*RRLMRRRM FSCFLHCP
13192	27093	A	13334	45	384	DPSVRINTLLALLLIRITF*LPQLNGYI EKSTPYECGFDPISPARVFFSIKFFLGA ITFLLFDLEIALLLPLP*ALQTTNPLPI GMASLLLIILALSLAYE*LQGLH*AE
13193	27094	A	13335	270	660	AGSRRPLRVPGFSLSMSPSLCRPVCVA QCIRVSFLLTVGAVLRPGFQCLDWPCLV YARLSGWTGFPPCRYGKGCCRYDEGCC FGEGCCRCDDRCRCGEGCCRCDDGCC YDEG*CRCDGCGCHYE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13194	27095	A	13336	298	349	KTPPFYGLRGSKIGTL*CSGVIIAH*SLKLLGSSDPLSLVAQAARTTGACHDQLTNAFFFFPLERVPTPLKNNPFLWVGKVKNDL
13195	27096	A	13337	865	518	KSATMRMVEDTHKMPAWGGYSGSLQOERGELSSLP*PESPPPLLI*FLKLPNPLPCSPLPCTQGPQPAPYVSIHTSLKFPNKLKSLVLSRAIEFS
13196	27097	A	13338	154	354	FNLQVKPDGYFVLFICHILPTDSKSGKAPGAPCHSRNFHIRKTLGWVQWLTTPVILALWET*FSHQENSGLGAHAHTCNPSTLGNQGGWIA
13197	27098	A	13339	262	11	QFHFSRKLTP*KM*LSAHSNSTHEAYVAFPKAHKPGLSKTA*LGTEAHACNPNI*LGQGGQITRGQAFKTSANMAKPRLY
13198	27099	A	13340	358	164	TKKGKPRFFLKNSKISRGWWAPVISGPWEQEGGAFV*TCRPKIWLTEVGPLPFFNLGKKKENPF
13199	27100	A	13341	147	2	FRPQKVSVRVGVLAHACNPITLGAQGGHII*GQEF*ASMANMVKPSSC
13200	27101	A	13342	367	17	TSRSWNLFHVLVRFPETADKIDREIGSFTKKRSLIDLITPYAWASFTLMMEGKKEQVTSSINGSRQKVRSSQSGELLSLTPSDPSWAHWLMPVFPALW*SETGSLFEVRSRPAWPTW
13201	27102	A	13343	166	492	EGTQETLCGCIICLVRGDALNLFHLKCSWVGWRGAICCMELRETAKQKLSVWKLYPFEIVFSFNNNPRPGAVAHICNPNTLGG*GGRIARAQEFETNLCNIVRPHLFR
13202	27103	A	13344	804	1124	TFFFCFFL*DRVVDVAPGWSSDMIMGPLQALTSWGSTDPTLGLQSGLDLQDTWPPYPTSFYFFLQGRGLTMLPRLVLNSCTQAILPPQPGQRSKTPISLKTN
13203	27104	A	13345	280	448	GGGGKKKKTPKPPLEKNNSFPPP*FFPPKKQIKPPPPF*GGGGKKKKTPKPPLEKNNSFPPPKPRKGIFFLPPLSWVKKKGDPPGGTRPLAPL
13204	27105	A	13346	232	400	AELLYRCSCGHFL*SMARYKTKPGVRWLTPIPVFWAAR*LHEPRSSRPASATQ
13205	27106	A	13347	138	332	RAVVKPSFEIFYFF*RAHTF**SCVCLCVCVCVCVCV*THTHTHTHKETHDY
13206	27107	A	13348	314	395	WLGIVAHAYNPSTLGT*GGWIT*GPEV
13207	27108	A	13349	388	371	IMNGWQDKELVSRVIQTGIKK*KPRNREFRAPP*WHERNGRKERERMGRKERERKKGKGRKRRKACIYKVKIEISNNLANLIINVER*DRRRPDILSWVLSRVS VFIALVTCLTSPQPFSLHLNLQILFPLGKNL
13208	27109	A	13350	412	40	LVFRFWMCLFSRELFGCFSHLLTKSMSQM*VVAFGDIMYTFDLLFIKKTNNCKLWQGCKEGLIHCWRECKLVQPL*RP1*RSLKKLQMGLPYDPAISLLETYPKERKSVY*RNICTSGRVG
13209	27110	A	13351	372	148	FFFFFFFFFFFFFFFFFATGSCRVA*PGVKWLISGTVPLLISTGVLTCISIDLGPVHTSLGNLVVPYSQELPY
13210	27111	A	13352	209	206	KKKKKNFFSFHGKNPGNGGPPGPPPPPF*TFKKGGGLPKGPPPKGFFWNPPQNG

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						GGGP*PGGEKKTTPKPSLGLVLLLLFFFFKFF KKRPTAFFFFLKKKIFF
13211	27112	A	13353	43	334	KKKKKKKKKKKKKKKKKKKKGGGPFIRISG GAQFFRGEKKFFFFFLGGGKTPRGFFFE KKPFFWGGNFWPPPPQKNFPFGEKKKFL GGGGGKNRVFFWGEKIFSLGFFLKKKFF* KKPEGKNFFFPKKNPVFSPPPP*KFFFF PKGBIFLGGGGPKIPPPKKRFFFKKPPG GFFSP*KKKKKFLPPEKLGPPRNIFYK RPPPPPPPPPPPPPPPPPPPP
13212	27113	A	13354	264	496	KPTILRVTHFLEGCEKYELLPAFNSF SEPLKRYYYWLGAEAHVCPNSTLEGROG QIT*GOEFETSLVMVKTCLY
13213	27114	A	13355	183	9	IRSPKIPETRVFFFSRWSYALVAQVGVQ WGNLS*MHPRARFQPLSSLSVPST*KY R
13214	27115	A	13356	208	378	EICLEFKIIDEKDCGKLWLTGAHT*N PITLGGQGGQTT*GRAFETSLDIMEKRY L
13215	27116	A	13357	256	341	KGQTQWLTPVIPTLWEA*AGLLESRSS
13216	27117	A	13358	78	344	IVGLFESESKKGQHVSGWIYLRLLIYR FLPPLFSLCKKFFFFFSPBTEFCFVPQ AGVQ*HNLG*LKPPPPQLKQFSLTLPS SWNYR
13217	27118	A	13359	259	291	AQ*LMPVVPALYEAEAGGSSLEPRSLLS VWAT
13218	27119	A	13360	448	121	RLFDLGNKKTSSFVQNSENAKYEDSLQF YCRIYIYVYIYVYICIHICVYM*TYMCM YICIMYTYTHVYTHVMCIHTYMCI*A YICVYIYIP*KACPLAISTLSSGH
13219	27120	A	13361	125	262	FSFQASVEFTSKTVSWQWLTPIISTT *EAQAGGSLEARNRSD
13220	27121	A	13362	362	46	ARAKGPKKIGFSGKMGPP*GAPPPKMGK KI*ITPPPKFLFFFLGKTKIKNPPWGF PFGFPKKKRGGAARR*KTPSPFREKPPP QKLKRFKTPFPPLFFFKNRP
13221	27122	A	13363	378	48	FKKAAREKVSTRKFRGFVCLFWDFFWRQ SHSVTQAGVQ*CDLNLHPPGSSDSPAAA SQVAWTGTHHTQLIFIFPCRNKISP SLLKKYKKNLPGVVAGACNPSSLGG
13222	27123	A	13364	174	396	SLIFILEKRECYPRSLFTVANFTVAKR *QTLNCPSTDKWINKMCHHTVEYYSID KRNEIPMRATCRQTLKA
13223	27124	A	13365	76	280	PLLPFKAWQWVGCHYVV*KLD*INCYFR ALLAFSEYMYIYIYIRTHHT*YIYIY IYKLTYSHLKVG
13224	27125	A	13366	133	324	YLL*ILVYCSHLIFSLLCLEGIILWVFI IATLITLNTSHLLINIVPIAILDLAAGQ AAVGLALLVSKKKKKGPPLKKPLGAQI SPANQRKKFPKRPKPIKTRRGTF
13225	27126	A	13367	488	190	FSYACFLPQCWFVCTFYIYLHAGFLLL IIFFENSFILCHSCWVCFLLQWFLLM NLFSFLMLMHPVS*MECSIYFSFSLI IFHFSMLLFFCFMI
13226	27127	A	13368	229	372	YYATKDFSRPRAVAHTCNPSTLGGGRGQ IT*GRQFETSLANVVKPOLY
13227	27128	A	13369	122	2	KEECVSGTWWVMPVIPAL*EAEGRGSL EPRSLRPATKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13228	27129	A	13370	43	412	RPTRPKRONYGDSENISGCGGLGKKGMN GKSTEDFEGSETTLVDAITVGTCHNKF I RSHIVYNTKSGP*HKLWTWGGHDVSV*V PQLRKTYHPGERCL**GRLSMYRGREYI GNLCIFCSLLL
13229	27130	A	13371	136	1	KSPTWPGAMAHTCNLSTLEGQGGWIT*G QGFETSLANMVKPSDAW
13230	27131	A	13372	228	385	GLLIHKLEFKHFWLGTVAHTCNPSLGG QGRHIT*GQGFETSLANMAEPCLY
13231	27132	A	13373	277	429	LETTTKAGLPTIIFTSSGQMSIWFQNK PWDSKKLFNLLSISSP**SSKNY*PWQS TVAHTCNPSLGGQGRWIT*GQFEISL ANMVKPARVGRHVIRGLQVS
13232	27133	A	13374	194	3	NQENYIYIYTHHTYTHTYIYL*LLLQ WVYLAYFLCLSYPSLFAQGFTHHTYTHT HMHTLL
13233	27134	A	13375	377	228	DRVLLLLPRLECRGIIMAHCLRLPLVSN S*APALSFQSAESTGVNVPVS
13234	27135	A	13376	255	465	NAWKCPFIYKITFVIFLIHVSCKKFRNY RQREWKLPTRPLSPS*AIIFPVCTYT SRWPEATKDPQKK
13235	27136	A	13377	336	38	VWWCPTVVPATQEAHVGGSLGRLRLQ *AVITLVNEHRESALASRRGPETSSVK PPLPTILAHTCFSLPRTGQDITSRFLAQ RNTBENLELQMEARA
13236	27137	A	13378	376	293	FFFFFFFFFYFFFK*KFLTCKKILSSQ YI
13237	27138	A	13379	215	16	HLTWSFTTATEGSKTIVTQHSVYRKALG LGAVTHTCNPSLGGGLGRWIT*GQEYKG IPPHGLEDVQ
13238	27139	A	13380	184	64	VDESLEGWMMDEWMSGWRGGCINRYMHA WMDG*GDGWIGG
13239	27140	A	13381	233	417	LKPITKGRKPRGFFLFPKPKQKKYFWGF KKKKKKKKKKKKKKKKSRAPF*KKG PQKTP
13240	27141	A	13382	34	360	RWNTNADHDLKDNILSPQINLYIRON SSRLEFCRH*QMDSKSPVKIPAGFVLYI* IYRYTHHTHTHTHTDSELYMETHTRMA NTIVRKNNLSLEHSYYLMLRMTIKLP
13241	27142	A	13383	214	71	QTLNTDSGPGVVIHACNPSNLGGHGGKI I*GQGFETSLANMVKRCLY
13242	27143	A	13384	352	312	DKQLTLHRTDSLIFITY*PPOSCEPIS YNNFPCLSQYLYLCPSLHTHTHTHTH THTHTHTHTHTHSVGRRLFFSGPHTB APRSRVSVYT
13243	27144	A	13385	393	271	IEGQIQYTSTIGNKFKDFYLILCKEGIM SREISPPSSCHLRQQ*RVRLRERDRERK RQREQRERE*GRSVLHPHVT
13244	27145	A	13386	180	440	PVEERTLCEDILCFPFVLLCIQFHLLI QHACFKYPNPNRFRGSGWGAHAHCNPS TLGGGGRWIT*NQEFPEARLSNMVKPRLY KNI
13245	27146	A	13387	190	47	EGERGVPSTILKMETLLGTVAYPCHPST LGQGGRGRIAEQBF*DHLE
13246	27147	A	13388	188	470	ARPPCKGRDSSAEGPPGPPFWSLGC WTRPPGRGEPIQAVRREESAQDWARP ELI KEWWPGLVAHTCNPSLGGRGWI A*A*EFENSQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13247	27148	A	13389	454	367	NKKKPPPRPP*PPPPPLGKTPFFFKKNP NFFRGGGNSPGSPSPGGGKGDPPGGF FPPPPYPRGEGGNPFFKKKKKKRASLD P*WSSQPCPAYEKELNFAFVLATVTLPP GHSS
13248	27149	A	13390	34	354	HTLLALLLIITF*LPQLNGYIEKSTPY ECGDFPISPARVPFSIKFFLVAITFLLF ELEIALLLPLP*ALQTTNPLIVMSSLL LIILALSLAYE*LQKGLD*TEY
13249	27150	A	13391	1089	792	THGFGPQVGSPLDLKQPKAMPQPSLG NPPPGCQQHSHGAGGP*VPPGPRQPVMA SRNLCLPLALPRTHTPPSPGQTRDKPRTQ DRSCWRDPNPGPV
13250	27151	A	13392	299	428	WIRCRGRGRSCLPVPHSAPALLSPLVVD GTRRREAGGTCCGGSGCMGAHWGLGGG EGSGCRSQALPREAAEARREFKHGGIPR H*LTESLVSVEFRHA
13251	27152	A	13393	382	413	HGKTHLYKKFKNKKPKATMPA*WLTPVI PTLQEAEEASLKPSSRPAAVWTWQDPS LQKI
13252	27153	A	13394	64	401	GGIFKEDSQAGFTGIGERQOGLVIPLL KNGQLSTDACVPPWGRVGVVERAGPPNPQ AGEGGGQGGQCSLGLLPEANRCHPCNPS TLGGRSGQIA*GQFEISLGNTVRSCTPY
13253	27154	A	13395	146	18	FSPGVVAHACNPSTLGGGQGGIT*GQAF KTSANTVTKPRPQ
13254	27155	A	13396	1056	679	DIQVPERPL*NVPEPAKGEPPDRAVGE HIDRDCRSDPAQQRKIFINKCERAGCR QREMMKLTCECSRNFCKHRHPLDHDC SGEGHPTSRAGLAISRAQAVASTSTVP SPSQTMPSCSTSPSR
13255	27156	A	13397	440	423	IHSPPTQRRV*QREERERERERERERH ALAEARNRTREGISGTTGERGNMLVGH LPGPLSSRRLGFCPDGFGGQHCLAQGDQ VRL
13256	27157	A	13398	2	256	IETLGSAREFIPYENTYQTYLKKQNRNS HMQSPNRRKHILKYIAAWA*WLTPVI PALWEAEAGRSLESRSRNPVSTKKKIQK
13257	27158	A	13399	102	922	LSFFLFSETGSCSVAQPEVQWCNHSLSQ P*TPGGPSMQFQLPQEQGQRTAVWHGGR A
13258	27159	A	13400	198	55	KDYSAVVHTCNPSTLGGGGGWIT*GQEL KTSQANMVKPHLYKNPKIEF
13259	27160	A	13401	19	447	ESALNLPASAGIIGVSHRTQPIFCILNAL ALGVILILERSPLQSPQVPPSHHTKPGS LPSVTPGRGPRPRAAEPTAQGRYNSN PVLISPGSVHPASFALPAEPP*TGAPST PRPCVLRPLLGNAMDLLCTKLSSRLPP YRT
13260	27161	A	13402	93	410	DSNLNYSLFFHGEADLGTNQVLTHTPSTT AMYFEHYCQPP*IVHGTINT*PPVVKRN PIHIITPSPCLRASTAINLLSHINCYS *ATPHPLGYQQTLYLPLTVHST
13261	27162	A	13403	55	387	SNSHTYSLKKSAGITKFNWHIVNCICI CQVVVFLEMVNRHTVILCQYFVKPRILY QHHTAILVTILTFTLRPGVVSHACNPST LGGGGGRII*AOEFKISLGNIVRPLY
13262	27163	A	13404	39	365	SGDRRVRLLLKIITF*LSQLNGYIEKST

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						RYECGFDPISPARVPFSIKFFLAITFL LFDLEIALLLPLP*ALQTTNPLIGMSS LLLIILALSLAYE*LQKGLD*AE
13263	27164	A	13405	32	350	HEFATSTSEMTKGTST*IVKRRIKHTLTC RRCGSKAYHLQKSTCGKCGYPAKRRKY NWSATAKRRNTTGTGRMRHLKIVYRRFR HGFREGTTPKPKRAVAASSSS
13264	27165	A	13406	326	668	LQPKIFCMPGIFTISEVSSMSN*RTAYG SQSPHKIVLI*LATFGQALSC*IL*IHL CYLKNKTKHRALVAHACNPNTLGSPRGR IA*GQEPETSLGSIVRLLSTKNLKKK NM
13265	27166	A	13407	170	472	KLISVWSEESSYCVHEGEPVVPQEKES WLEIGKAEMERSTLESLLGATLEALSSN PTRKMQGLKLKLQASAFKEEPWLGVA HACNPSTLGG*GGRIA
13266	27167	A	13408	178	422	FYNRYF*YTKTYQTENIYCKIMSFRLLV *KI*SLPGAMAHACNPSTLGGRGRII* GREFETRNS
13267	27168	A	13409	274	444	LFSQYIVFVHYSSFVLILFV**LFSQYI VFVHYSSFVLILFVILHNYTYIYIHTHT HTYTLIFLLIFSQISLGWMLIL
13268	27169	A	13410	205	23	KEFLKFHRKCICQOVKKIWPRAVAHACN PSTLGGQKKRIT*GQELETSLANVEKPH FSNS
13269	27170	A	13411	25	426	SVWWSLETRSSRLRLKKI*NLQNKRR KFHRHAQRKYDLETQGBDAIYKLRER RKEEE*EKEKKRRRRKKEKKKKKPTL LCLKQORNQHLDLRLPASRTVKKLISVV *ATHSVVPCYGPSKLIQOSIH
13270	27171	A	13412	227	52	EIGSHSCHPGWSTVAQS*LTLTNSN*TQ LILPQPPPRELHYNCPVPPPAFCRQALA MF
13271	27172	A	13413	345	67	SKCCYVVAHDCILLDLICLYFLELVGCV DCFSSSLGHY*PLFV*IFPLSPSLFWY SHYBHCVPHFSAKPFIFLHFFPSPEFP FLCIEMVYV
13272	27173	A	13414	345	33	KVFFFLIICKMRMKNQKKNHIGICLLNS AMNTCISFPLRQQIMTTWLEVTQIWGV LFYLFHFIEMGSCPGWSAVA*SQPSATP VWSQVILLPQPPEDLGNS
13273	27174	A	13415	187	415	FNQGWAFLEFFCVIFSYPWKDRNRTIFS IKITSFQESVLKLCIFEV*ILKIGLG QVRWLTVPVIALRRRQADH
13274	27175	A	13416	143	50	CMKLQSSIVMLGVVAHACNPSTLGGQGG WIT*GQGGWIT
13275	27176	A	13417	170	17	KQMRKEGNGLLTISKVWKQPKSPSQS* *IKKM*YICTMECYSALRPEFPE
13276	27177	A	13418	7	163	IK*IWI*TMYYSAMKRRKIMSSAAIW MKLRAIILGEVMQEWTKNLMFISGS
13277	27178	A	13419	901	709	SGRKTSLGNIARSCLYTKSFKIHCLPVP PATQAEAGGSLKPRSLRLQ*ARSHHCS PVWVTRP
13278	27179	A	13420	236	4	VIRAKTGSNSLFPHTFFQGNLCFF QKKKKKKIYIQSKPGAMAHACNPSTLGG QIT*DOEFETSLATMVKPNLY
13279	27180	A	13421	46	141	NSVISAHCNLCPLGSSDSPSSASRVAGI TGWC*HCNLCPLGSSDSPSSASRVAGIT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GWC
13280	27181	A	13422	604	1121	LGSGDLP*EINPLSSCSLLREKDPPTTS GPQTDQPKKHLTNFKSAPYKTTIDAELR VTLTVEAHLHPGEINSHVAHTKPVWWSL HTDAHEIWCSDSLKLVPTLPLIPLEAA LRNITHSLSTIPPPKNFRPNTSTLFCVI FLINIRRQEQASEPKPSHRIPCDLHVY AQMA
13281	27182	A	13423	214	22	IRESSSTPSSPTLPESCNSIPFPF*KFI WSGVVAHAYNLNTLGG*GRKIARAQRF NSTRAGLW
13282	27183	A	13424	397	330	SEYNSECS*VQWHTLVVSATQEAEEAGS LEARSSRLCALIIPVNCHCTPAWAFPM
13283	27184	A	13425	729	885	AKCYPVRNLSLWPGAVAHACNPSTLGGQ GGRT*GQEFRTSLANMVKPHLY
13284	27185	A	13426	231	2	ASVFFKATLVDLHW*YIYTYTYTYTYHI YTHYTHYIYIYIYIYIYLVNMQYICLYV HINANQQGYIYTGRTPICPF
13285	27186	A	13427	184	171	LS*YIYIYTHYTHYTHYTHYIYIYTYE QPSSQSS
13286	27187	A	13428	372	166	CKFRPRKINTTFSHICGS*KVDIEAA* HWLGTVAHACNPSTLGGQGRWTI*VWEP KASLANLLTPLLQ
13287	27188	A	13429	391	437	MYSLGVGPFPHSTI*LLKDI*FWSGVVAHT CNPSTL*GQDGRIT*GRKLETRPGNRAK LYLYKKNSN
13288	27189	A	13430	39	254	EFIPRAQDLETSQGNRVRPRLYRKFKNN *VWVCASVVPAMWEAEAGLSEPGRLRL HSNMDNGERSCLKK
13289	27190	A	13431	336	488	DIWPGMVAHACNPSTLGGQGGRIA*A*E FETSLSNMARPWLKKKLARHSGA
13290	27191	A	13432	154	481	FFFFFFFQKQNGFF*KGIFFFKLEGR GAI*PNLTLPG*GKSPASPL*KGGKK GGAPPP*LIFFFLKKKLPLLQGGGLKL RALGKPPPPPSQRGGINGVKT*PFGL
13291	27192	A	13433	388	280	KSKLKGCCVALCLLGLI*SVLLA*PKT *LPCVSLDMYIDTTCSLISISYLSIYLS IYLSIYLSIV*SVS
13292	27193	A	13434	187	48	SISSTKGPGAHAYNPNTWGGGGGRIT *GQEFETSLANMVKPRNS
13293	27194	A	13435	71	309	DSVSEEEEEVELAHPLAAERYHCERA ET*VKALLWLELCDERVSSRSHTEDCT EELDFDLHARDHCDVHKLFPSNLK
13294	27195	A	13436	18	375	RPAVGRPRTRPINTLLGLLLIITF*LP QLSGYIEKSTPYECGFDPIPARVPFSI KFCLLAMTFLLFDLEIALLLPLP*ALQT TNLPLIVMASLLLLIIILALSLAYE*LQK GLD*AE
13295	27196	A	13437	373	27	THPYSHQEQSP*PLTGALSALLMTSG LAM*FHFHSITLLILGLLNTLTIYQ*W RDVTRESTYQGHHTPPVQGLRYGILF ITSEVFFFGAFF*AFDHSSLAPTPQLGG HWPPGTITPLNPLEVPLLNTSVLLASGV SIT*AHDP
13296	27197	A	13438	575	699	LGTVAHTCNSSSLGGRGGWIT*GQEFET SLANMVKTCPOKK
13297	27198	A	13439	247	168	LENLIYTRVLERHREAKVHFFFSNISYS DKRTDTFVLTKTH*HTHTHTHTHTHT

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						HTRGSHFFY*HTHTHTHTHTHTHTRGSHFFY
13298	27199	A	13440	391	168	TKKKKHPSPRGAREVFF*QPPPPFCVL*FFIVFFLSQGGGGGGEFFPPFFPPPTSPSPPPPRGVWKTTPFS
13299	27200	A	13441	403	246	LPPTAIIIGPPGPPPPF*NPAPFEFFWGPKKKKLSPPPAIKMVFFKGPPP
13300	27201	A	13442	305	414	KNNFHP SILGG*GGWIT*GQALTTSLG NMVKPHIY
13301	27202	A	13443	269	409	PGTVAHAYNLSTLEG*GTMITQGQEF*I.SLVNTVIPHYLQKKKKGR
13302	27203	A	13444	295	37	DPSYLAHVMVTPHQVSTQHTLPRPRCLPEMNFLVSLKIWCQWPGTVAHACNPSTLRGRGWIT*GQEFETSLANMTKTRTRGSAR
13303	27204	A	13445	256	388	FCGFWPGAEAHACCPCTLGGRGWIT*GQKFRSLAHMVKPRVC
13304	27205	A	13446	277	374	SRLTATSSRGWIT*GQEFVTLANMVKPLLY
13305	27206	A	13447	14	387	PQVIHSPWPPKVLGLQA*TTQAWWLTPVIPALWEAKANGSLEYRSS
13306	27207	A	13448	185	379	HFGRRPADHLRPGATNHPGQGETPSLL*NTKKKRRGRPPKKKKLQSLVWQNKIFFLAELKLLW
13307	27208	A	13449	168	346	ISILRTNNMISIKINLRLFIDELKKRDPFIFPYFFFFFFFFFFGGNHS*SLIVIFLIC
13308	27209	A	13450	57	176	VAESRPGPGGTATELVPPSTRLLTRAPRDLITGKRKPPPLGRMSRARVQWHNHF*TESCSVAQARVQQRNLGSL*TLPPKIKQFSCLSLLSSWEDCLSQRVRDCSEK
13309	27210	A	13451	411	241	PPLFFFFFFKQKFPSP*GGGQGWDFGS LQPPPPRVKQIFCPKIPPPWPKKGGVPG
13310	27211	A	13452	307	298	PTHSIVRNKSL*IN*TSSMCSGLKVMRR*SQQEDP*SGVVAHACNLSTLGGRGWIT*GQEFSTFLCPSA
13311	27212	A	13454	191	108	GWSQTPGLGRSSLLSLPQWWDYRMQCRGVILAPHCGLDLLGSGDPPASASQVAGTA AFENCATSFWLP*FLNTQCFKIYKTKN
13312	27213	A	13455	242	400	IATLLDYLQIPNTGPGAVAHACNPSTLGGQGRWII*GQEFENSLANTVK3CL
13313	27214	A	13456	1	346	YVTTARCSCWAGTESHMGAKDFYRQEKHPFHADSGIGWA*DLRQRYGRPGRRM*F SWARGAGEKHS LA*AQNLMFVVTTFWEVKEGRSLEPRSLRPAWATWRNVSTKIKKKKKG
13314	27215	A	13457	166	289	VRSSKLNWVRWLVPILTLWEA*AGGFLEPRISRLVWATQ
13315	27216	A	13458	220	76	TASLKLSKSWLDVVAHACNPSTLGGPGRWIT*GQEIKTSLANMVKPSP
13316	27217	A	13459	219	46	SPPLKKNNFFPPGVMGAPRFFLKGPPQNFFFFFFF FFFFLKQ*EQTFLLIY
13317	27218	A	13460	126	1	VVSLGAVARSCSPSTLGVQGG*IT*SQEFETSLANMVRTLS
13318	27219	A	13461	330	420	NICSWAQLTPVTPAL*EAEAGGSPEVTSS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: In USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predicted end nucleotide location correspond ing to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13319	27220	A	13462	577	766	AQWHTSIVLAA*EAAAAGLLBPRS*SRL KCTMIIPINSHCTPAWQHMRPCLLKKNF SNSFISK
13320	27221	A	13463	206	387	VTVGETEAEAGRGHGLLTCCVLKTQKWL GTVAHAYNPSTLGG*GGRIT*DQEFETS FLGS
13321	27222	A	13464	167	41	DFWLGAUTHACNPNSVGG*GGQIT*GQE FETSLANMVKPWN
13322	27223	A	13465	480	79	SRVISPLILNSVISAKSLLPVGSQKGS KGQVWSTQEERLEPGVMGEFTPGPCPCL VSQGPSPCLCPSPPPYSFRWSRLSQAPGSI RVLI*RPAAATSAPPPAQLGLDPTAFPP PILLSRDGQWAAGRQGDGRDKGLP
13323	27224	A	13466	3	373	DAWVAHASAHASVCLIIDTLLALLLIIT TF*LPQLNGYIEESTPYECGLEPISPAR VPLYIKFFLVAITFLLDLERALLPLP *ALLTTNLPILVMSSLLIIILALSIGY E*LRKGLD*AE
13324	27225	A	13467	214	55	TRQKIFNLFSS*KKFLIPPAPAKDFLFF IFFFFFFFFFFFFFSCSRILLHR
13325	27226	A	13468	111	358	VMKVFI*IGELVTOAYIFVKSHQIAHI LFHSMYVLP*IKMFWPGTVAYTYNPSTL GGHSRRIS*AQEFETSLGNIVSPHLY
13326	27227	A	13469	199	607	RIRGTSQKLLLLKLLISLIPKSQPTRG P*TTFPPTNTNFPFPVAAATAPDPSPA HFVSSPYNPDLGSP*PECPSGRLQREI EQCKKDIQNFPPTTSRICNDLSLKGS ASRRRGHLFCERFVNQFRSPKPKK
13327	27228	A	13470	128	256	EDWMMWLTPTVITPQVEVVRGSLEPRSS ELQ*AVIVPCTPSE
13328	27229	A	13471	94	388	KGEGKTEELWSWRSHRGTHLCLLADISA LPLHYYYYYYFQWRSLPDQPGQHGET PCLPKIQIINRAYWHVPVPTDQEADAR *LPEPNRQSRQPE
13329	27230	A	13472	359	73	ATEPGQLFYF*ESESHNVTQAGVQWLDH GSLQPPPTGLKPSFPLIHTGITAAASHYT WLNQLLPMNVSLTTFYESPQLKIQRSHI LCNSIHIKPLE
13330	27231	A	13473	332	10	ILSKRGFPKPGRYCEVNPFLCVQGA*V RP*EDTSLHCEIYHTHTHTHTHTHTN LKP*TSKELIPQKTESLFFSLCIKKSL RFQTFPDAGSTGNSVGCACFISK
13331	27232	A	13474	355	385	IMVCIKQSCVH*KNN*FWPGTVARVCNP RTLGGQDRQTA*AQELKTSLDNMAKPCCL YKFF
13332	27233	A	13475	297	425	RKSAWWLMPVVSPL*EABAGGFLEPGSL RSAWATWGDPHLYKK
13333	27234	A	13476	160	1	KSTGRGLMVAHICIPSTLGSQGGWIA*A QEFETSLGKILSLPEIQKSASLITW
13334	27235	A	13477	334	79	GMKEQINFLYQKRGIKPNKLAENVVLI HYN*KLLSNSFK*LQDTASI*YFFGNYL NRPGMVAHACNPSTLGGRGGWIT*GQEF L
13335	27236	A	13478	234	385	YAKFHVSINEKKPDVAHACNPSTLGGQG KWIT*GQEFKTSANMTKPRIY
13336	27237	A	13479	408	129	KRSINRRKGGELSSSHFLLLLPLPLDEE PSPPPFCPLPPFPFPCRLPQSG*GAC GRLHPC*MDLGPCKCPARKVFSHLSCSL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						VLQVCRSP
13337	27238	A	13480	251	384	TITPWRGAVAHVCNPSTLGGQSRQMT*G QEFKTSLSNMVKPRLY
13338	27239	A	13481	164	300	AGDDSDNSMGLLGRHEIKFFKCLGPCM TTKFIVPALWEAEVGGWLEPTSLRLR*A LIALLQCTPA*GTVDYKVYRPSLTGSR GRRMA
13339	27240	A	13482	2	30	TGCHQFRFLNPPSPHPVLQLVSPGDC LIFRYFKF*LHQLM*INPNANFCGARSF LCKFRVWIS*LRYPSLVALSVLFVFK*S VQI*VKKKKKKKKKKKKKKKKKKK*K
13340	27241	A	13483	39	199	LDVGTCSPIVPASQEAERLHEPTSLR LW*AMIVQLYYSGLDRARPCLYLKK
13341	27242	A	13484	18	72	TRRSYPGSTGCGQLHTFGLVSLYNCVSQ FLITNLYISYRDIY*YIYIYLYREIYL YIYIEIYTYIBRYVYIHI*ILGLQVANC IPLD
13342	27243	A	13485	266	496	LDSASDITQAGVQWCNHSFL*PQTGPLK *ASTSAS*VABITGLSQHVWVKIIMSVS LSSYTFIQLPSILLYGNTAP
13343	27244	A	13486	286	72	HILSHCTVLWFLTPHHGTTTHYKNTTGQP SIVATHNLSTLGG*GRWTT*GQEFKTS LANTVKCSDAWVDRD
13344	27245	A	13487	309	6	RFFFFFPFGKKGVFQRFFFGFPFGFP PRFFKTGPEIFFFGPLKKKNFPPPGGK IVFF*RGAPPPPPPPPPFFLFFFFFLK KNYLLLEKVSPEKEG
13345	27246	A	13488	183	459	RRVKKICKCIIWQNNYL*KGINICSMPO KKKKKKKKKKKKGAPFKKKKKKIS*G GGGPPF*KTKIKPPGGRGFFFFGGEKIM LFPVFI
13346	27247	A	13489	348	1	CEGKDLPIQFASWFKYAGFHSLESIFQ SFCQTKKLEAPKELSPCSQLRYRNWQLT CRRMKLDPHLLPYTKINSRPGAAHA*N PSTLGG*GGWII*GQEFETSLTMGETP PTRP
13347	27248	A	13490	313	320	KQGGPPLAQARVQWYNLSSGETSLPLPG SSNPPSATGVAGTTGSPPLA*LIIFFFL *DRENGDQRKL
13348	27249	A	13491	187	350	GNPVKK*IKNTSSSGVWWLMPPIPAL WDABVGGLEPRSLRPAWATERDSVS
13349	27250	A	13492	211	83	EYAKNGKLLSWRYL*SVVCVVCVTTTC VCVCVVCVTTICKNI
13350	27251	A	13493	286	407	LGVEAYACNLNTLGG*GGRIT*GQEFET GLGNTARPCLYF
13351	27252	A	13494	897	1033	KFIFKMQWDDHSSLQP*TPCLKQSSCL RLPSTWDYRREPLHLAM
13352	27253	A	13495	265	3	HLILLEEDLTWQRGKWLKGRVSLCSLGS *TQSLTVLKKGRGLGVVAVAPSTLGGRG RWVALAQELETSLGNMVKLSLSKIQKLA GMV
13353	27254	A	13496	319	1	CFKLWDTCAQCAGLLHRYTCVMVVCYTH HPEPCYNIMGLPKYMWSYLWPKCHAVY HFRYIKNLLPGCVAHACNPSTLGGRGW IT*GKEFKRRMKTIV*IGIYFI
13354	27255	A	13497	265	11	VLGEVSNQHLGAPSNRTPSEVPLAQAA QGRPSLVPPSAIVFPSTYFTICYAFLSIS MPIIP*VWEAEVGELLEPRSLRQA*ATW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
13355	27256	A	13498	164	22	GIKRKLKSGVVAHARNSSSLAGRGGWL T*GQEFETSLAKMMEIPSV
13356	27257	A	13499	277	363	TYLCYIFNICLFVGEIEKQR*LI*PHRS TLNGHILYVRPVPSPNPQAVASFVCTCY MPTWPEVVESQKK
13357	27258	A	13500	1	270	YTCSVLLLVTVNLLCLLIYKLNFIIGML RKKTIVYIYIERIQYLLKFOASTGCLGVY PTV*PYMYTTYMYMYMYIYIYIYIIL CLCLDG
13358	27259	A	13501	170	383	ILYSSKLTYPSPQIVIFFCGKST*GWVW WLMFPVPAI*EAEVGGSLSTSLGQAWA TGRKAFFVIFYKEYKN
13359	27260	A	13502	31	402	GDYLYLREGWQEPARREQHAQNLFPNRT F*PHLICLTNYRLFSLAWSECEERRNET TDKNQTVKDLALDMKRVLPFS*GHQKVI KVGVVAYACNPSTLGGQGWITRGBEFK TSLINMAKPYLY
13360	27261	A	13503	232	446	RNRPGAVAHACNPSTFRGRGGRIMRLGD *RS
13361	27262	A	13504	196	390	VNKAEEKHLYFVARKEILRPGVVVHTCN PSTLGGRGGWII*GQEFETSLPLPKTQK LAECGRGCL
13362	27263	A	13505	146	7	LKYVLYWLGAMAYTCNTSTLGGQGGWIS *GQEFETSLANMVKCLF
13363	27264	A	13506	177	18	SNFGRPRQDHFRLDGRHSETPSLOEK VKKLTRHGGACVQSLLERLRREDHLGP GGGGCSVP*SVNII
13364	27265	A	13507	117	338	NKILKKKKGGRFKESKFTSPGLQGNF FMGPPKLNLRAGV*QRREGKNLGPVQLK PFEANPLFARGPNTKNP
13365	27266	A	13508	306	443	LARYEPAVRTRAC*AQWLTAVIPVL*EA EAGGPLEARNLRPAAWAT
13366	27267	A	13509	146	390	KMFKGHEQAHRKKKKRGRFKGSKFTS ACLQRNIFFLGPPKLNLRAGV*QRGDWK NPGVTQFNRFENPLFARGPNTQKP
13367	27268	A	13510	119	356	NEDRNLRGGCPGR*LLRTEGVCSNPAGW SGIRWCEESGGLFNRVVRGTESVLFSGL FVCCVFAQEKAKATGRAEVS LCP
13368	27269	A	13511	221	21	EDLQRDKPLGSCYSTCGWAEQWYLQHPG GAGSKCRIWLGAVAHAYNPSTLGGQGRW IT*GQEF LSL
13369	27270	A	13512	163	418	TFPDDQCLMLQDHACVKRSIQSA*YLTP AVLAHWEAEAGGLEPTSLRPAAWAT
13370	27271	A	13513	239	21	FGNLGGPGGRTACTIQFSLGNIVRPYFYK TKPKPKPNQNTKIS*AWWCMPIVPATR KAEVGESLEPRRSRLQ
13371	27272	A	13514	135	11	KFFFWPGVLAHAYNPSSSLGAQGGRT*G QEYETSLANMVKS
13372	27273	A	13515	162	57	EGTLRSRRPPLGGWVT*GQEFETSPANM VKRCLY
13373	27274	A	13516	424	54	PKRGFFPTPIWVPPVFPPLPPFPKPPPR IFFLGGPPKKKFFSPPPGKIFFF*KGPP PPPPPPPPFFFLFFFKKKKRLGGFFFFF FWARPFSFLSLFFFKETIPLYNIWMHK DSCKAVIHYYH
13374	27275	A	13517	310	349	GGGPLKKKLFFSRGGERFFFF*GAPFFF FFFFL*SSKIFIFFLKSPPPPPPPPFFC FFFFFSQILFFISSPCFVFFFLNYTSRT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CSYVCALILFKGNTYSRKARHILW
13375	27276	A	13518	273	393	IKCLSYRKKATTLGGQGRWIT*SQEFETSLSNM*KPOLY
13376	27277	A	13519	450	139	IPPIALVSPFAKHTWQQMGLVRRSSKGNMMSKGWEI IHPSRIFCSNHTLLRLALWLGAVVHTCNPSTLVGRGGWIT*GWFKPKSKTSMERFCILSRHKTRGS
13377	27278	A	13520	47	427	KMKQLFEMLVFQNWITFLSHSIFRTIR*LTLPLMFYFYFKQ*RTLPLPKF*DRVWLCHAGGCL*CSGTVSAHCNLRLLGSSDPSTSAS*VAGTVGAGHHIWLILNNRELPKQKFFINSSRNLPFT
13378	27279	A	13521	199	98	SLPSVKLSICCEFFEDIVSKDFIPVVLVVKRESCSLCALPNLLPK*EKTNIQVP*VFQSTIKAKAQIGMVAHACNPSTLGGRGWIT*GLR
13379	27280	A	13522	314	18	QTLNFIYILKIYNIISLVHC*IFEARFQILV*V**NYPF*SLICFTFSWHETQNT**KNLIIWAGAVAHTCNCNTLGDQGRRIALAQEIEPSLGNIAIQ
13380	27281	A	13523	18	231	CPPAVFGTSIEBQIQLYKDIKD*KIGOAWWCAPVPGTQAEVGGSLERSSRL*CAMSTSMNRHCVPAWAT
13381	27282	A	13524	239	465	RVQVSECLLHREKCLYFQLGLS*LIPQTGWLKQQLPGTVAHTCNPSTLGRGRKRI T*GQEFETSLANIVKPRLY
13382	27283	A	13525	388	468	SLRLGTVAHTCNPSTLGG*GGWITRSG
13383	27284	A	13526	342	369	CTLNTLLYSISDFGVSAFLATGGDITR NKVRKT*LRGLTVAHTYNPNTLGGQGRRLT*AEFKNSLSNIGRPHLYKTKTKKT
13384	27285	A	13527	241	231	EYVCIWSHSSLYFSSSLYIHM*VCVCVYIYVHTNSHIYTHMYIHTHTHTHICIKYKEKYKEL
13385	27286	A	13528	241	231	EYVCIWSHSSLYFSSSLYIHM*VCVCVYIYVHTNSHIYTHMYIHTHTHTHICIKYKEKYKEL
13386	27287	A	13529	34	299	SAPASASPWGIGVLYRPLACPEDRFSPGPEANCGEIETTELRLVTLSPRLECSGTITAPCSLDLQGSRDPPPSAS*VSETTGASHHAQL
13387	27288	A	13530	158	45	SGHRSRARWL*PVISALWEASAGGSPEIKSLRNRRPG
13388	27289	A	13531	342	1	CFFLKGAPPPFFFFFFNFFFFFLVGTDLKILKVTWKWKGPKIDKAVPKNNQARGLP*PDIKIFYKVLGAVANAYNPSNLGG*GGWIA*E*EFETSLANMTKPQYKYYKLA
13389	27290	A	13532	589	742	RIMKMLRIKICGTGPGMVAHAVNPSSLDGWIT*DQEFKASLANMIKPHLY
13390	27291	A	13533	74	446	HVGIPSRLTSVSHPRHCKHPRTESEHVCATIEARHYQCKVSRPSDAGSEGRPRDMTQDEVADTPPPNISSITATRTMATIGVGVAHAYNPNTLGGQGRRIA*AEFKTSLGNLAKPCLYKH
13391	27292	A	13534	1941	1040	AFHLLPYLSSGFYCSLGPFCFLGSSHMAAWHKEPLHNACSDSRSSAPIRQGLGSPSATHDTHTRTLAHICKEIFKERLHEIKEREIDS*RG*NTQR*VEREEAENKYKPTETI

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						NTETENHKQOEMLRHAGEERENSPREAE RKCRNEKCEIKSRNSRKEARLRKKVKFK TNEKGKG*QIITVHKEKREVGRRGRQ NKKRTKSTQHVTQKQDMR*SVKEEPHLR RAKRNSNKMKNERYVLQDTHSCQKE KMRQRHTRKKLARETWKVRHTLNREQR AKPRKKEIKEIHSAILKC
13392	27293	A	13535	1192	1476	EIKRKWGPASCHACNPITGRPRRDHL RSGVQGPQGRGETPSLLKNIQISWAWW CAPVI*EIKRKWGPASCHACNPITGRP RRVDHLRSGVQGPQGRGETPSLLKNIQ ISWAWWCAPVIPATWEAEAGGSLETGSG GCTEPRSHHCTQAWVTE
13393	27294	A	13536	55	132	RAESCSLAEDGVQ*GNLSSLQPPPPK
13394	27295	A	13537	7	325	SPVEFRLGEPTKGTSSFGKRRNKTHLC RRCGSKAYHLQKSTCGK*GYPAKRKRKY NWSAKAKRRNTTGTGRMRHLKIVYRTFK HGFREGTTPKPKRAAVAASSSS
13395	27296	A	13538	259	274	KFEAAVCYHCTTSL*CHTVCFLSFFL LEIGYHYITQAQSGAMIAHCSLKLGGSS NPPVPAF*VAETRSACYNALVVFVKFLM GL*ELWKDMS
13396	27297	A	13539	3	68	QASVLPQKQLMSWQKLESTFVKFNLV KTGRLGEEISCLLVREYYSISDCLATI KLPAHLKSMRKPRLKDFKSTFLISTKNQ GNHGHGTGNEVNNFQQRISV*KTYFKK YNNRPGAVAHTCNPSTLGG*DWIT*GK NCQNQLS
13397	27298	A	13540	268	468	YRRLISKKFFKHRWKSVSFFKFSFFWL EVAHACNPSTLGGQGGKIA*AQEFLLSL GNIVGPCLYKK
13398	27299	A	13541	308	437	FSWAFEIGSQAEVQWHDHSL*PLPPRF KRFSHLPLSSWDYR
13399	27300	A	13542	7	244	AKTAPLFF*FETVSCFVAQARGQWHD SLQPRPPGQETSMIKTSSDPPPPASQVA GATGMGHHAQKI*FLVETGSPHVSQGG ALLK
13400	27301	A	13543	50	175	ALPAHTAVGQCSVEGFCVLSDPEDGGA ARMKLVRLMKLSHETVTIELKNGTQVH GTITGVDVSMNTHLKAVKMTLNREPQV LETLSILGNNIRYFILDLSPLDTLLAD AEPNVKSMNREAVAG*R*G*AREIFDEI ES
13401	27302	A	13544	47	362	VAFQGLQVPATNPANFFFWKGGFFVFP QGGRGGEKIGLRDPWPPGVRIKPGPTLS GTREKGA PPPPIYF*FWKKGQKGGP GGF*TWDPKGPSPPTPKGGD
13402	27303	A	13545	97	351	NKKKKGPPPPFF*KKRVGKKKKGARAGG PPKPPPPFGGPRGGGPRGQNSKTPRPG GNPPFKKKKKRNI PPAGPMGLKGGGHL
13403	27304	A	13546	214	32	NYIKISSVDGGA KIK*WT*NLKCLVLSV KNITRWVDCSSGVQDPQGHGETPSLL KTRKTSWA*WRLGLIQWRKMPWPSR
13404	27305	A	13547	350	159	QTGTLTQKTKQKQAQWMTVILGL*EA KAGGLLEPKSLRPAWATWQDPIYKKKFF LERKTRW
13405	27306	A	13548	367	149	FFFFFFFF*TGSHYVAQNWTQIPGLNLP ASASQVTATTGMHHHTRHTPPPSLTSH

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						QSVSTASWTYLQNSGRH
13406	27307	A	13549	321	2	GLVKVTHHGYDRNLGYPDSQASVLSFFY TA*MVQ*LQLPDKVQIYPAPHLFINDMP P*WLLKIPSGPGTVAHPYNPTLGGRG RRTTRDREFETSLANVVKPHLH
13407	27308	A	13550	216	13	GYSGETVFSMRKGQSGPCLQGSPSPM GKAGINQII PKTTLGGRGGWIA*GQEFK TSLANTVVKPCLY
13408	27309	A	13551	199	391	KDFSIFIAFCFKRPFITGSQGOEWLIFP HAYNPSILGGRGRQIT*GQEFLLPARLG NMVKPCLY
13409	27310	A	13552	70	239	ATCVKN*RTSWAWWCVPVVPATHEAAAG GLLEPRSSRLQCSVIASVERHRTSVWTT
13410	27311	A	13553	105	257	GQAQWLMPIPALWEAEAGGSFAPRSLR LA*ATVPGPNFLKRAFHSLLNLFPL
13411	27312	A	13554	499	165	Y*MESHFVTQGGQLQWCSLGSQAPPPEV GGWLELGRQRLPMKPKIAPINTPSPG
13412	27313	A	13555	415	719	YTDKSIRSISLLPVKGSTHSMCPVKFIQ LOEAGGIHMAKLSGQRVDREWRLGTVAH TCNRSHLEGKGGQIT*AOVFKTSLGNNMA KSCCLKYQKLSWIWQH
13413	27314	A	13556	224	523	DKVSLCHPGWECGWQSQSLTTASISQG* TILFPQSPE
13414	27315	A	13558	355	1	QVSLQLPYCVLFQFHIYNKQAALLQRCY VSATNLLINAIWQYVNSLKMCEENQNV LQNMPP*HRNYFGEAGHGGSCS*SQLLG RLRH*NCLNLGGGCGSELRLRHCTPAWA TKASPS
13415	27316	A	13559	73	259	KYVPHKGKISERRLCSVAQAGVQWCDHG SRSLEVLGSNDLLASAS*VAGITGCWGS SDPHTT
13416	27317	A	13560	205	21	VVKISEDFLLGDAKKWAYQEDIKRLRLG RGAVSHTCNPSTWRGRGWIT*DQEFET SLPKC
13417	27318	A	13561	254	481	LMALLPGSSDVLSEYGEWHFNFIILIS KEIFILLFF*DGVSLLPRLCSCGMISA YCHLCLOGSSDRRDLKKQ
13418	27319	A	13562	174	369	TFFSPSMFVEPGPYIIAQAGVRNLTGA IIVHCSLKLALSDSPTSAS*VTATTGM PPHLAFTVK
13419	27320	A	13563	371	109	LFSKAGRCILQNLCCMVSGKCPMNGI DVTREYPTFIAHRVLTAAATSGSDFLGQ AQWLMPIPAI*EANAGESLEPKSLRLA *ATVPGPRSLSQTLHRSELCLG
13420	27321	A	13564	206	486	RQLAAVHILVTPLDPHVTWANYVTSLSL LSSSENGVNNDNTHFIGLLLRDYK*GWV *WLTPIPALWEAKVGRIARGQBLENSL GSKARPRFV
13421	27322	A	13565	212	398	SRVRGCFPPNLPKSSCI*ECGQGAHAHA CNPSTLGGRGQIA*AOEFKTSQGNVAK PHLYKI
13422	27323	A	13566	26	395	YSPVHTDKSGVRKLGFFFFFEKEPH FFSPAUKARAKIGLNGTPLSQGKNFRP KPPKRGKRGAPQPGKILNFKKRGFS MGAKVNPNGFKGNPPP*PPKGAGKGG TPRPGFFFFF
13423	27324	A	13567	400	195	ATRVSLAPTNNKINWGWPTPVIPPPQE GEAGEFL*PQKWRVRLNKIVPLSRPRD

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						KTRLCKFKKKKN
13424	27325	A	13568	316	154	SQPFPLRWEDRLSRGVQNPQKQ*LMPV IPAFSGAEVGSLEPRSSKPA*ATNNLK SKVIIGGQICDKASKVSIVESSWWGWGC
13425	27326	A	13569	297	475	FDYFFIY*ETKSHSAAQAGVQ*CKHSSL QP*PPGLKQSLLPWPPKSAGLTGVSYGT WPI
13426	27327	A	13570	116	332	NRVLLLPKGEYRGITSAHCSLKLGSKR PPTSAA*GDETTGVCHHTPV*FLKTFP IEIRPGYVPRVGHWR
13427	27328	A	13571	233	405	TVPELRASCRLKKKKKKKKGEKNLKKIK GFPGPGRV*GPEAKNPGGGGPGIPKGP G
13428	27329	A	13572	408	3	TFCDYFKTPPPGKFFFIINGPPSFFLNRG PSFFFFPGFPFLKNFFFPPLVVFKG GYKRGVFPKKKGPQPLFFFFFLI* KKTRPGTVAHPCNPSTLGGQGRWIT*GQ EFLSSLAKMAGRVVRPGNCBSV
13429	27330	A	13573	273	406	IKFKAERGHS*NTSTFGGQGRWIA*S QEFETSLANMVKPHLY
13430	27331	A	13574	385	38	KNSPPPPGKNFFFP*GPPSPFFFP FFFFFLLGGKTFPPPSRFFFLKP FPPKNQGPKNFFPPKKKIGD*ARPPPLT GGAKGAPLFKKKKKKKLKVRPGAHAHT CNS
13431	27332	A	13575	230	53	HWKVLKENKQIFTKISFKMNAIKDSVGQ AQWLMPVIPAL*EPDMGPFVEPKSLRPA WAT
13432	27333	A	13576	406	33	VNSIVWVSSPFRVSTFISFFELKSCSVT QAGV*WHDLSLLQLQTPGLKRSPAPSRG LSFYLLSIFYPHSSQTELFVGTINAASF TNSRLLYLSLLCGKYHPLVPSLPLSTI WYPSLRVSHHFP
13433	27334	A	13577	426	294	GGFSPFPVKPPQFFFGPLKKKISPP PPGEKKIFF*KAPPP
13434	27335	A	13578	268	3	LQAKGPAMGEAGARCSSEVWGWRKGF L*VSR*PSFDSHVRIGRVQRLMPVVPV WETEADISFEPCCSRPAWASWRKTYIQ PQRI
13435	27336	A	13579	395	49	EKKKFFVCFPGFPGNPPNPSPQFF*KGL ISPSGSLRTRRGFFP*RVFFFLKKQFP LSPRVECNIGIPDP*PPFGEVSTPQVA GAIGPPPPPRVNFYFFVKGFNLVGMF PFF
13436	27337	A	13580	68	466	GASPAQGSTLHLVILPRYFFKIPTVRTE SFGSLVTSPPPLHFLPLNKERGGPGIP LPCPQLQLVGGTSLPPVPSLEPDSQDK WPLHGVPPGHVCS*PLAGDGAWPPSPHW IPLNPGTSKSLQAPPPNSA
13437	27338	A	13581	67	249	ATAPGLLCYKIFSCQLQWCVPVTQLAW ETEAGGSLEARSRL**TMITPVNRHCI LAWAT
13438	27339	A	13582	359	3	KQDSQWVAAAPASVAVSTCWRGLPLPWS GGQNRGKGSPLQVHRGA*GTENKNQGG TPRPGGPGPSAPRGSSLGHRKLPVHH TTLSSRSALPPTPRHPAPSSPPCTBEF HRTPI
13439	27340	A	13583	174	1	FFFFFVETESHVAQARVLEYSGAIPAQ

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						CNLDNLSSSELPASAS*AS*VAAXTGT*KR
13440	27341	A	13584	192	206	LEFFLEVGSCYVAQAGFEFFPGSGHLP LSA S*VVGSTGVPHHTQLV*SFSSLYNLERN C
13441	27342	A	13585	244	28	KKPENQEIYNYIFYHLFNVHEQIRISLGP GAVAYNCNPSTLRD*GGRIT*AQEFKTN LGNMAPRTRGSTRTF
13442	27343	A	13586	312	701	RGPEET*PRTRKSSPRPTRSCESVSKLA RPPRRCSAAPAQVPRLSLRSPKDPDP RV SSAEKCAPLELLPECSETGALPRNSFLC QNASSPLLSLGLPPSPVTQALQPRALHQ HLGSTNKEDAHVAPAKK
13443	27344	A	13587	410	292	GYMIKQOTVYHECRM*ANSHLHLPPPEGL LRAVTLWRRAP
13444	27345	A	13588	428	36	TPPPPPFFWAQKKKIFPPPGGKIFFFL KGPPELFFFFFLFFFLKFFGLK GPPFFVQD*QGLEBNPKGSSSLGWEKLGR ALLPQQRSFVPGLGPTRLFVGLVFWFFG FFFLPFGLCFFALIFNC
13445	27346	A	13589	3	364	TAPDDQGRPYQAGEPAAHVRADSTHGLG A*RRVAGHLPPRVGAPHHPGASSREGAP PLHPPPNL*HRRPNGSCRFLPGPAAPPQ GAEGGRGRDRRGTHSVAQTGGPGGFGSG VTPSWRSS
13446	27347	A	13590	778	910	DRIRRS GAVAHTCNPSTLGGQGERTA*G QEFKTS LGDMVRFLY
13447	27348	A	13591	230	3	KLVNILVEKSLVAMKSTVSEGKMVIRSP ASLGMVAHTHSPSTLGGQGRQIA*AQEF ETILGNMAEPCLYKHSVY
13448	27349	A	13592	223	340	LTPIIPEPWESEVVGSL*LTGPVAVTHA YNPRTLGI RSGRIT*GHEFQTTLSHTMK TRLYHELL
13449	27350	A	13593	35	220	DRASLS PRLECSGMIVAHCSINLSGSSD PLTPAS*GDGTTDTCHHARLIFTGADFC IDASS
13450	27351	A	13594	87	369	NVQKTECEISGKMQIWQKGSVTKCSNG LFNFFIFSKKIASCKVKLTRE*KYKSQ ARWCTPVIPATEAEVRGQLEPRSLRPAW ATYQPHFKS
13451	27352	A	13595	261	489	SWVNERMVVG**KHETSQAQWLMPITPA LCEAEVGGSLARSWETSLCNIVRLHLS KKKRGKGRKRGGNQIAPSRE
13452	27353	A	13596	238	2	NDCLWWLFRIPANVSTFGLLHMSLKVNT PGNRNFKSELGTRCLIHTCNP SILGGQG GWIT*QGEFVTSMQKGSVKNQ
13453	27354	A	13597	36	687	RDVHRSTYQAGSKQDWGPGEABRLSSSR RGAYSCPVPITFAEGKTRMGRDKMRLIL GLSWGPSLTLLLPITNAPRRPGM*EPAL PGNSTS*SGAVRFPGGGRK*EDSAESWS CFCSHPSSSGNPPSPPSAVCMPLGLS GLQR*PKQLSPPPALS LPVSSLLVRLSP WPPTSSHLLPQALPQSLHPQGSRAVND SFSM*GMVLGSRNRNRCMEA
13454	27355	A	13598	367	468	KKQRRGREPWLTFAIPALWKAKAGGSP* VQSSRP
13455	27356	A	13599	183	380	LTSMLAVDNSSVEKTCPOAMRISRP GAV AHTCNPSILGGQGGLIA*VQEYETNLGS

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						MAKTHLYKN
13456	27357	A	13600	161	657	LIQGCWCSLFFSTRVFLAAIGMKSQWCR PVAMD LGVYQLRHFSISFLSLLGTENA SVRLDNSSSGASVVAIDNKIEQAMD LK SHLMYAV*EEVEVLKEQIKELIKNSQL EQENNLKTLASPEQLAQFQAQLQTGSP PATTQPQGTTPPAQPASQSGGPTA
13457	27358	A	13602	121	423	MIKNSFGLYLYSQVIYIIMKYTAIY LKDFFFKDGVLRHPRWNTVTTQCSLEI LGSTDP PASAS*AAGTTNTSHHGQLYSY FKKRPTYAEMEYKIKK
13458	27359	A	13603	1889	1717	VPRIPLSWTFPSSI*RPKPPSSTFSHP GKPSMGPPGLNRCVPQRALLPGWYQHCG R
13459	27360	A	13604	81	267	ETCCIKNNTLK*I*SQMLWCAPIVPATW QAEVGGSLDPRSSSL*CAMITSVNNHCT PAWAR
13460	27361	A	13605	267	418	THASGMVTHTCNPGTLRVSAGRIT*GQE FKTSLGNIARPHLYKIIINKYI
13461	27362	A	13606	428	24	CPESNPRKREPTLKSEPIITLPTGLIL DDGNSPTAAAGSVFAETLQPCSSLCC* VKSSPWPTASLPQPFGSAPQTLPVRYAL IPGSLVSTSLGPRLAPGLPGSPSPSP QVTLDSEYPSPTPCIAPALD
13462	27363	A	13607	267	442	RPPPTLKVPWLGVVHACNPRTLGGQGG SIS*AQKLENSLSNLRPHLYQKQKQKQ KK
13463	27364	A	13608	3	280	YRLSVICEDPMRREQTCFPPPPSFPFN RYCSTRDGGMEGSQDFRKGPPA*APCR SGGWRGCCSPAGAPGSPLCGSSQGGPV SPWGQKRS
13464	27365	A	13609	291	248	EKRAHGSQPMKGRERNMCKSSSEFRVVA WSLAGVKGDGGR*GSGAGGSPKLG*AV* LDPEGHAGQAVFCGEAGARTQIGKKG*R RDQAPLPLSPNLCSGSCLP TKHSLAMP LRVKSYSQAQLGRTTCTRPSPTITFDS S
13465	27366	A	13610	267	3	HTDLLYNTPTHPISPRCDPKHTAIPDKQ SLLFFFFEMESCSVARAGVRWHDRLSLR PLPPRF*KFFCCSIPSLYCGRSRGSSQT YTS

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13470	27371	A	13615	197	428	KTMVGLKTSASFHQDFIQIPLNHNLSVP *TMLGSQPRFLFPPGTVSHICNPSTLGG RGGWIT*GQEFETSLATMVKP
13471	27372	A	13616	445	550	ISITRGRARWLTPVILVLWEAEAGGSP* GRSSRLP
13472	27373	A	13617	3	435	TMVLSPADKTNVKAARWKGVAHAGEYGA EALERMFLSFPTTKTYFPHFDLSHGSQAQ VKGHGKKEADALTNAAHVDDMPNALS LSDLHAHKLKRVDPVNFKLLSHCLLVTL RHLPAEFTPAVHASLDKFLASVSTVLTS KYR
13473	27374	A	13618	719	918	CEGREKWKIGRERKGRGRKGBQMGRE GKGREDGGRKRPCTSRPRSSSRDRSNII ISEHASAVEA
13474	27375	A	13619	847	938	WLMPAVPALLEAEVGISLEAQSCRPPWA TQ
13475	27376	A	13620	349	409	NLWSWFGAVAHVCNPSTLGG
13476	27377	B	13621	25	189	MVLSPADETNVKAAWKGVAHAGEYGA ALERMFLCFPTTMTYFPDFLIHGSQAQ*
13477	27378	A	13622	142	356	RIVENEKINAEKSSKQKVDLQSLPTRY LDQTVVPILLQGLAVLAKERPNNPIEFL ASYLLKNKAQFEDRN
13478	27379	A	13623	18	1353	AGAAQCEVVSAGEAGARTMSEADGLRQR RPLRPQVVTDDGQAPKDGSSFSGRV FRVTFMLAVSLTVPLLGAMMLLESPI DPOPLRQISGIALFCSFKBPPLLLGLV LHPNTKLRQAERLFENQLVGPSIAHIGD VMTGTADGRVVKLENGEIETIARFGSG PCKTRDDEPVCGRPLGIRAGPNGTLFV ADAYKGLFEVNPWKREVKLLLSSETPI EGKNMSFVNDLTVTDGRKIYFTDSSSK WQRRDYLLLVMEGTDDGRLLLEYDTVT REVKVLDDQLRFPNGVQLSPAEDFVL VAETIMARRRVVVSGLMKGADLFVEN MPPGFPDNI RPSSSGGYWVGMTIRPNPGFSMLD FLSERPWI KRMIFKLF SQETVMK FVPRYS LVLELSD SGAFRR SLHDP DGLVAT YISEV HEHDG HLYLGS FRSP FLCRL SLQAV
13479	27380	A	13624	18	1353	AGAAQCEVVSAGEAGARTMSEADGLRQR RPLRPQVVTDDGQAPKDGSSFSGRV FRVTFMLAVSLTVPLLGAMMLLESPI DPOPLRQISGIALFCSFKBPPLLLGLV LHPNTKLRQAERLFENQLVGPSIAHIGD VMTGTADGRVVKLENGEIETIARFGSG PCKTRDDEPVCGRPLGIRAGPNGTLFV ADAYKGLFEVNPWKREVKLLLSSETPI EGKNMSFVNDLTVTDGRKIYFTDSSSK WQRRDYLLLVMEGTDDGRLLLEYDTVT REVKVLDDQLRFPNGVQLSPAEDFVL VAETIMARRRVVVSGLMKGADLFVEN MPPGFPDNI RPSSSGGYWVGMTIRPNPGFSMLD FLSERPWI KRMIFKLF SQETVMK FVPRYS LVLELSD SGAFRR SLHDP DGLVAT YISEV HEHDG HLYLGS FRSP FLCRL SLQAV
13480	27381	A	13625	1	384	QSFRGTGRKRERERKMSLSDWHLAAKL ADQPLTPKSIILRLPETELGEYSLGGYSI SFLKQLIAGKLQESVDPDELIDLYCGR KLLDDQTLDFYGIQPGSTVHVLRKSWPE

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						PDQKPEFVDKEAMRD
13481	27382	A	13626	980	1089	KRIRIQLTGGLYPVPPHPPPPQSPPIFP RPTSPTRT
13482	27383	A	13627	116	587	VGELRADSWFVPSQPEQASGPQKQAFI WPEAPRSARLPITYTDYWSRLQTQES QMLGSMARKKPRNTSRLPLALNPLKSKD VLAVLAERNEAIVPVGAWEVPASPGSSE IPAYTSAYLIBEELKEQLRKKQEALKHF QKQVKYRVNQITLRKQ
13483	27384	A	13628	150	484	VAEPQASRGVRKTEVGEQQGGTACGGC GHQCPPTWHIQRAHCVPTGAGGWHL QGRASCRRPPSPQVYQTQVGRQDPHF GVGRDSRGELAWSSFIHPYLLSVCNPL
13484	27385	A	13629	330	397	ARCEWLTVPVIALWEAEAGGSH
13485	27386	A	13630	10	137	SFTGAVILIIAHGLTSSLLFCLANSNYE RTHNLFFLNDFFFS
13486	27387	A	13631	380	98	FQWLVSFTATLWFEERHRKNKIEREERR AKGERGDRKEERREEGGEERGRRGERS DKREP KKKSKESNHPKVVKFSFICSFC FLTPFFPVFF
13487	27388	A	13632	56	827	PLFEAFTACGFVHDCGLLIHPEETCGLO PISSDYIEAILQSELKRCPSGDMKGQWI VPCLSCSDNRTCDWREITWQPHNCQYGV LTKPQLQQCLGGRKILFIGDSTNRGIMY YLIERLNETLQEWQKVHGTIFYHNVNGG KTLISYSYYPQFWISPSLRPTFENALEH LLQSRPLENTGQTVLVVGGVQWLSNH LQIIHKVLKSPFTTLNQPVTKSCLQAIY FPRLSPTLHSNCLDLVYSFTKSFNIYFV VQFLN
13488	27389	A	13634	3	2718	SGPCRTTVAPLLRAAPVEHCVAALRPTD STMLKKFDKKDEESGGGSPNPFQHLEKSA VLQEARVFNETPINPRKCAHILTKILYL INQGEHLGTTTEATEAFFAMTKLFQSNDF TLRRMCYLTIKEMSCIAEDVIIVTSSLT KDMTGKEDNYRGPAVRALCQITDSTMLQ AIERYMKQAIVDKVPVSVSSALVSSLHL LKCSFDVVKRWNVAQEAASSDNIMVQY HALGLLYHVRKNDRLAVNKMISKVTRHG LKSPFAYCMMIRVASKQLEEDGSRDSP LFDPIESCLRNKHEMVVYBAASAIYNLP GCSAKELAPAVSVLQFCSSPKAALRYA AVRTLNVKVMKHPSAVTACNLDLENLVT DSNRSIATLAITTLTKGSESSIDRLMK QISSFMSEISDEFKVVVVQAISALCQKY PRKHAVLMNLFMTLREEGGFEYKRAIV DCIISIIIEENSESKETGLSHLCEFIEDC EFTVLATRILHLLGQEGPKTTNPSKYIR FTYNRVVLEHEEVRAVASALAKFGAQN EEMLP SILVLLKRCVMDDDNEVRDRATF YLVLEQKQKALNAGYILNGLTVSIPGL ERALQYTTLEPSEKPFDLKSVPLATAPM AEQRTSTPTITAVKQPEKVAATRQEIQ EQLAAVPEFRGLGPLFKSSPEPVALTES ETEYVIRCTKHTFTNHMVQFDCNTNLN DQTLNVTVMQMEPTAYEVL CYVPARSL PYNQPGTCYTLVLEPKEDPTAVACTFSC MMKFTVKDCDPTTGETDDEGYEDEVLE

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						DLEVTVADHIQKVMKLNFEAAWDEVGDE FEKBETFTLSTIKTLEEAVGNIVKFLGM HPCERSDKVPDNKNTHTLLAGVFRGGH DILVRSRLLLDVTVMQVTARSLELPV DIILASVG
13489	27390	A	13635	118	629	LWALQLHPEPELPSRRGTGAAGVWTGVA MIRFILIONRAGKTRIAKWMQFDDDEK QKLIBEVHAVVTVRDAKHTNFVEFRNFK IIYRRYAGLYFCICVDVNDNNLAYLEAI HNFVEVLNEYFHNVCELDVLVFNFKVYT VVDEMFLAGEIRETSQTKVLKQLMLQSL LE
13490	27391	A	13636	57	221	LHHCTPPWAEVEETLKRQSQKGVQGI VVNTEGGWEPLGHCGDRSRPPAQGCP
13491	27392	A	13639	344	544	LSGGHAGALSSLWVHLYCLSSQQLIGN VLVTVLAIHFGKEFTPEVQASWQKMTG VCSALCFRVH
13492	27393	A	13640	319	623	DMEEAEGGGNDRVRNLQSEVEGVKNIM TONVERILARGENLEHLRNKTEDEATS EHFKTTSQKVARFVWKNVMIIVLICVI VFIIILFIVLEATGAFS
13493	27394	A	13641	2099	769	TRLAGRVSVASRRCRGPVAGGLLVERSK ARRPLLESRVAMAAPPELLQQQEEDRSK LRSVSVDLNVDPSLIQIDIPDALSERDKV KFTVHTKTTLPTFQSPEFSVTRQHEDFV WLHDTLIETTDYAGLIIPPAPTKPDFDG PREKMQLGEGEGSMTKEEFAMKQELE AEYLAVFKKTVSSHEVFLQRLSSHPVLS KDRNFHVFLFYDQDLSVRRKNTKEMFGG FFKSVVKSADVLFTGVKEVDDFFEQEK NFLINYYNRIKDSVCKADKMTSRHKNVA DDYIHTAACLHSLALEEPTVIKKYLLKV AELFEKLRKVEGRVSSDEDLKLTLLRY YMLNIEAAKDLLYRRTKALIDYENSNA LDKARLKSQDVKLAEAHQQECCQKFEQL SESAKBEELINFKRKRVAAPRKNLIEMSE LEIKHARNNVSLQSCIDLFKN
13494	27395	A	13642	210	772	SVKMVRYSLDPENPTKCSKSRGSNLRVH FKNTRETAQAIKGMHIRKATKYLKDVTL QKQCVPPFRRYNGVGRCAQAKQWGTQ RWPKKSAEFLHMLKNAESNAELKGLDV DSLVIHQVNKAPKMRRTYRAGRIN PYMSSPCHIEMLTEKEQIVPKPEEEVA QKKKISQKCLKKQKLMARE
13495	27396	A	13643	168	2172	SPLCEVSVPSFCFRVFCCKHKKHKS LYEYVEKPLKLVKVGNEVTELSTGS SGHDSSLFEDKNDHDKHDKRKRKRKKG EKQIPGEEKGRKRRRVKBDKKRDRDRV ENEAEDLQCHAPVRLDLPPEKPLTSSL AKQEEVEQTPLQALNQLMRQLQKDP AFFSFPVTFIAPGYSMIKHPMDFSTM KEKIKNDYQSIIEELKDNFKLMCTNAMI YNKPETIYYKAACKLLHSGMKILSQERI QSLKQSIDFMADLQKTRQKDGTDTSQS GEDGGCWQREREDSGDAEAHAFKSPSKE NKKKDKDMLDEKFKSNNLEREQOLDRI VKESGGKLTRRLVNSQCEFERRKPDGTT TLGLLHPVDPIVGPYCPVRLGMTTGR

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						LQSGVNTLQGFKEDRKNKVTPLVLYLNYG PYSSYAPHYDSTFANISKDDSDLIYSTY GEDSDLPSDFSIEHFLATCQDYPYVMAD SLLDVLTKGGHSRTIQEMEMSLPEDEGH TRTLDTAKEMEQITEVEPPGRLDSTQD RLIALKAVTNFGVPVEVPDSEEREIFQK KLDETRLLRELQEAQNRRLSTRPPNFM ICLLGPSYREMHLEQVTNNLKELAQQV TPGDIVSTYGVKAMGISIPSPVMENN VDLTEDTEEPKKTDAECGPGGG
13496	27397	A	13644	1032	207	PADVTPKPATEAVQSEHSASPMSINEV ILSASGACKLIDSLHSYCFSSRQNSQV CCLREQVEKNGELKSLRQVRSDSQV RKLQEKLELRRVSPYPSLLSPSREP PKMNPVVEPLSWMGLTWLSDPPGAGTYP TLQPPQYLEEVHISHVGQPMNFNFNSF HPDTRKPMHRECGFIRLKPDTNKVAFVS AQNTGVVEVEEGEVNGQELCIASHSIAR ISPAKEPHVEQITRKFRNLSEGLQEQTV SMATTQPMTOHLHVITYKKVTP
13497	27398	A	13646	148	380	RGSWREVPESASLPSRGAKGKWRGLCCC CCCCCCCCCYHCHQBQGLDKHQADL WRSGRTQNCAGIWOEHQTLLEG
13498	27399	A	13647	2099	769	TRLAGRVSVASRPCRGPVVGGLLVERSK ARRPLLESRVAMAAVPELLQQQEDRSK LRSVSVDLNVDPSLQIDIPDALSERDKV KFTVHTKTTLPFQSPFVSVTROHEDFV WLHDTLIETDYAGLIIPAPTKPDFDG PREKMQLGEGEGSMTKEEFKMKQELE AEYLAVFVKTVSSHEVFLQRLSSHVPLS KDRNFHVFLFYDQDLSVRRKNTKEMFGG FFKS VVKSADDEVLTGKVEVDDFEQEK NFLINYNRIKDCVKADKMTSRSHKNVA DDYIHTAACLSLALKEEPTVIKKYLLKV AELFEKLRKVEGRVSSDEDLKLTLLRY YMLNIEAAKDLLYRRTKALIDYENSNA LDKARLKSVDVLAEAHQECCQKFBQL SESAKEELINFKRKRVAFPRKNLIBMSE LEIKHARNNVSLQSCIDLFKN
13499	27400	A	13648	1	1206	MSTSQSPCESICDVTSHDKSNFTDMIK LNILRCEVILDYPAPGGGSLGAKHCCSC YTVSSGVTEGERNAGEKGVKLNADGARI RGTPGRGRRAEAEASSPAPAAVAAACV AAAAASRQLASGNRTRVSSGVPAFAFLG TMNPNCARCGKIVYPTKVNCLDKFWHK ACFHCETCKMTLNMKNYKGYEKKPYCNA HYPKQSFTMVADTPENLRKQSELQSQ VRYKEEFKNGKGFVSVVADTPQLRIK KTQDQISNIKYHEEFKSRMGPSGEGM EPERRDSQDGSSYRRPLEQQQPHIPTS APVYQQPQQPVAQSYGGYKEPAAPVSI QRSAPGGGKRYRAVYDYSAADEDEVSF QDGDITVNVQQIDDGWMYGTVERTGDTG MLPANYVEAI
13500	27401	A	13649	3	394	GDGGGHLGSGRNGGSMNAPPAPESFL FEGEKITINKDTKVPNACLFMTNKEDHT LGNI I KSQLKDPQVLFAGYKVPHPLEH KIIIRVQTPDYSPEAFNAITDLISE

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13501	27402	A	13650	1	471	LSLLEERFRVRAGPGGAD SRPTGLREAGSGPREAPRRSGCKSPGL GTVGMLRPKALTQVLSQANTGGVQSTLL LNNEGSLAYSGYGDITDARVTAAIASNI WAAYDRNGNQAFNEDNLKFIILDCMEGR VAITRVANLLLCMYAKETVGFGLKAKA QALVQYLEEPLTQVAAS
13502	27403	A	13651	1334	82	CYTGGTQSLWPGSSCASSVARPSSLFRS AWSCEWSVRCARACTMSVPAFIDISEED QAAELRAYLKSKEGAEISEENSEGLHVD LAQIEACDVCLKEDDKDVESVMNSVVS LLLILEPDKQEALESCEKLVKPREGE RPSLRQLLSNLPHGMDKNTFVRITVYC SLIKVAASCGAIQYIPELDOVRKWD WNLTTEKKHTLLRLLYEALVDCCKSDAA SKVMVELLGSYTEDNASQARVDAHRCIV RALKDPNAFLFDHLLTLKPKVFLGELI HDLLTIFVSAKLASYVKFYQNNKDFIDS LGLLHEQNMAKMRLLTFMGMAVENKBIIS FDTMQQELQIGADDVEAFVIDAVRTKMV YCKIDQTRKVVVSHSTHRTFGKQQWQQ LYDTLNAWKQNLNKVNSLLSLSDT
13503	27404	A	13652	1	377	TTASGRSGVKGSTMSAEVPEAASAEQK EMEDKVTSPKAEAEAKLARYPHLGQKP GGSDFLRKLQKQKYFDSGDYNMAKAK MKNKQLPTAAPDKTEVTGDHIPTPDLP QRKPSLVASKLAG
13504	27405	A	13653	424	596	SLKNIYGLSCRKKKKGAVKKIILVQAWW LMPVITVLWEAEVGGLEARGLRPTRAT W
13505	27406	A	13654	190	448	LRSPAPHLGSPELRIRKGRGHSHCLAG AAGPQRTALCGLSAPLCPSPPTPPGAGA PRYCSGSDAPPCLLRGAGPPIPGMGDP ETS
13506	27407	A	13657	1612	563	SMPGWRLLTQVGAQVLGRIGDGLGAALG PGNRTHIWLFRVRLGHGKSGTWDEHLSE ENVPFIXQLVSDDEKAQLASKLCPKDE PWPPIHPWEPGSPRVGLIALKLGMMPLWT KDGQKHVVTLQVQDCHVLKYTSKENCN GKMATLSVGGKTVSRFRKATSIIEFYRE LGLPPKQTVKIFNITDNAIKPGTPLYA AHFRPGQYVDVTAKTIGKGFQGVMKRWG FKGQPATHGQTKTHRRPGAVATGDIRV WPGTKMPGKMGNIYRTEYGLKVRINTK HNIIYVNGSVPGHKNCVKVDSKLPAY KDLGKNLPFFTYFPDGDDEBLPEDLYDE NVCQPGAPSIITFA
13507	27408	A	13658	128	2626	NSHRVWYVRARRRRRGKQREQPEDRGV PMKRAAMALHSPQYIFGDFSPDEFNQFF VTPRSSVELPPYSGTVLQGTQAVDKLPD GQEQRIEFGVDEVI EPSDTLPRTPSYS ISSTLNPQAPEFILGCTASKITPDGITH EASYGSIDCQYPGSALALDGSSNVEAEV LENDGVSGGLGQREKRRKKRPPGYYSY LKDGDDDISSTEALVNGHANSVPNSVS AEDAEFMGDMPPSVTPRTCNPSQNSTDS VSDIVPDSPPGALGSDTRTAGQPEGGP GADFGQSCFFAEAGRDTLSRTAGAQPCV

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						GTDITENLGVANGQILESSGEGTATNGV ELHTTESIDLDPKTPESASPPADGTGSA SGTLPVSPKSWASLFHDSKPSSSSPVA YVETKYSPPAISPLVSEKQVEVKEGLVP VSEDPVAIKIAELLENTLIHKPVSLQP RGLINKGNWCYINATLQALVACPPMYHL MKFIPLYSKVQRCTSTPMIDSFVRLMN EFTNMPVPPKPRQALGDKIVRDIRPGAA FEPTYIYRLTLVNKSSLSEKGRQEDAE YLGFIPLNGLHEBMLNLKLLSPSNEKLT ISNGPKNHSVNEEEQEEQEGSEDEWEQ VGPRNKTSVTRQADFVQTPITGIFGGHI RSVVYQSSKESATLQPFFTLQLDIQSD KIRTVDALLESVARESVOGYTTTKTKQE VEISRRVTLEKLPVLVLHLKRPVYEKT GGCQKLKINIEYPVDLEISKELLSPGVK NKNFKCHRTYRLFAVVYHHGNSATGGHY TTDVFQIGLNGWLRIDDQTVKVINQYQV VKPTAERTAYLLYRRVDLL
13508	27409	A	13659	42	382	TLWLKTIQIYLTISLGLGSDYGLAGFSA LGCHQAQAVKMLTAFILIQGLDLGRSHFQ AHSGCWQDSFPDCSRIHGGLLLVQOES PWFQSAERVSCITKCNHRSDTHLCSIL L
13509	27410	A	13660	178	349	DMGFCYVAQTVLKLGLSSDPPTSASQEA GTTCHHAHLLSHPPFLMIYRNFSFIQCLE T
13510	27411	A	13661	268	2	RQQKVLSSSGSLMSEMGRTVLPLKSPG MNPSSPLLASGGCWKSLACGHIIPFSSF ILMWPSPLCVSVSSSLPMRKPLLLHLRS TLFQ
13511	27412	A	13662	112	483	AGVGALRMVQRLTYRRRLSYNTASNKTR LSRTFPGNRIVLYLTKKVGKAPKSACGVC PGRLRGVRAVRPKVLMRLSKTKKHVSRA YGGSMAKACVRDRIKRAFLIEQKIVVK VLKAAQSQKAK
13512	27413	A	13663	2	873	SVEEFDRCCTGRGCGADARAGAAVMKIS FQPAVAGIKGDKADKASAPAPASATE ILLTPAREEQPPQHRSKRGSSVGGVCYL SMGMVLLMGLVFASVYIYRYFFLAQLA RDNFFRCGVLYEDSLSSQVRTQMELEED VKIYLDENYERINVPVPQFGGDPADII HDFQRGLTAYHDISLDKCYVIELNTTIV LPPRNFWELLMNVKRGTYLPQTYIIQEE MVTTEHVSDEALGSFIYHLCNGKDTYR LRRRATRRRINKRGAKNCAIRHFENTF VVETLICGVV
13513	27414	A	13664	118	3	AWSLIPVIPVREAKAGGLLEPRSLRPT WATWQDPVST
13514	27415	A	13665	1	2876	IRQRINFSRKNKWDNRKLDQAGVSELAT NQKILVCGRYEGIDERVIQTEIDEEWS IGDYVLSSGGLPAMTLIDSVSFRIPGVL GHEASATEDSFABGLLDCPHYTRPEVLE GMEVPPVLLSGNHAEIRRWRLKQSLGRT WLRPELLENLALTEEQARLLAEFKTEH AQQQHKHDMADAEAGRTFLRADFNMI EGDRI MVCLSGGKDSYTMLEILRNQQS APINFSLVAVNLDQKQPGFPEHVLPEYL

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						EKLGVEYKIVEENTYTGIVKEKIEGKTT CSLCSRLRRGILYRTATELGATKIALGH HRDDILQTLFLNMFYGGKMGMPKLM DDGKHIVIRPLAYCREKDIQRFADAKAF PIIPCNLGSGQPNLQKQVIADMLRDWDK RYPGRIETMPSAMQNVVPSHLCDTNLFD FKGITHGSEVVNGGDLAFDREIPLQFA CWQPERDENQLDELRLNVVEPDGPRHRH APDARRFCOYL RHQARYLLSVVPLDVA VTEPLANGDGLNVLKREVVGFRANTVE KTGENQYRVWPNEMPADLHKIRPHHPLN RNLDFHFFPLDLNSTFSGGYVHVLLKGV SDDLKLSFQKMGYVRDSDHRLMVTALP PACQLVQVALGCFALRLECEILGEVLAQ LGTSVLPAEELLQARRASGDVASCORLA QDEEPPPLPPRGSAAAYRAPLDLYRDLQ EDEGSEDASLYGEPSPGPDSPPAELAYR PPLWEQSAKLWGTGGRAWEPPEELPQA SSPPYGALEEGLEPEPSAFSFLSLRREL SRPGDLATPESSAAASPRIRAEVGPAS AYRSVSEPPGYQGTQLPVPWRPAHPLLR HLSPAACCPLCSPARLPSRPLAACAWR RPAALVATACTDGHSAQQPRGFALGQL GPRSRALGRQLPWCPSLGRGLGLWLPC PWGSPGHSRGLESPGQPLLEVGLSVYGR LQQQA
13515	27416	A	13667	76	289	SGTPASPCLEMDPNCSCSPVGSACAGS CKCKECKCTSCCKSCCSCCPVGCACKAQ GCICKGTSCKSCCA
13516	27417	A	13669	2	667	GRVDAEQSRLGATERAAAAAMNPEYDYL FKLLLI GDSGVGKSCLLRRFADDTYTES YISTIGVDFKIRTIELDGKTIQLIWDT AGQERFRTITSSYYRGAGHIIIVYDVT QESYANVKWLQEI DRYASENVNKLVLG NKSDLTTKKVDNTTAKEFADSLGIPFL ETSAKNATNVEQAFMTMAAEIKKRMGP AASGGERPNLKIDSTPVKPAAGGCC
13517	27418	A	13670	176	398	RILKTQLQENNQPTTTTKNRQKTRTDTL PKGIYRRHISLWKLGTNLTPVIPALCEA NAGGRLESRSSRPVWATY
13518	27419	A	13671	149	247	RKGLALSPRLDCSGAITVNCSLNLQGLS NIPI
13519	27420	A	13672	257	359	VASLHGWAQWLTPVIPTLWKTKEGFE PRCSR
13520	27421	A	13673	142	1	HLKGSGLAKHQWLMPVIPALWEAEVGS LEPRSSRPVWATLQDPIS
13521	27422	A	13674	619	168	MFIESCCTPKIYTSFVLRSQSHSFAQGV QWLDLGSLOPLSLGSSNSPASASCIQVL FVIYTSVKLGVGGRGLGNKKVMSNKKPV CECRGWIILPFSVPSLRFQDGGWDHGV SAEKALQAGRTAGHRVGPPLGAPCGGA PCTTPPAWRS
13522	27423	A	13675	3	370	ARALLHPRHLHQWQCLCHLQGTGGCPQOS PSSEGRADLLSPAEEGYPPASGCFIP HFLCGCSIFNCLFPPIMRHAHSPDALLE TLGFCRAWRLMPVIPTLWEAKVDRLLLES RSSRPSWPTW
13523	27424	A	13676	3	281	IGLRPELSVSLGRQRLTAIRLQPLPAR

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						TPCGFLRARVALALMADETDLPPLPRLE YSGMITAYCSLDLFGSSDPPTLGSGVAG TTENCCED
13524	27425	A	13677	272	389	YCRQIEKSKKKRCWLGTVAHACNPSTWG GRGGRITRSRD
13525	27426	A	13678	261	363	NSSWGHWRLTSVIPALWEAEVGGSEPV RSLRPV
13526	27427	A	13679	149	44	SCVMSVSVLKKMYWLGAVAHACNPSTLG GQGGRTA
13527	27428	C	13680	118	267	MSHCTWLMCVVCVCVCGVYAYMYTYSF LRWDLPMLSRLECSGYSQAQ**
13528	27429	A	13682	16	346	NHHLTQPHPHLDINDFFFFFFFFFFFFFFF FFFFFFFFFFFFLKKSPRPAQKKKKKKKK KKKPRFFFLGGAPPPLFFFLINFFFFFFF LCKIISLVYNRRGGPCLSKRFFLKERKS PL
13529	27430	A	13683	244	140	GRVDVFHHVAQAGLKLSSGDLPAWPPK ELRLQV
13530	27431	A	13684	191	777	NSDEHVYRCLYGHKLSFLLSKYLKSGLA GVLLPLDAAVDMEKIEEQFANLHIVKCS LGTKEPTYLLGIDTSKTVOAGKENLVAV LCSNGSIRIYDKERLNVLEFGSGYPGLL NGVRFANS CDSVYSACTDGTVKWDARV AREKPVQLFKGYPSNIFISFDINCNDHI ICAGTEKVDDALFGGFGDARMEFLQN
13531	27432	A	13685	150	253	VGWGLWLVPIPAFWAEAKMGESLDPNRL LPCWAT
13532	27433	A	13686	500	321	IEMGSHYVAQAGLELLSSSNPPTSVSQS AGIVGMSHHALAAISKSSDASITSHHPM TTP
13533	27434	A	13687	6	424	MSLLQCGGIRCFRMPPEPAKSAPAPKRG KKAIVTKAQKDGKKRRSRKESYSVYVY KVLKQVHPDTGISSKAMGIMNSFUNDIF ERIAGEASRLAHYNKRSTITSREIQTAV RLLLPGLAKHAVSEGTKAVTKYTSSK
13534	27435	A	13688	178	293	TGYSSQAQWLMTVLATWEAEAGGSLQP RSLRPATWQ
13535	27436	A	13689	663	144	KELSAVSAGIPHSQSGGCGGGSVAACV PAAPAAAGLCSGRAQKVPPPSLAGWPP GVNAPPPPVCSVRLHVCQSDRLWVRLA ARRGILALLRSALKAAATLAGCQSVRWSV RPSESLRPTSNAASLFRSSVPTVLSHSV PLAASLGKRRACGGREHASVAVYLSVCL SLPT
13536	27437	A	13690	125	3	FAHQGHAPGQAWLRLPVPVLRREBLGG RPEPRSSRTARA
13537	27438	A	13691	136	24	GGPFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFPGKLQDFQYVVK
13538	27439	A	13692	144	1	MLKIVQSGECLTLKFNCLLSLCTLP TLIALTTLLPISPILILL
13539	27440	A	13693	1476	380	NSWSTLASELTWAAATSADPERKSQAAS AAMWATLPLLCAWLLGVPCGAELC VNSLEKFFHFKSWMSKHKTYSTEEYHHR LQTFASNWRKINAHNNNGHFTFKMALNQF SDMSFAEIKHKYLWSEPQNC SATKSNYL RGTGPYPSPVDWRKKGNFVSPVKNQGAC GSCWTFSTTGALESAIAIATGKMLSLAE QQLVDCAQDFNNHGCQGGLPSSQAFEYIL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YNKGIMGEDTYPYQGGKGYCKFQPGKAI GFVKDVANITTYDEEAMVEAVALYNPVS FAFEVTQDFMMYRTGIYSSTSCHKTPDK VNHAVLAVGYGEKNGIPYWIKNWGPQ WGMNGYFLIERGKNMCGLAACASYPIPL V
13540	27441	A	13694	87	2	PGWAWWFTPVILALWETEAGGSPEFKSL
13541	27442	A	13696	130	2	CNIIIIIIQVCWAWWMLPVI PALWHAEP GGSPEVESSRPALV
13542	27443	A	13697	282	107	GLTKCPGTVCRLKVVVISYQLSTICLSM MEHSGTILAHCSLKLGSDDPPTSVSRV AS
13543	27444	A	13698	198	3	CSITVNVKVMVMTLFRSSMSLEIVCDIDL AVLRRDLGSLQDPPPRFTPLSCLSLPSS WDYRRPLV
13544	27445	A	13699	2	120	ARGDGVSLWLPRLKNGAISAHCNLRPT GSSDKNFKTRF
13545	27446	A	13700	60	341	PDMGLEDERKMLTESGDPEEEEEQEEL VDPLTTVREQCEQLQKCVKARERLELCD ERVSSRSHTDDDCPEELFDFLHAKDHCV ALKLFNNLQ
13546	27447	A	13701	6	540	KNSRTLQCGGIRGSLCRPRKPGVGGTQ TRAVRPAVCSADSARPHLPRLRRADMKDS LVLLGRVPAHPDSRCWFLAWNPAITLLA SCGGDRRIRIWTGEGDSWICKSVLSEGH QRTVRKVAWSPCGNYLASASFDATTCIW KKLTLRIYNIILRKLEACIKPLCCALKYG CLEEKQLHS
13547	27448	A	13702	239	346	AKRGWLMVPI PALWEAKVGKSLEPRISR PLWATWQN
13548	27449	A	13703	210	300	LMPVISALWEAKARGLLEPRTLPAWAT W
13549	27450	A	13704	141	440	PSAFEHFKEKINLYFLKFCISQGFPERQN NRDREIHRERYERDRERHRYERGLRE LAHVIVEAEKPHHRPFITWETLGCWWSG SVQVQKPWEPGKLMV
13550	27451	A	13705	204	438	LLNVLLTQLFFLFLSLRQSCSVAQARGQ WYNHGSLOPSTHGASNPTASQSVGTT GMSHDHGLFLHFSTLDFSSSL
13551	27452	A	13706	1707	1821	AKAGGSQHLLEILANAVKPCLYWECKMAG PWWCAPVGG
13552	27453	A	13707	167	334	IRANFKILTEIGWTQWLTPVIPALWEA EGGGLEPGSPSLVFLFFILTTILMRKK
13553	27454	A	13708	224	344	KDTAMEEEIKDTEKTGKPLGAVAHACN PSTLGDQGRQIA
13554	27455	A	13709	1476	380	NSWSTLASELTWAATSADPERKSQAAS AAMWATLPLLCAWALGVPCGAELC VNSLEKFFKSWMSKHKRTYSTEEYHHR LQTFASNWRKINAHNNGNHTFKMALNQF SDMSFAEIKHKYLWSEPQNC SATKSNYL RGTGPYPSPVDWRKKGNFVSPVKNGQAC GSCWTFSTTGALSAIAIATGKMLSLAE QQLVDCAQDFNNHGCQGGGPSQAFYIIL YNKGIMGEDTYPYQGGKGYCKFQPGKAI GFVKDVANITTYDEEAMVEAVALYNPVS FAFEVTQDFMMYRTGIYSSTSCHKTPDK VNHAVLAVGYGEKNGIPYWIKNWGPQ WGMNGYFLIERGKNMCGLAACASYPIPL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						V
13555	27456	A	13710	763	257	YEKILKLTADAKFESGDVKATVAVLSPF LSSAAKHSVDGESLSSELQQLGLPKEHA ASLCRCYEEKQSPLOKHLRVCSLRMRNL AGVGWRVDYTLSSSLLQIRGKSPWCHCG WKVATCPQGPQAPACLPFPSSKTKFPR SSLARTESRPKTLMKLPWABEKGVPFV
13556	27457	A	13711	133	401	VLSKSGNPYWGSLSTNHEIKQEGCAWQL TPVIPALWEAEAGGSLEPRSLRPAWATS WLPREIKDLLKNGCGPSKITQGGPMVA GSLKL
13557	27458	A	13712	212	74	RRINLAPPRVFLKGPPIIIIIIIIIIIII FFAWGNPLFLFNSTFGRT
13558	27459	A	13713	324	141	DRVLPRLCSGVITARYRLNLLGSRDPP TSASLIAGSTGTCHHAWLSFSYLYTYVF FIIL
13559	27460	A	13714	299	431	IRLIWLSAVDHACNSSTLGHHGVQMTKG QDFETNLANTANPHY
13560	27461	A	13715	133	1	ILVWAWWDMPAIPVLWEAETEGLLPRRS LRPAWATWKNITSTKN
13561	27462	A	13716	18	165	IPLHTHTHTHTHTHTHTGYLLALSGTEFL SVLYMASERECRTYNMLNK
13562	27463	A	13717	119	1	KPNVSOAQWLAPVIPALWEARVGVLFKP RSLRPTWATQQ
13563	27464	A	13718	271	64	VLRISTLTNEILAKTRNPLQILMKPRK RWGTVAPHLRAPVGDQPDQHSSTPSLLKI TKISWVWVWRTPI
13564	27465	A	13719	21	209	KDGPKGTTGGSETNESVEMTECCSVTQAG VQWHDLSLQPPPPGFKRFSCLGLPSSW DYSRND
13565	27466	A	13720	391	151	RGFFLKGEKKKNFFPIILGKKILGSPGK KGEKKKKKRGKIFFFLKNPLGFFPKKKV LGEKKNPYSGVWGGKKKRGPPPH
13566	27467	A	13721	109	2	RRLGVAHACNPSTLGGEVGGSGQPGNC GQVTKVS
13567	27468	A	13722	69	369	RDILQADGAHSLPPTPSLNAYIIFSSP IGPHTHRPYHATPTLPPYTNLIKKKK KKKKKKKKKKKKKKKKKKKKGGGPF KKTGGAPIFGGGGK
13568	27469	A	13723	58	1208	FWNENSPASELAPNGGGSVTSVPRLEDY LTRPQLYKLTGVEGPSRANSRDSFHDRK TYKTPSANMMVLKVEELVTGKKNGGEB GEFLPEDFRDGEYEAATLEKQEDLKT LAHPVTLGEEQWKSEKQREAEKKKKLE QSKLENLEDEIIIIQLKKKKYRKT PVVKEPEPEIITEPVDVPTFLKAALNK LPVVEKFLSDKNNPDVCEYKRTALHRA CLEGHLAIVEKLMEAGAQIEFRDMLBST AIHWASRGGNLDVLKLLNKGAKISARD KLLSTALHVAVRTGHYCAEHLIACRAD LNAKDREGDTPLHDAVRLNRYKMIRLLI MYGADLNIKNACAGKTPMDLVLHWQNGTK AIFDSLRENSYKTSRIATF
13569	27470	A	13724	400	135	KWNGKBLNGVDGIGWDWNEMYWKGLEPH ETEWNBLENGLEWNGMSWDGIKCNGIK WNGIECSGMLWNGMECIGMECPMEWIR VEWN
13570	27471	A	13726	186	344	SASLGLWRCDRCRRSLVHSLNVAQAGV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QWRDLSSLQFPFPPSRLPWPPKVL
13571	27472	A	13727	380	168	APPQKKVFSSKFPQGGFFAPPNRKKLFF SPPRKIVPPPKFFLWAPPLFFFFFF FFFFFFWYSRTDYK
13572	27473	A	13728	324	219	RIMFFIFFYFFFFFFVFPLFFFFFKR PPPPFY
13573	27474	A	13729	2	270	RLQEASLSPVPEILGGALPSAKRTSYLL LSTLCLLLSETASRGNLTGLGHRSDHY NSVRSQQSLYSACPIVTTIHGTCYGGK AKCK
13574	27475	A	13730	134	3	AVHRCCKWGRGWRLTPVIPTLWEABV GGPLEPRSLRPALAT
13575	27476	A	13731	429	641	RKKAVCFMNDLICFLDNTFKNNVLSQAW WCVHLVPTIWEAEAGGSLEPRSLKLQCP VVAPVNNCTPAWAT
13576	27477	A	13732	188	32	IFFFFLFFYFLFFFFFPSSRHCTLQP GQSETRSQNKQKTKNKQTKNLP
13577	27478	A	13733	341	3	GTVTPEEPKMGDQTPRGLPRPERTLGR LSTSESVDPTPRVGGSSGGRTAPWGP PRERGRVAGSSLHRACNFTSNTIISVG LWLTPIVITLGEAEAGGSPEVRSSTHAS
13578	27479	A	13734	208	2	KLYKNFFFRFTKNPPPLKKGFLYNPF FKKKKI VKKKKKKKKKKKQKKKKKK GRPLAIKNYPRV
13579	27480	A	13735	16	212	EGVSLLLPRLECRGTISAHCNLRHGR CTPASASQILRLKQENHLNLGGGGYRD PIKLQRTAS
13580	27481	A	13736	22	214	PDRPALPTRPGGWITWGREVRDQPGQCG ETPSLLKIEKLAGCDGTCLBQNCQNN SNNKVGIR
13581	27482	A	13737	386	51	WGNSTQQALFEHLCSGHTSLPAVPCP HQACFPPLICRGIIAHCNLGLLGSS DSPISASPIDGNTGLHPLRLFSFLWY RWGLTMMPKRSLSPGLKPSSRLADAW
13582	27483	A	13738	204	431	SQHFGISRADHLSSNVGDQPEQHGNK LYKYKKNQGWAWLTPVIPPLWEGQVG GSPEGKELKTPLNLGKPHL
13583	27484	A	13739	69	159	IKKEALSWAWLTPVIPALWKANAGGSP E
13584	27485	A	13740	32	285	FFLSFFLFFFPFGGGKKTKKFFSQD FLGPPKILGGGFPSPFPFGPPFLKKGK KSPQNLFFLKKNPFPFPFPKPLWGF
13585	27486	A	13741	372	213	YRSCVLLQONPPLFYQSWWNFSLCVCVC VCVCVCETGSLKKFLLTQKKR
13586	27487	A	13742	29	237	TKRKGYTKNGYWAWLTPVIPALFY AEGNLILQMCKQAQPEAGCGVCVCVCA CMCVCVCVKVFF
13587	27488	A	13743	322	183	HTHTHTHTHTHTHTNPIHVFWLLKY PKIQSHQPHISAFQDPLL
13588	27489	A	13744	305	373	VGWGWLTPVIPALWEAKVGS
13589	27490	A	13745	172	1	KNKIEBQMKWEMRQEAHAHSCNPSTLGG QGEFETSLVNMMPCLYKMKQKISQVCS C
13590	27491	A	13746	285	1045	FQHPFGLSSEMAAVKASTSKATRPWYS HPVYARYWQHYHQAMAWQSHHAYRKA VESCFNLFWYLPALLPQSSVDNEAAYP QSFYDHHVWQDYPCSSSHFRSGQHPR YSSRIQASTKEDQALSKEEEMETESDAE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VECDLSNMEITTELRQYFAETERHRER RRQQQLDAERLDSYVNADHDLYCNTRRS VEAPTERPGERROAEMKRLYGDSAAKIQ AMEAAVQLSFDKHKCDRKQPKYWPVIFLK F
13591	27492	A	13747	2	305	GRVGSFSVRDVELSDPARERGERMPVAVG PYGQSQPSCFDRVKMGFVMGCAVGMAAG ALFGTFSCLRIGMRGRELMMGGIGKTMQ SGGTFTGTFMAIGMGIRC
13592	27493	A	13748	2	305	GRVGSFSVRDVELSDPARERGERMPVAVG PYGQSQPSCFDRVKMGFVMGCAVGMAAG ALFGTFSCLRIGMRGRELMMGGIGKTMQ SGGTFTGTFMAIGMGIRC
13593	27494	A	13750	238	423	AVSWDQLTWGTGVQEKKIQAQAWGLMPV IPTLWEGEVGGSPEVKSSRPACPHGKTP FLLMQ
13594	27495	A	13751	455	248	ISVGPGLFQNLFCFLPYGTFLEKKFF IMETGSRFVIQAGVQWGSYSSPQPQFFG FESSLKPPHSGVK
13595	27496	A	13752	2	98	IPTPTIHTHTSHHTHTHTHTSFLYMP PDLK
13596	27497	A	13753	196	2	IWAPPKIFLKKPPLFFFFFFFFFFFFFFF FFFFFFFFIISFIPWPLTRKQKLSRWVF FKDSACSA
13597	27498	A	13754	917	379	KYKCSLQKNLLLVGCKKYSILCYRRHL HLVTHGERKKPAVNSFFLFFSFFFLN LVRNTEITKKRVNLHETKADAESCNDQD TTSSETASELEQIRSGKHNKGWAGEGA AGRRERGERMEWTEMRGARGRRGRER EMERARVRGGEEREKEIDLYKKVTSKIE ETKLGNNLLKG
13598	27499	A	13755	175	21	KKKNFFPPRVILGPPKVFVKRAPLFFF FFFFFFFFFFFFFLKKSRLAI
13599	27500	A	13757	234	341	EIGWVQWLMFVIPAVWEAEVGGLEPRS LRAARAI
13600	27501	A	13758	1	365	PAPNRGGHIQDRATNSTELGANQCFFP SPRPPSLEKKTPEINKEPRPAPQPSNPG NLGTREGGDSWAGTTRCLRRDTDEGDTYR TEPPTALSWGQTRAFFFPALPAGKKRH RNLLKTQFF
13601	27502	A	13759	87	181	SHHTHTHTHTHTHTFTYLVHVIHFDMEI LGL
13602	27503	A	13760	1	228	ARGERERERERERERERERERERERE RYREGGRLLTMGEGETERATDLYHTPP PSIKAWRLCEPRPRAGILCGRNIF
13603	27504	A	13761	383	197	RCDPPAWVSQSARITGVSYRAQPATSVL MGEEDFLEDPVIAFVRLAPAVLLSKLSE VSVAMT
13604	27505	A	13762	276	57	YAVLGGGGGRKNLFVVFVFLFFFFFFFFFF FKKQGFGLMPLGEDRGPNMGFFYPFPMVG DKTKLFFKKKKKKRPR
13605	27506	A	13763	377	209	PRPAYGPAFLFTEGFSWNPFFFQMESR SVAQAGVQWCYLGLQPPPPWFPPTLLN
13606	27507	A	13764	160	202	MEKYNVPHSGILHSHEKEQAALFTIAK RWRQPSYPSIDWKNMISHTVBYTTAM KRKNQLYSQ
13607	27508	A	13765	390	284	ESGGHFLSLSLSIYIYIHIYIYVCVYIY THTSHTI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13608	27509	A	13766	350	41	YVVILQENRNTQNRKLLPKSTELCMLLQ MLLFILNTTNYPLPLWQCYHRFCSFFLK TGSFYVTQAKVRWLFMTGMITVHCSLKLL DSSHPPKWLVLQELATVAS
13609	27510	A	13767	330	156	KITQAWWCVHVVPDNRREAVTGVIRLGR MRLPLEGACTNCVPSWEKQDPVSHNEK K
13610	27511	A	13768	25	292	KCFFLSWRGGSRQLSQHFGRPRRADHLR PGVDPQPGQHGFLLVKMSDKPDLSEVEK FDRSKLKKNTTEKNTLPSKEIFFSLVG VNIQD
13611	27512	A	13769	585	680	KCLGSRTRWLTPVIPTLWAEAGGSLRP RSS
13612	27513	A	13770	488	359	PSPRERKFLPFFKKKKGWGPPPPKKNR GRGPQKEGFPQKPKP
13613	27514	A	13771	794	515	PDMGLEDEQKMLTESGDPEEEEEEEEL VDPLTTVREQCEQLEKCVKARERLELCD ERVSSRSHTEDCTEELPDFLHARDHCV AHKLFNNLK
13614	27515	A	13772	130	397	VVGLTFLCFMCRASLPRHSPQARKTKK KKKKKKKKKKKKGGSLKKIFGGAKKS GATKKKNFPKKRGQKNKNGPFFKNEIFF GGGAI
13615	27516	A	13773	376	145	TRVGGGCSEQRLLCHCTPSWATEPNPVS NNKIPLELFPNSQTFHFVRNWKRGNN WLSNYSISSTVTRHFPTLPQF
13616	27517	A	13774	1	247	GLQSLADLLSGLLQKVLPLSNGIMDLY LLYYLFTFTGSCSVAQARVQWCEHGS LQPHTSASSDPTSTATTCHHARLIW
13617	27518	A	13775	376	145	TRVGGGCSEQRLLCHCTPSWATEPNPVS NNKIPLELFPNSQTFHFVRNWKRGNN WLSNYSISSTVTRHFPTLPQF
13618	27519	A	13776	107	468	EKARSPERARDQEGGTERDRNSEREKIL PKLREELPWVSGGWRCWPWHQGWSHWED NPGWGIPTGPSVGWGEKKGPGEGRSHKY GTGRTKCELGVSIGNSAFTLLHFYFKH RKREKQI
13619	27520	A	13777	125	2	NIFFPLFELYYPKCHWARWLTPVIPALW EAKEGGSPEVRSS
13620	27521	A	13778	166	74	GRICYSHSLSKHTHTHTHTHTSHISF IP
13621	27522	A	13779	1	341	ARGERERERERERERERERERERERE RERERERERERERERERERERERERE RERERLSFSLGGGALKKKRIFLCVTL GKHLPLTHTGFFGENTHTLSMKTREGG FICAGGDERRSASVMRAYIYRECEPHTH V
13622	27523	A	13780	614	337	RRCSALCYRRHGNHKVKIRSKQGASVS PHEHLRILSLLEVRNVGLGHSIFPHSLR MYVCMYVCMYVCISYLSIYLSIYLSIY LSISISSR
13623	27524	A	13781	390	158	VLIRLSWGRICFQAHSQWQNSGSCSHK TEGLCLLLAGSCSWLLGALKGWASKEE FYTMQHSCQSDTTLSPPLYSIH
13624	27525	A	13782	308	163	TKFYLLFFFFFLLFIFFFFFLLKKKF LFFIQGGGKIKTGTLTLFG
13625	27526	A	13783	45	277	IASGRPFFFLHLPLPFQKAFVFGGGGT PFEYQNFVAYIKGQGNPFLFGCGDLFN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						APOLIKQLSOLGQKYPKPLL
13626	27527	A	13784	413	218	PNFPFFLFFSGKFFFAQNLPGFFPPPG GEGKAFPGQGPCVGGGGFAGPTFFFGPP APPEILYFF
13627	27528	A	13785	1011	1368	IDWENDLTPMVLCHGPSIYNKYSFQNI FPISANFFPIAHINLTLLQLVSELSHKI ILRHFIKPIKDILNLYLILPGVWLFDL CKSTAICRYLCVCIYIHLIYHITHIHI YTHIRL
13628	27529	A	13786	161	425	RWGSCYCPGYPHLKIFKLLLLVLVLEM GVLPLLPRLECSGMITVHCNLEPLGTSY PPISVSQTKKKKRPFTLPLPLNLQIGLP LRGE
13629	27530	A	13787	70	311	DLISITALVISPNKFYIYLSIYLSIYLS IYLSIYLIYFISTNLLWVLSLWETLNKT RLNLFLTQNNIWNPKLLVSALI
13630	27531	A	13788	25	219	RNMAAATLTSKLYSLFRRTSTFALTIY VGVMFFERAFDQADAIYDHVNEGKWK HIKHKYENK
13631	27532	A	13789	279	138	RRSLALSPRWDCGLQWRNLGSLQALLPG FTPFSCLSLSSWDYRPF
13632	27533	A	13790	138	28	GGWVRWLTVPVLPALWEARVGGLEPGSS KKERGKKEV
13633	27534	A	13791	133	7	YSCQRCLTHGQAQWLTTVISAPWEAKAG RLLEPRSVRSAWAT
13634	27535	A	13792	86	290	EHVHRTLIEASVSGWGWLTVPVISAWE AEVGSLEGOEFELSLGKSETPSLTIT TTESLGSFAATS
13635	27536	A	13793	150	37	KIYVPSQARWLPVLPALCEAEVGRLLLE PSSRLAWAV
13636	27537	A	13794	216	77	PTQHPTEGYMIKQQTVYHECRMWANS CLLPEGLLRAVTPWCHAP
13637	27538	A	13795	251	347	VARAWGLAPVLPALWEAEVGGSPGRSL KPAL
13638	27539	A	13797	177	274	VQWHMSVVPALQAEAEVGGSPPEPSLRPA WATY
13639	27540	A	13798	307	406	KFKKGWANWLPVLPALWEAKAGGSPES RSLRP
13640	27541	A	13799	194	3	FFFFFFFFFEMGSHYIVQARVQWLFTDA NIVHCSLQLLASSDPPVSTSQVGLQACA DDAQNPE
13641	27542	A	13800	333	198	LPSVFFFFFQTESCSVTQAGVEWCDLGS LHSSLGNRRLCLKIK
13642	27543	A	13801	1	335	ETERGRERETERGRERETERGRERETER GRERERERERERERERDRERERERORGE GKKNRDRENNRRERETRVGDVVCVCPHP NLILNCSPYISHVLREGLGKTYLNYGGS FPTLCSG
13643	27544	A	13803	14	454	RVFFDRSRYRSRTLGSTHASALLGILVY RSHLISSLLCLEGIILSLFIATLITLN THSLLANIVPIAILVFAACAAVGLALL VSKKKKKGAPVLKNPWGAQSLRGQARKY FFPYREPKNLPGNLGKEPFLGGGDILG QPPYKN
13644	27545	A	13804	1474	1661	TDFHNSHLLKCKNCIFSTLNYYIRREH FSIVFIFCYICVVKVHYIRRELFCLYF LLYMCC
13645	27546	A	13805	360	3	LWGKRGGPFSPPPFFFFLELFFFLKKMG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion; \=possible nucleotide insertion)
						GGGFFGGFFWGPCKGEIFFFVFFWAPQK KKKKKPPPIFWGGGPPFFFPKQK KKKNKKKKKKKKKKKKKRAARWPA RSRSA
13646	27547	A	13806	1	425	RLGGVALRSAADGAFVSGEFCGGKLLRW CLVTDFFPDSCCTCSYRRSTPGCSPGG SRGLSEGESSVSLQSRVLSAMKHVLN LYLLGVVLTLLSIFVRVMESLEGLLESP SPGTSWTTTSQLANTEPTKGLPDHPSRS M
13647	27548	A	13807	5	313	EKPYLQGITPTSKTHLIYEFTPTIIV KEYSTNYVLLIGNTQITKIYHIVFRKFS MTPIYKFDLAQWLTPVIPTLWEAKPGG LLEPRSLQSSYSLIILIL
13648	27549	A	13808	182	314	VITQLDKTERAQWLMFVILVLYEAEVGG LLEAMSSRPAAWATKW
13649	27550	A	13809	219	1812	LPPFESGAMSGFNFGGTGAPTGGFTFGT AKTATTTTPATGFSFSTSGTGGFNGAPF QPATSTPSTGLFSLATQTPATQTGTGFTF GTATLASGGTGFFLGIGASKLNLNTAA TPAMANPSGFGGLGSSNLTAISSTVTSS QGTAPTGFVFGPSTTSVAPATTSGGFSF TGGSTAQPSGFNIGSAGNSAQPTAPATL PLTPATPAATTAGATQPAAPTPTATITS TGPSLFASIAAPTSSATTGLSLCTPVT TAGAPTAGTQGFSLKAPGAASGTSTTTS TAATATATTTSSSTTGFFALNLKPLAPA GIPSNTAAAVTAPPGFGAAGAAASSAM TYAQLESINKWSLELEDQERHFLQOAT QVNAWDRTLIENGEKITSLEHREVEKVKL DQKRLDQELDFILSQKLELDLLSPLLE LVKEQSGTIYLQHADEEREKTYKLARNI DAQLKRMAQDLKDIIEHLNTSGAPADTS DPLQIQICKILNAHMDSLQWIDQNSALLQ RKVEEVTKVCEGRRKEQERSFRITFD
13650	27551	A	13810	134	263	KNSLFKKKNNGRPWPLMPVLPALWEAEA GGLLEPRGLRPTWVT
13651	27552	A	13811	210	51	TLSHRKPISFEAYFARVRGFILVSETR NPPICGWRWLTVPVLPALWEAEAGG
13652	27553	A	13812	241	139	LHEAGLAPMIPALWEVKVGGLEPRSPR PAWASW
13653	27554	A	13813	539	256	RTTQMSTAAGFTEAPNWKQPRCPWTEEQ TNKMWSLHAMECASAMKWEVLIQPAVR MARENSRRKPGDMHDWVWSAGEWLPGL LGRSTGKGS
13654	27555	A	13815	63	369	VRETPLKTHYLEEISSPASPTAIPOSL FSFFISPPSSLATGSGHSGHPVHSLHHP PETEPSVCLWAGPKVPPGAAGKGS SNPLVIRSLAPPASL
13655	27556	A	13817	258	3	AESAPFFSTNSLFFTHTHTHTHTHTH THSLRTRWAPSQVCRPQTSQRGGECVG PTAFAPSPTLLKPHHPSSHVHLPSQPRR
13656	27557	A	13818	516	665	WFKSGSFWLGMVAHTCNPTLGGGGWI TSGRSRTSVTTTTTSTQTCAPA
13657	27558	A	13819	295	361	WLTPVIPALLEAVTGGSLBPRS
13658	27559	A	13820	166	368	GWATQHSAYVSSSSIGALCLGESCS VTQAGVQWCDLSSPQPSHPGKFRFLCLS LPSSWDHRGDL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13659	27560	A	13821	133	530	RKYCGQCLNMALNNVSLSSGDQSRVAY RSSHGDLRPRASALAMVSGDGLVSRPE AIHLGPRQAVRPSVRAESRRVDGGGRSP REPDGRGRSRQARFSPYPPIPAVEFDLLR SVLQQRLLIALGGVIAARISV
13660	27561	A	13822	76	1958	RQELIWPLCSPPPQDRFLQKSWIFFRPV MADKLTRIAIVNHDCKPKKCRQECKKS CPVVRMGKLCIEVTPQSKIAWISSETLCI GCGICIKKCPFGALSTVNLPSNLEKETT HRYCANAFKLHRLPIPRPGEVLGLVGTN GIGKSTALKILAGKQKPNLGKYDDPPDW QEILTYFRGSELQNYFTKILEDDLKAI KPQYVDQIPKAAKGTGVSILDRDETET QAIVCQQLDLTHLKERNVEDLSGGELQR FACAVVCIQKADIFMFDEPSSYLDVKQR LKAATIRSLINPDRIIVVEHDLSSVLD YLSDFICCLYGVPASAYGVVTPFVSVREG INIFLDGYVPTENLRFRDASLVFKVAET ANEEVVKMCMYKYPGMKKMGFEFLAI VAGEFTDSEIMVMLGENTGKTTFIRML AGRLKPDEGGEVPLNVSYKPKISPKS TGSVRQLLHEKIRDAYTHPQFVTDVMKP LQIENIIDQEVQTLSSGGELQRLVALACL GKPADVYLIDEPSAYLDEQRIMAAARVV KRFILHAKKTAFFVEHDFIMATYLADRV IVFDGVPSKNTVANSQPTLLAGMKNKFLS QLEITFRDPNNYRPRINKLNSIKDVEQ KKSGNYFFLDD
13661	27562	A	13823	3	292	KCWYVHEPPRPAPMQTYQVDLRCCFVS TINLLVCGERASLPSVESLVFSGLAEW MKAVLAPSRRESGLVLQVQPEYAEAIWG ARPACRGLVFSA
13662	27563	A	13824	245	91	YKVNFGPPRGSSFFRPPPPFFFEVHFHFF IIFPPPPPPPPFFSFFLGCFMVV
13663	27564	A	13825	276	100	PGQKKKTLSPKKKSIYLYIHTHIYIT HTHIYKYIFVCVYICVSIYIHTHIVPR IFS
13664	27565	A	13826	202	375	IYNTYIHTHTHTHTHTNVLYIQSGDC IYAVLLGELSFIYIFVFLSSLISILPHL TY
13665	27566	A	13827	278	34	KPRGLSPAGVSAQRANGPHSCPRLPDPR TELQVRQIPALVGSSAFQGRGRKGPVG GSGPSRPRAPPQPRPGCCQCTLLQI
13666	27567	A	13828	62	307	GGARAIFLNVPHLKRPMFFLELCLSTKC PVGTEFALDSSLRLYNSTFCNVQWLMP TIPALCKAEMGGLLEARSLIPAWAT
13667	27568	A	13829	386	478	NRIGMVSHACNPSTLGGQGRIRMRSGDQ DHS
13668	27569	A	13830	364	484	NFNIWLGWAWLMPVIPALWEAKAGGSL EVRGSGPAANMV
13669	27570	A	13831	33	486	PARSAEFGTRRERERERERERERERE RERERERERERERERERERERERERG VICVCPCALLCVRESPLSQKCYCVCF VVRITESLALSPFLGRCLALLIFLEGM WRKIWAPSLSLCVGALFFSQHPPFFWC LCVLSLVRPLPLSLSGGVFVSQRALI
13670	27571	A	13832	6	718	YSAVEFAMAGVGAGPLRAMGRQALLLA LCATGAQGLYPHIGETEKRCFIEIPDE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						TMVIGNYRTQMWDKQKEVFLPSTPGLGM HVEVKDPDGKMLQVLSRQYGSERFTF TSHTPGDHQICLHSNSTRMALFAGGKLR VHLDIQVGEHANNYPEIAAKDKLTQL RARQLLDQVEQIQKEQDYQRYREERFRL TSESTNQRLVWSIAQTVILITGIWQM RHLKSFFFEAKLV
13671	27572	A	13833	17	130	RLQEFGTRRERERERERERERERERE RDTHSFLHG
13672	27573	A	13834	283	460	LVVRLATCKNYSLKRETEPGSVAHVYNP STLGGQGGRTARGQEFKTSLDNIARPPS LQK
13673	27574	A	13835	3	435	WPRFCTALQEFGTRRERERERERERE RERERERERERERERERATSLSRARPSF LFPSACVSHTPYVGERENLSLHTLKHTH TREKHSLSYTNASARDTRARFSEGRAPP IYSVYLTHGVFFFFFSLCLSVRAEGL AHV
13674	27575	A	13837	351	57	RTLVIHISKFTGNLSDLVYVQSEWQDLGT ADLSIMTSVLHCLPSLESIKNTDSWPSS VAHTCNPSTLGGRCRCDQHGQHSKQPS LLKIQKIARRCGG
13675	27576	A	13838	336	150	TFCYKKYLWGAHCFIFRTGLPIKNFVF GQAWCLLPVISARWEAETGGSLEPRSLR VAWAS
13676	27577	A	13839	310	454	HCSLGLPQVLLIILYKILGLWARWLTPV IPALWEVEAGGLLEARSSRP
13677	27578	A	13840	163	297	IIFFLDLKLQGANITYYSIYLSIYLSI YLSIYLYTHTLWNTLQL
13678	27579	A	13841	33	316	LDQHPTPRSPLLCHSLRKTSSSQGGKSE LVKQSLKKPKLPEGRFDAPEDSHLEKEP LEKFPDDVNPVTKEKGGPRGPEPTRYGD WERKGRCIDF
13679	27580	A	13842	4474	2586	DGSGGCVKMEFPGGNDNYLTITGSPHPF LSGAETFTHTPSLGDEEFETPPISLSDSP SLAVSDVVGHFDDLADPSSSQDGSFSAQ YGVQTLDMFVGMTHGLMEQGGGLSGGL TMDLDHSIGTQYSANPPVTIDVPMDDMT SGLMGHSQLTITDQSELSSQLGLSLGGG TILPPAQSPEDRLSTTPSTSSLHEDGV EDFRROLPSQKTVVVEAGKKQKAPKKRK KKDPNEPQKPVSAVALFFRDTQAAIKGQ NPNATFGEVSKIVASMWDSLGERQKQIY KRKTEAAKKEYLKALAAAYKDNQECQATV ETVELDPAPPSQTPSPPPMATVDPASPA PASIEPPALSPSIVVNSTLSSYVANQAS SGAGGQPNITKLIITKQMLPSSITMSQG GMVTVIPATVVTSRGLQLGQTSTATIOP SQQAQIVTRSVLQAAAAAASMQLP PRLQPPPLQMPQPPTQQQVTILQPPPP LQAMQPPPPQKVRINLQQQPPPLQIKSV PLPTLKMQTTLVPPTVESSPERPMNNSP EAHTVEAPSPETICEMITDVVPEVESPS QMDVELVSGSPVALSPQPRCVRSGCENP PIVSKDWDNEYCSNECVVKHCRDVFLLAW VASRNSNTVVFVK
13680	27581	A	13843	54	251	EFYRMNSPSPPLWLVCVCVCACLFMCCLC ALTCMCVWYKSLLSNLQVLSKIFYDS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ISPAENPGK
13681	27582	A	13844	154	26	DPHPVPTTERSEGSQARWLFPVPTLWEA EACGSPEVKSSNST
13682	27583	A	13845	475	225	GHTELYGGALFQLLQAAIPEGGGTSCLF NPSSDGGSSAAGGVVGGAGDLARSSRP SPTSSRPVPSDPSPPSLYLTPWKETH
13683	27584	A	13846	479	319	RDCRRSLTHSVLSGAQAGVQWRDLGSLQ PPPSRLPWPPKAPRWQPLPGHHPI
13684	27585	A	13847	182	499	LLCVKLCDSNENKALREQTRAQVQGGH SRAQVQVQGGHSAHTVVQIRSAASRRK AFSTCSSHLGMVLLFYGTGSSTYMRPTT RYSPLEGRLLAAVFSILIPTLN
13685	27586	A	13848	388	494	RDSWERWLEPLIPVLWEAQAGRLLEPRS LRLAWAT
13686	27587	A	13849	198	63	HHATTWMNLEDIMFRKVSQTQKNKYMI PLIWKTKKVLSHREQK
13687	27588	A	13850	555	353	RCPPGAQAPLPAPSPAPPVHIALSPISC GVSWPRELTAHPPEPPPPFFFKIHHPHQ LSVGKRGQMTF
13688	27589	A	13851	169	66	LLAGSTGQARWLTPVIPELWKAQVGGSL EIRSSR
13689	27590	A	13853	12	105	IASGLHDFPKKKIKKKKKKKKKKKGG AL
13690	27591	A	13854	256	363	ICLFIKSDRGQTQWLTPVILTLLWKAEA GGSLPKS
13691	27592	A	13856	23	436	IDRLSDSHEERERERERERERERERE RERERERERERERERERERERERE RERESSLLCVRHTCFAPPTYIFLWETLR VCPTPCVNGALSVSHTERARIFFYTCG GSVARAPVCAHTRIFSSRARARALCARP PLSRERRAHTRVFFI
13692	27593	A	13857	91	428	PDPDTSPLTDRGETPLGATLPSCYCGG QQSFEPKTKTTNQKKKKKKKFTPOKK NPKIFPPKPCPKGPRGENQPKTONQP KKKKKILGGGPAPNSPLGGKKNSWAGF
13693	27594	A	13859	465	43	KRVTTENPOHICSAETAIPWSLQNCNF HILWGHHPNHPIYITTSIYIYIYIPIHY GMVYIYTRICMCVCIYVHICITHTHIY IYIHTHTIYMERERETVSCSVAQAGVQ WCDLGSLOPPNKLKRFSCSLPSSWDY W
13694	27595	A	13860	290	52	WYKYLPGTRGFLIWLNLKICIGRIELLV GYFSFIYLSIYLSIYLSIYLSRSIAQP GVKRCNHSSLQPRTPGLMHLNS
13695	27596	A	13861	108	22	IFFLFSVAKTRFSYAFPKFFPYRMNHVS I
13696	27597	A	13862	167	33	VFTVPGTYMCVSVRDLGQAWLTPVIPA LWEAEAGGSLEEPLRT
13697	27598	A	13863	448	355	FFFFFFFFFFFFFFFFFFFFFFFFAKN PLN
13698	27599	A	13864	321	445	SQSTQAWCLMPVIPALWETKSSSEFEP SLRPAWATGHNP
13699	27600	A	13865	380	80	MILSPSPKFFSFLSFLSALLLWHCLEL PFLSNVKGQMNDPVGLSPTSTPSDLR IYLFFCFVCLFVCFETGFPSVAQAGVQ WCDPLGLKNFLPPQSP
13700	27601	A	13866	372	264	KMENPEDKNFFIFEMFFIVFLFFFFFL FCLTQFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
13701	27602	A	13867	161	304	LFIAEMTSHYIAQAGLELLASSNPPTSA SERTGITDGATEILPQLRL
13702	27603	A	13868	230	348	VSFIONLVFCVERVYRVPDFGVWRGSK YNGSTELHSK
13703	27604	A	13869	168	260	EVIAECYNGCFQTLSLCVCVCVCVCVCV CY
13704	27605	A	13870	140	16	LKYGQWRDLGSLQPPPPRFKQFSCLSLL SSRNCTMTDRHE
13705	27606	A	13871	143	30	KILKVVVSQAWWLIPVIPALWEAEVGGG LEPRISRLA
13706	27607	A	13872	158	59	HLHGCIHLLKLRLDAVSHACNSSTLGGO GGRIA
13707	27608	A	13873	232	115	APFFFKGAPIFFFFFFFFFFFFFIIFLIR GKPGNDVGVEG
13708	27609	A	13874	1619	1375	KTTWRRHLEKLQDMSLLRHRVHVDSSQG LFPPFQROGLLPRLKNGDIIPYCNLKL LGWSNSPASAFRVARTTSLCRHTWL
13709	27610	A	13875	219	84	NPLQSTSTICNRAWDRVTCLWSQLLRL RWEDHLSPGVPSCSAL
13710	27611	A	13876	166	496	KKKKKKKKGGGGLKKTGGAAGINRGRK KKIFFQKGGQKKTGKILKKPFLGGGK KGNPPKKIKGLREKKKFKRGKAKPAQ NPWGKKISPPGFFLKKFFPRGRGFFI
13711	27612	A	13877	132	348	PSKKKRGKGGPKRTPGGPKFNGGKGN FPLMGGGIKPNLGLGKNPYLGGGTNGN NPPTETKGFGEKKKF
13712	27613	A	13878	287	134	QQGPFISPGPKEENRMGPPSPGWNGPI RSPPGAGPNPGAFQDGMFPSSKKQ
13713	27614	A	13879	333	480	VHPLRSAEGPRPESNMLHLTLKSKQQL TPVIPALWEAKAGGSGQGEIE
13714	27615	A	13880	1	227	PKIHCKIQHIVLVLSFFPSFFLSFFQGE SCSAAQAGVQWHDLSLQAPPPGFKWFR FIELLGLGFHSRRMRGKDS
13715	27616	A	13881	276	378	GWPWWLTPVIPALLEAEVGGLEPRSLR LALAT
13716	27617	A	13882	126	389	GSVLGTGCCGSLVLTVCRGSVLGTVLIA SATPDRYLRLSSGSLTRITNSDLVPWL TPVIPALWEAEAGVSLPRIWRPARETW EDPH
13717	27618	A	13883	414	150	ARQAPKWGNPTGSPPPGFLNPPPKNFFL GPQKKKIFFPTPPPHFFFFKGPPPPFF FFFFFSSPHASGILLCHPGRIAVAQSW LTE
13718	27619	A	13884	197	363	DLGVVVVNTFMLKFKCLNVSRGHVQWLI IPVIPILWKAAGRSKPRSLRPAAWT
13719	27620	A	13885	101	236	NIHYANFPYPGLACPEYIVRALQKKYTQ THTHTHTHTRTTHSL
13720	27621	A	13887	17	140	TVHLKMVKIGLHMVAHACNPSTLGGRGG PIMRSGALGNFCL
13721	27622	A	13888	135	1	VLHAGLKLGSSTSPTSASKGAGTVGIH YHTQLAFQFFLFCFLIR
13722	27623	A	13889	411	276	TLYFKHGEMGFHHVQAGLELLASSDPP ALEFETSLHNKVRPRL
13723	27624	A	13890	216	54	EFKLCYTLFDHSYFPLEELVSGQVWRLR PAIPSFWEAKEGGSLEPRSSKHEIV
13724	27625	A	13891	3	149	SSDRPSSSWLAWVGLWSMVWRVPFFLL PILFLASHVGSPLSPSPHF

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13725	27626	A	13892	166	1	LFSKI FWWLLPVTIPALREARKVGELLEPGSSRPAAWATWKNPVYTKNTKISQAWOCT
13726	27627	A	13893	128	2	FSTTYPNFIKLPHPYLPPLTLFLDSAHLHPSEINSLVAQKKK
13727	27628	A	13894	225	391	HLSTHILTFPFSLEPQWWLVPIIPVLWEVKMGGLLEPRSSRPAAWATQDPPQVSRK
13728	27629	A	13895	192	1	TLVVCVSSSVFKNYNNICLACWFMPIIPA LWEVESGSLLELKSSPPAWPTWWVPLKS KNTKISLA
13729	27630	A	13896	152	245	DQSIADVLMYYTHTHTHTHTHTHLQNVPG
13730	27631	A	13897	270	406	ISTRFFLYRDRASLCHPGWSAGVQSWLP GSSNSQAQAILLPQPE
13731	27632	A	13898	232	73	EAEGPRDVTSSTFHWRLYDQTYNYHECR MWANSRLRLTPEGLKVTIPWCHAH
13732	27633	A	13899	107	7	LGQAQWLMPIIPALWEAKAGGSLEPRTS RPAWA
13733	27634	A	13900	62	224	PTRPILAHCNLCVLGSDPPASASQSAG VTGMSHCAWSNLIHLPSTRTAICTL
13734	27635	A	13901	450	194	KRQVKSHSEVKTTHVQWPGIDPGSPAWE ARILPLNHQRLSGTTFWRITKSNHKDL ETVLSGFFKCRCLKANKDIQTKCVFIGNF Y
13735	27636	A	13902	300	404	AAPGRAPQKKKKKKKKKKKKKKKKKKAP FIKRGR
13736	27637	A	13903	131	29	ALGSLQPLSPRFKRFSCLSLPSSWNSTA LTVTMT
13737	27638	A	13904	267	74	VWVLVPFPTS YGVLDKPI LIVNNIYVHV CVCLCMCVCCVCCTVIRRHCHWNMI IISQHDQ
13738	27639	A	13905	193	64	IRSHQIHLHFKFRILGWTWLTPTVIP APWEAEGRSPSPSS
13739	27640	A	13906	309	424	QSTDFLENRRVGVWAWLTPTVIPALWEAE VGGLPEIKNS
13740	27641	A	13907	404	251	SCLISLRSDYRHVPFPQANFVFFFFEM ESCSVAQSGVQWQEENSISKINK
13741	27642	A	13908	471	59	GPPQAKKGKGFPTPGPPQKKGQPKSG VLGFSPPPLGPCPGLGPPKGNFPGGSP FFFFFFRKWEHKNELFPFSKTEKPRRAG EARKGSQSTKYAGLSRGERQASPTLRPG HLAASAGGWLQYTRWQGLPEPGN
13742	27643	A	13909	479	231	QBYCMLIFCEHFGDFDLNIVFCEKKMV GVIADFYLLSFTGRPQWLMPIPTLWE AEVGSLEAKSFTPAWATWQDPI SMF
13743	27644	A	13910	167	19	CIVLGIMLDSLWEPRQWVPSWVRWFPTV IPALWEAEAGGSPEVRSSNS
13744	27645	A	13911	328	446	GSFSKITDLSQTWWYVPVVLALQSEVGRSLEPRSSRLQ
13745	27646	A	13912	145	460	NAFMSTGCEVLSYSELQRNLVWVWLPV IPATPQAEAGRLLGPRSSRPWATKGV RALSHKQNTKTNKLSHSTGVSVFVTHHI HSPGILWRLSQWLLAMNLATN
13746	27647	A	13913	319	210	KLGFKGPPLEFFFFFFFFFFFPGFL TVSCNFTL
13747	27648	A	13914	372	10	PNTTCTPITYGKKCCPREISYYLCHEFI RIRILTFDGCSCYIAQAGLKLGSRSPT SASGVAGNTDVCHHTQPIFYILETG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LALLPRLILNSWSQAILLPPQPLRSYFNFWLFFCLYN
13748	27649	A	13915	594	471	PSYIAYMCICMCVCVYVYINICVCIYTHVHTPYNPVISK
13749	27650	A	13916	235	3	EANNLRKTYTSGWFORTSKRPPAVRRMKVLFFETESCVAPVGVEWHDSLQPRPPGLNRSSHLSPSSSDYRWA
13750	27651	A	13917	272	184	KTTAWAQWLTVPVISTLWEAKVGGSLAEGS
13751	27652	A	13918	46	321	SRVQGTGGHGRGCIQAGVGEQAEKRETBGPPWRWLTVPVISKLWEAKAGGSLEPVSRRATWNLLKRIYYTDEREYLIPLALNTSQGSTFSF
13752	27653	A	13919	387	484	FIETIGWARWLMPIPTLWEAEAGGSPEVRSS
13753	27654	A	13920	142	321	FLFSIHFLSCWGLFSNVQSLSIFSYLKVRLYGQAWWFTPIILALWEDKAGGSLDPRSL
13754	27655	A	13921	270	412	IEDRKIYSILHTETLERGQARWLTVPVIPAFWEVKAGGSFEPRLRPV
13755	27656	A	13922	304	396	NFGWAQWLTVPVIPALWESEAGGSLEPRGLRS
13756	27657	A	13923	305	387	VWVLTVPVIPALWEAEAGGSPEPRSSRP
13757	27658	A	13924	103	3	NKSPELGWAWLAPVIPALWEAEAGGSPVRSS
13758	27659	A	13925	195	400	CLLILSGLVASCIERHKGQAWWLMPIPTLWEAKVGGSLRLNLSAWGTWRNSISIKYTEQLAQQ
13759	27660	A	13926	294	489	KWAKMQTLHKGRYACVCICVCVCVYTYTDIYIFYIHIPMNTKCSMLLVIGEMKILSRMWSNQ
13760	27661	A	13927	363	2	NWGPFGFPFFFLKTGVPVFFIFGAPKKKFFLSTPRALKFVLLKGGPLFFFFFLWVFLVKTGSHCVAQPDLELLSSNPVLVSQGAGITGMSPQVQPLDLFFFSFFETGSRSYAWADAW
13761	27662	A	13928	1	218	LRPKKRKTNPKMWSVHTMEYHSALKRKEIRTQTRWINLEDIVLSEIRVAVTGRILYDSTQMRNLEESNL
13762	27663	A	13929	219	408	TFCHFIAFLHVKMFVVPFFSFIMFFPPLNCNKAFERKKKKKKNNKKKKKKRKKISLSPPAPP
13763	27664	A	13930	161	22	WHPPASASHVAGTTGACHHERLRQEDHFSLRVQGCSEPRLCHTTP
13764	27665	A	13931	116	1	INTGWARWLTVPVPAFWEAAVGGSLPRSTSQAATWK
13765	27666	A	13932	181	38	PWPQRATQPKISPLPPAISALWEAEAGGALEPRSSRPAAKSDAWVD
13766	27667	A	13933	267	397	TVFDRTLFFIKKIIHSAWPLTPVVPALWEAEVCGSPVRS
13767	27668	A	13934	129	12	NIGVGWALWLTVPVIPALWEAEAGGPPKVRSSRTARPMS
13768	27669	A	13935	179	1	KTYYGGIPIPPGPPKGEKKPPFFFKKFFLFPIISFFIFFFFLRQSLAKMQSASVWKVS
13769	27670	A	13936	245	616	DDKKKKEAAQKKATEQKIKVPEQIKPSVSQPPANSNNGTSTATSTNNNAKRATAN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NQQPQQQQQQQQPQQQQPQQQPQPQPQQ QQPQQQPQALPRYPREVPPRFRHQEHKQ LLKRGQHFPVEF
13770	27671	A	13937	121	292	NTDLDLALALIVRVLTSDDNFKNWGWVQ WLMVPVFPAPWEAEVGGSSSEATNLRPANAT
13771	27672	A	13938	421	202	GPREAPLFPSTQGISRPLFFFFFETES RTVTRAAQWHNLGSPQPPLCSLDILKT SQSVCMPAAAILVSQIT
13772	27673	A	13939	205	543	ILESRRRLGWSEALPENQLLCRASSWES LGPPDPCLKPPSPAPWGAAGGWAKST SVSEPVFVGTLLVALFLEMAVGLLLGLP FCFHSGLGAPHLCEPDGPSVLPABARQSR
13773	27674	A	13940	140	2	LSQHSEYTLPPPLYLEKESRRPPPPQH TTPPPPPWPHWDIADIQ
13774	27675	A	13941	47	303	GLIFLIWTCTIVKTSTDFPRMEDCSQCI HQVTEESNKRMGFLSYIANPHHGSRLL WPQHAAPWDDGRRGKPVPSLGFVSFPFP Q
13775	27676	A	13942	1488	1719	PLVSFSKNTYPCLGNVKQKQKTFCSRW KLHVLSSNLSSPAEVTVVASINLVVSEQ SFQNSQLPAMLCILVHLQMS
13776	27677	A	13943	127	402	QVTHPPNRTMCSSMIFLFLYLCLFLSL PFPSHLSLYAPPKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKAGGGGPPK KKIHFPFGGRIIPFY
13777	27678	A	13944	852	209	EQTVCYTRIDLQQLVFLRLAEFLLSQ GDPGSPMMCQLQQFDLWVLRLGVLNFGGE TCPGLFLYTKVEDYSKWITSKAERAGPP LSSLHHWEKLISFSHHGPNATMTQKTYS DSELGHVGSYLQQRRTITHSRNGNSSR DSLDRKDVKEGRSPASVQPLYDY YGEVGEGRIFAGQNRLYQPEEILGSL RACFLFAAVSSPGATPPN
13778	27679	A	13945	68	260	INIFWHCVLLVILYVILYISQFLFPCKVN IASWLGSVAHACNPSTLGQAGESLEPR NLRPAWAT
13779	27680	A	13946	420	156	FLPPGVKYGSFKRAPPPPPPPFLVET LSCYIAHTGLELPDSSNYPTSASQSAVI TGMSHHTWPLEGACLAIPQALRIILLVLV PLH
13780	27681	A	13947	317	17	AGHGGSTCNPSQPIVTAVPINLWGRDLL QQWGAQAFIPEQLYSQSQHTMQEMGYV PGMGLKKNLKLKPLQAEQONSHQGLG YNFSWQPLLQLNL
13781	27682	A	13948	55	224	NFRLTSSFSYLKMSFWLGMWLTVPVIAL WEARTGGLFEARSLRLVWVQSKKAGSHL
13782	27683	A	13949	1464	805	RATSVRGAGRERSCGAANSFASIGPFLR RSVLENAHFRSSREGGMAASTDMAGLEE SFRKFAIHGDPKASQEMNGKNWAKLCK DCKVADGKSVTGTVDIVFSKVKGKSAR VINYEKFKALEELATKRFKGSKEEAF DAICQLVAGKEPANVGVTKAKTGGAADR LTDTSRYTGSHKERFDESGKGKGIAGRQ DILDDSGYVSAYKNAGTYDAKVEK
13783	27684	A	13950	356	98	NAGPGIYFWGPIKKILPCPPAGVKLGSL KRAPLFFFFVEMGFHHVAQAGLKLSSR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DSPIPVSQSIRITSTCEPPCLAKIKSSLRL
13784	27685	A	13951	194	48	NFLEGWPGQRLTPVIPALWKAEGGSLEPKTFRPVWAMWRDLRKPQH
13785	27686	A	13952	341	418	DQPGQHGETPSILKIQKLAGRGSTCL
13786	27687	A	13953	158	323	TWLKKYFQSTNQLPPAHLNLVQPLLPFG LPLPLPKKKKKKKKKKKKKKKKKKKKK
13787	27688	A	13954	231	355	VFLPQKQKQNCPLTGKWNNSNWIHTL EYYSAVKGMQLI
13788	27689	A	13955	493	39	PAAFSSWGWAAGSSLLKKTTPASWPPGL LPPAPVSSMAAPDLDSFPLPLCWTFRLV LCRVFSSSTLAFLSCVSTSFGLTPAAS SNIFSLPHWASPPLPTARLTSAVSPE PLPPLPSRLQRQPRGAPSHPGMSMGPIIL DATSNSTTSR
13789	27690	A	13956	497	372	NTKISWASWYAPVIPATWEVSNSRPQAI HSHQPPKRIGLQA
13790	27691	A	13957	438	301	GTTYLDIDMTCDYVSVCLCIYICTROQS YIITYVYTHTHTHMYI
13791	27692	A	13958	84	466	QPLGRSGKVPQLHLWEMQRLPAAFFRSF AAQQLGESVHINTPTSLSLRGRPFISS GPGARARVTCAPCLHAARILCCFWRGLH RLKCSNVISAHCNLRFGSSSDSPASASQ VAGITGRSSLEQLLE
13792	27693	A	13959	216	28	KYVKNYVLSSII FWMQEI FHNFKSSRT QWLTPVIPALWEAEAGGSPEPRSSRPAS SIQLENS
13793	27694	A	13960	320	943	VLSESLSDRAQRCNCRMGKQNSKLAPV MEDLVKSTEFNEHELKQWYKGFLLKDCPS GRLNLEEFQQLYVKFFPYGDASKFAQHA FRTPDKNGDGTIDREFICALSITSRGS FEQKLNWAFNMYDLDDGDKITRVEMLEI IEAIYKMGVTIVMMKNEDGLTPEQRVD KIFSKMDKNDDQITLDEFKEAKSDPS IVLLQCDIQK
13794	27695	A	13961	191	8	GLFRFRRLSEEVKHCCCCCCCCCCCC CCCCCCCCCYLRLAPQSPAAPAPELH TPLPGSRRNR
13795	27696	A	13962	203	28	VWGNQHFVFPVPRKKVFCFFPLNKLIR GGFFFFFFFFFFLVFIDNSWVFLGEGDLA GS
13796	27697	A	13963	18	171	GIRHEERERERERERERERERERERERH PAREIDMCVSKRDTRGALCALF
13797	27698	A	13964	25	299	HDFCTRRERERERERERERERERERERE RERERERERERERERERERERERERE RERERERERERERERETHLSLYIYMCV FLYIPLYFSFLYIHTQREAPPPLSATLS LSIL
13798	27699	A	13965	246	410	AYNGQSGRGVTPVIPSLWEAKTGGSLP RSWRSATWHTPPVPGPSKEISLYI
13799	27700	A	13966	91	26	FCCCGCCCCCFYCKKEKTLV
13800	27701	A	13967	158	24	PFCHIIYFLESCFVAMLECSGKILAH YLRLGSSNSLVPSLA
13801	27702	A	13968	129	7	SWAQWLMPITLWEHEAGRSLEAMSSR PAWATQQDPVSKK
13802	27703	A	13969	445	268	KIQLTKLKNASELPSRINQAEKISGW AWCLMPVIPVLWEAKAGGSLEPRSLRRG QVT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13803	27704	A	13970	1628	1309	HRRKKCAGYSSLSSALLRERERERERERERESVCVCLGTITCFRRQYCVIQGISGVRQNCVQIPALSDPDLPLFLSLSVLHSENTWVVRPTLRVTERNKGAMCV
13804	27705	A	13971	314	140	QCHNCYILTQLVKIKGDQAWWLMPTIPA LGAKAGGSLEAGSLRS AWATWRAPMSTKIF
13805	27706	A	13972	292	482	YKSVRTQDSCAAGVDRLVKGIRYVNLFVYICQHS DGR TWLTPVIPPLWETKGGGSSEVGRSG
13806	27707	A	13973	502	303	STAIGPSFSPFLCTHGSFHGFLFFFCFCFPLVEMGSHYVAPAGLKLGGSSDPPASASPSHLGLQV
13807	27708	A	13974	493	289	IPPTALGTSFSPFLCTHGSFHGFLFFFCFCFPLVEMGSHYVAPAGLKLGGSDPPASASPSHLGLQV
13808	27709	A	13975	405	121	IREAAQSESLFVRAAPHTGLISGPCITIEYAVKDTRCMQRRILVRELECAAHGLTECLSIDTHTHTHTHTHTHTHTHTHTHTHTHGTRWEAGQSLKGES
13809	27710	A	13976	135	254	TVTCTNSSWSLTFTSFLFLMPGWIQGR RVCVCVCVCVC
13810	27711	A	13977	179	58	VPLSINSPQRQCIFCCCCCCCCFLVLQKIISERSWAEIG
13811	27712	A	13978	97	186	KIIFWLGVVAHACNPSTLGGQGGGRIMRG RD
13812	27713	A	13979	289	420	ELGLKIHGFPSQAPWFMPIIPALWEAEA GGLLESRSRIA WAMW
13813	27714	A	13980	421	106	SGGRNFFFFLGGGFYKKKFPFPPFLRGK KKKPPLPKKNPTPIFFPPGGGPPFSPPPKKGGGKIFFPPGGKNFIMQNFPGFPPLWGKKKKFLPKKKNPLFFFFF
13814	27715	A	13981	309	135	KHIYIYLSIYLSIYLSIYLSIYLPAYLPTYLHAHPLIHANAYKNIHIDYPPKKGFEY
13815	27716	A	13982	231	21	QHMYCLKSIWHKKLSRKPYCIITSEYSS MVKLRVSIQVQWLMFVIPALWEAKAGG LLKARSSRFMWAI
13816	27717	A	13983	209	359	HLHTHTHTHTPNGVKQIMTQIPILPLTG PLILEKFLNFSKPLSHPGKRD
13817	27718	A	13984	391	249	IWPILPPQRIFFFFFETESCSVTQARVQ WCNLGS LQPPNPVFP SLAK
13818	27719	A	13985	181	403	YLVLDSPSTLGLISQPKDYITKDQTLT FRPVVVAHACNPSTLGSQGNITSVQEV ETS LCNTARPCLYQYKN
13819	27720	A	13986	441	358	ETGSRVCVILAGAQRDLSSVQPLPPRFK
13820	27721	A	13987	7	233	ASIPCIYQRTKIPNTKQTKNKNKIPAWWCTPIAPATQKAEIPPLHSSLGDFLRLSPKKKKGGFNWAPTSPKFF
13821	27722	A	13988	152	44	PKAPLFFFFFFFFFFYETRSHSVAQAKVQRHDHGS
13822	27723	A	13989	188	379	NVSCHAAETRVWWEKERPLVPFPGAYLL DGMPLVWLLSASSILSIWLSIYLSIYLSIYLSIYF
13823	27724	A	13991	296	53	SSILFHASKYHFSGRFLSLLSCKRRNILQLVPHMYSPLYMYIHTKHIEYMYVHIYIYMNLRNCRIYLHSCTPKENQAR
13824	27725	A	13992	37	290	RLGSPASRRHQIQCLIRACLKDGTLGWV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						WWLIPVIPALWEAKVGGSLPRSTPAW ATQGDILKKDGTLLQCPHVAKGHSSHS
13825	27726	A	13993	189	370	SRNALFKKRWESSCQSSFNLSGVFPQAA TKGWVRWLTLPALWEAKAGGSLEPRS SRPA
13826	27727	A	13994	179	25	SKHNKKNIQICLLCSKRSMFVHVCIH ICVYVRYAYIYIGMCIHIYIHS
13827	27728	A	13995	159	2	EDPLSPGVQDQHGHRKSLSGRGKISL GQEFKSSMAAMYFGRSGGCKLERR
13828	27729	A	13996	307	99	FIWEHFVNYTMFFTYKKPTSQAWWLMV VPALWETEAGGSPEVRSRPPGQHDDVR PLGPSLHVYLQMD
13829	27730	A	13997	218	21	FQHFGRPRVDHLSLGVQDQPGQHGETP SPLASSILDLPFPFIDEVDLAFQSV TLGVQDITS
13830	27731	A	13998	227	404	GYSVTLLGLTQLTQRIAHGTRKGERER ERERERERVCSCLMHESHLFFFL FRE
13831	27732	A	13999	400	668	PVGRRWELQGMGLGVRTWQSSLPQCGPT SSSVLSLGRGTPGISNTCLPPRSATELG LPAQVPFPNVQSQDQLSFLGCFPTY NRQTL
13832	27733	A	14000	225	414	NRVLLCHTGWSTVAILAYCSFKLLGSRD SPTLASRAARTIVKCRNVWLKCKKKK KGGRRLL
13833	27734	A	14001	397	118	LFSGPFFFDKSECFQEPVFPCLLLYNQ MQPYLLRSFVDSYMYDSFLDRVSC QSGWSTVAPSRLLTAALNSLAQVILLPOP LNVLCGISR
13834	27735	A	14002	3	173	YVFYRQKMVCIFYKIRIKMFMNRNLNL GQWCVPVIVPATQVAEAGGSPBPTSLRPI
13835	27736	A	14003	440	290	YTHLYIYIYIHTHTHTYIYLYCTYWG QFDLLVLDNKLYKEIYIYLSVFI
13836	27737	A	14004	2	116	ARLVAMPFKYEETKDFLLTARRKDAKSV KIKKNKSAAV
13837	27738	A	14005	279	422	SAKAPLSCLRTNSLLKNGLRGAWWIT PVIPTLWEAEVGGSPDVTSP
13838	27739	A	14006	3	497	GGIGDSRCGSTRASSSPQLAGRSSSVLP AAAPCTPTMDVFKKGFSAKEGVVGAV EKTQGVTEAAEKTKEGVMYVGAKTEN VVQSVTSVAEKTKEQANAVSEAVSSVN TVATKTVEEAENIAVTSGVVRKEDLRPS APQGEASKEKEVAEEAQSGGD
13839	27740	A	14007	1	292	SLGGGGCNDPRSYPHCTPAWATEQDTS SLSIYMSVRVCIYMYMCVCIRIYTYI HTHIHVRVYIYIPIYIYIYIYVDLV IYMGWCGCPPPSI
13840	27741	A	14008	57	250	KIFFFLMNTWGGVPVVLATWEAEVGG LEPRSLGLQETMTSLLSRLPRQGEIL SLILKRN
13841	27742	A	14009	184	2	AVPGRWPCQVPGLLPSTQDTLKQGRG QWLTFTVTPMPWEAEAGGSLDARSLRPAW ATGK
13842	27743	A	14010	123	3	KEPSRPGRWLTSTIPACWEAEAGGPPEA RSSTRBFRTAK
13843	27744	A	14011	403	168	GTGLRASRCISQPVMSGLLSPSEFPFPE IESHLHVSQRETAARLRDRERERARE RERERGNASSGKPPGSASCV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13844	27745	A	14012	207	422	EIRRGSLAGPLSLNFI LSVMSGSHSKYLR KVIGRAQWLMFVVPALWEAEVGLHELR RLGHTWAAW
13845	27746	A	14013	200	405	WLCVLGWSLLALS PRLECYGPI SAHCNL HLLRSSDSPASASQALQEA WYQHLLMM PQAAS TQVGRKK
13846	27747	A	14014	319	176	KPSTITFLFLHLFISSRESRPVTQT EVK WLNHSS PQPPTPRFSLPSS
13847	27748	A	14015	63	401	EQENKNTLNSPGWDGVHIVLRLNTRM PLGHLSPSEGVS GSGSGRRRCQAGAGR SATAAARPCQCLGLKGLPAVPSCGLEG KAPERAGYSASHPHGCETGNWVLYVN
13848	27749	A	14016	416	63	VSKVYPRKINHRTQRTVRHETFKIAMPKY SNLCSILRFNKDRLAFMRHYTKQCSRTS ITEYIAMFFVCLFVLKIGAHCHPGWNE VVLVCSQVTAAS T SRAQAILPPQPPKIL GMQQA
13849	27750	A	14017	196	425	SLMFRPPLFSFCCFCIRYPPIFVFFSLL CFAFSWC SLLFFHYLKL FLLFLLEFF LPVLLCLDSPLVHDFLLSS
13850	27751	A	14018	3	233	SSRMGRGKTIAFDMRWSCEVDRARHRD REREREREREREREKGAEPQFFVISPW VDRPCLAGILHLKCGCGHRL
13851	27752	A	14019	163	1	AERWHDQICVEREINGWVQWLMFVTPVL WEAKAKNLLPKNLKLRNRRPGNSR
13852	27753	A	14020	203	83	LKKKKNK SQAQWLT S VVLASQAEAGGS LEPRNSRPAWAT
13853	27754	A	14021	179	3	VTWQRELRLQME LRLICRAWLTPVIP VPWEAKAGGSPEPRSSRP AWETRNRPG NS
13854	27755	A	14022	358	431	WHKKKNQNLGTGAHACNPSTLGG
13855	27756	A	14023	98	3	GRFAGWLTVPAPT LWAEAMGGSLEPRSL GHE
13856	27757	A	14024	254	385	RENWABPSSHSLNIFLQLGTVARACNP STLGGRGGWITRSGD
13857	27758	A	14025	140	1	KGVLDPGRGLCVPCFCFFFLCVCVCVCV CVCVWRRSLTSLPRLQCI
13858	27759	A	14026	579	852	QREWVGWAGKEGEGWVSHVPASAQLPAN GQRGQPHPSPLGGTGSTWAQEGAYCCLS SCSHCCCCSSCCCCPPGFC LPPSLGAI CHLYHL
13859	27760	A	14027	30	663	LRIRALRELPA SHIPGSLTICCVPRPPL PCSSTKPDAGYKPLAQQLGSGRTGPC LGHAPCYSPLWELRGHGCS PYGSPSPGS VSLWQEA MRLPKNTPREKDRRTAALQEG LRRAVSVPLTLAETVASLWPALQELARC GNLACRSDLQVAAKALEMGVFGAYFNVL INLRDITDEAFKDQIHHRVSSILQRAKT QAALVLDCLETRQE
13860	27761	A	14028	1	267	AVGVHHA FHLPHCFFASLLESVPSPRLA MDPNCS CAAGVSCTCAGSCKCKECKCTS CKSCCSCCPVGCSKCAQGCCKGASEK CSCCD
13861	27762	A	14029	46	1746	PAAGAATMEFRQEEFRKLAGRALGKLHR LLEKRQEGAETLELSADGRPVTTQTRDP PVVDCTCFGLPRRYIIAIMSGLGFCISF GIRCNLGVAIVSMVNSTTHRGHVVVQ KAQFSDPETVGLIHGSFFWGYIVTQIP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1. 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						GGFICQKFAANRVFGFAIVATSTLNMLI PSAARVHYGCVIFVRILQGLVEGVTPA CHGIWSKWAPPLERSRLATTAFCGSYAG AVVAMPLAGVLVQYSGWSSVFYVYGSFG IFWYLFWLLVSYESPALHPSISEERKY IEDAIGESAKLMNPLTKFSTPWRRFFTS MPVYAIIVANFCRSWTFYLLLSIQPAYF EEVFGFEISKVGLVLSALPHLVTIIVPI GGQIADFLRSRRIMSTTNVRKLMNCGGF GMEATLLLTVGYSHSKGVAISFLVLAVG FSGFAISGFNVNHLDIAPRYASILMGIS NGVGTLSGMVCP IIVGAMTKHKTRBWQ YVFLIASLVHYGGVIFYGVFASGEKQPW AEPEEMSEEEKCGFVGHDLQAGSDSEME DEAEPGPAPPAPPPSYGATHSTFQPPRP PPVVRDY
13862	27763	A	14030	240	63	VFTAQSNNGVELNRFNEGPLSAVLKGRV AWAQLTPVIPTLWEVKAGGLLEARSLS PA
13863	27764	A	14031	289	414	HAEMGRVQWLTPAIPALCKAEAGGPPEP RSLRPAWATY
13864	27765	A	14032	386	1765	LGDARAPEKMSAIQAAPWPGTECIAKYN FHGTAEQDLFPCKGDVLTIVAVTKDPNW YKAKNKVGREGIIIPANYVQKREGVKAGT KLSLMPWFHGKITREQAERLLYPPETGL FLVRESTNYPGDYTLCSVCDGKVEHYRI MYHASKLSIDEEVYFENLMQLVEHYTSD ADGLCTRLIKPKVMEGTVAQDEFYRSG WALNMKELKLLQITIGKBEFGDVMLGDYR GNKVAVKCIKNATAQAFLAEASVMTQL RHSNLVQLLGVIVEEKGLYIVTEYMAK GSLVDYLRSGRSVLGGDCILKPSLDVC EAMEYLEGNFVHRDLAARNVLVSEDNV AKVDFGLTKBASSTQDTGKLPVKWTAP EALREKKFSTKSDVWSPGILLWEIYSFG RVYPYRIPKLDVVRVEKGKMDAPDGC PPAVYEVKNCWHLDAAMRPSFLQLREQ LEHIKTHELHL
13865	27766	A	14033	619	414	EQARCLEQHACTSPRQPRPQLQCSELKG HSLGMEHQGHVPCILHPCSPCPPVKASPA CWSSNPAPLCPH
13866	27767	A	14034	2	614	LESRPDGRPSSTHPASPSAFSAPGKPHP PEAKMSSKRAKAKTKKRPQRATSNVFA MFDQSQIQEFKEAFNMIDQNRDGFIDKE DLHDMLASLGKNPTDEYLEGMMSEAPGP INFMTFLTMEFGKLNCTDPEDVIRNAFA CFDEEASGFIHEDHLRELLTTMGDRFTD EEVDEMYREAPIDKKGNFNYVEFTRILK HGAKDKDD
13867	27768	A	14035	1	254	AVEFGPAGPGSLGRAAAMIIPVRCFTCG KIVGNKWEAYLGLLQAEYTRGDALDAG LKRYCCRRMLLAHVDLIEKLLNYAPLEK
13868	27769	A	14036	494	148	FRFLSDCGVFAEGHIELQVBSGVPLGFS TMAEDMETKIKNYKTAPFDSRFPNQNT RNCWQNYLDFHRCQKAMTAKGDISVCE WYQRYVYQSLCPTSWVTDWDEQRAEGTFP GKI
13869	27770	A	14037	130	3969	IMGDVKNFLYAWCGKRKMTSPSYEIRAVG

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						NKNRQKFMCEVQVEGYNYTGMGNSTNKK DAQSNAAADFVNLYLVRINEIKSEEVPAF GVASPPPLTDTPTDTANAEGDLPTTMGG PLPPHLALKAENNSEVGASGYVPGPTW DRGANLKDYYSRKEEQEVQATLESEFVD LNAGLHGNWTLNNAKARLNQYFQKEKIQ GEYKYTQVGPDHNRSFIAEMTIYIKQLG RRIFAREHGSNNKLAQSCALSIVRQLY HLGVEAYSGLTKKKEGETVEPYKVNLS QDLBHQLQNIQELNLEILPPPEDPSVP VALNIGKLAQFEPSSQRQNVGVVWSP QSNWNPTSSNIDEGPLAFATPEQISM LKNELMYQLEQDHDLOAILQERELLPVK KFESEILEAISQNSVVIIRGATGCGKTT QVPQFILDDFIQNDRAECNIVVTQPRR ISAVSVAERVAFERGEEPGKSCGYSVRF ESVLPRPHASIMFCTVGILLRLEAGIR GISHVIVDEIHERDINTSFLLVLRDVV QAYPEVRIVFMSATIDTSMFCEYFFNCP SLKLWRTYVPQYFLEDICQMTFVPPP KDKKKDKDDGGEDDDANCNLICGDEY GPETRLSMSQLNEKETPPELIEALLKYI ETLVNPGAVLVFLPGWNLITYTMQKHLE NPHFGSHRYQILPLHSQIPREEQRKVF PVPVGVTKVILSTNIAETSITINDVVV IDSCKQKVKLFTAHNMTNYSTVWASKT NLEQRKGRAGRSTAGFCFHLCSRARFER LETHMTPEMFRTPLHEIALSIKLLRLGG IGQFLAKAIEPPPLDAVIEABHTLRELD ALDANDELTPILGRILAKLPIPRFGKMM IMGCIFYVGDAICTIAATCFPEPFVNE GKQLGYIHRNFAGNRFSHDVALLSVFQA WDDARMGGEABIRFCEHKRLNMTLRM TWEAKVOLKEILINSGFPEDCILLTQVFT NTGPDNNLDVVISLLAFGVYPNVCYHKE KRKILTTEGRNALIHKSSVNCPPSSQDM NYSPFFVFGEKIRTRISAAGMTLVPP LQLLLFASKKVQSDGQIVLVDDWIKLQI SHEAAACITGLRAAMEALVVEVTKQPAI ISQLDPVNERMLNMIRQISEPSAAGINL MIGSTRYGDGPRPPKMARYDNGSGYRRG GSSYSGGGYGGYSSGGYSGGYGGSAT PSGRI CAGVGGGYRGVSRGGFRGNSGGD YRGPSGGYRGSGGFQGGGRGAYGTGYL DIEEEVAAIKLGVVSSVCRQ
13870	27771	A	14038	431	542	EGITPGWARWLPVPIGLWEEAAGGSPG REIDIGLAN
13871	27772	A	14040	238	362	RRCITFLSFRMLAPRVYSVVGKRAFSPSV CVRAGHKCDYSYS
13872	27773	A	14041	6290	3514	FRAAGSSSTNSGRICPLPFGALLYQSEG LLARPHGKGSFQVGRQOQAVRVGSAHA SSAGYVCVSAFFPVFLRFCVGGGPGISR VYALFYGECNPTREWAVSSELSPSPQEQ NKMNVKVEKQSQESVSFKDVTVTQREW QHLDPSQRALYRDVMLENYSNLVSVGYC VHKPEVIFRLQQGEPEPWQEEFPSPSQF PEVWTADHLKERSQENQSKHLWEVVFIN NEMLTKEQGDVIGIPFNVDSVSPSRKM

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						FCQCDSCGMSFNTVSELVTSKINYLGRK SDEFNACGKLLLNIXHDETHTREKNEVL KNRNTLSHRENTLQHEKIQTLDNHFEYS ICQETLLEKAVFNTRRKRENAEENNCDDYN EFGRTFCDSSSLFHQISPSRDNHFEFS DCEKFLCVKSTLSKPHGVSMKHYDCGGS GNNFRKRLCLSHLQKGDGKHKHFEKNEC GKAFWEKSHLTRHQRVHTGQKPFQCNRC EKAFWDKSNLTKHQRSHTGKPFECNRC GKAFSHKSALTQHRTHTGKPYQCNAC GETFYQKSDLTKHQRTHTGQKPYECYEC GKSFCMNSHLTVHQRTHTGKPFECLEBC GKSFCQKSHLTQHRTHTGDKPYECNAC GKTFYHKSVLTRHQIHTGLKPYECYBC GKTFCLKSDLTIHQRTHTGKPFACPBBC GKFFSHKSTLSQHYRTHTGKPYECHEC GKIFYNKSVLTKHNRTHTGKPYECNEC GKTFQKSQLTQHQRTHIGKPYECNEC GKAFCHKSLIVHQRTHTGKPYKCNRC GKSFCVKSGLIPIHERKHTGKPYECNEC GKFFRHKSLLTVHRAHTGKSKQCNEC GKIFYRKSELAHQRSHTGKPYECNTC RKTFQKSNLIVHQRRHIGENLMNEMDI RNFQPVQVSLHNASEYSHCGESPDDILNV Q
13873	27774	A	14043	187	422	LTIPKLHSAQEPAGPVSPPPPPSPFTQI GGRSRAEPRNQYCPQVAPVPLRGCLPL SPGEPHPTDSSPRHLTCGGIVF
13874	27775	A	14044	340	442	NKFLSWVRLIMPVITPFWKAVGGWLEA RSLRNQ
13875	27776	A	14045	3	1240	LVEGAAGQGVSDGARLRKCGTRSFPGSE EVLSSMARGSAFPAAALWLSILLCLLA LRAEAGPPQEESELYLWIDAHQARVLIGF EEDILIVSEKMAFPTHDFRKAQQRMPA ISVNIHSMNFTWQAAGQAEYFYEFLSLR SLDRGIMADPTVNVPLLGTVPHKASVVQ VGFPCLGKQDGVAAFEVDVIVMNSGNT ILQTPONAIFFKTCQQAECPPGCRNGGF CNERRICECPDGFHGPHEKALCTPRCM NGGLCVTPGFCICPPGFYGVNCDKANC TTCFNGGTCTFYPGKCICPPGLEGEQCEI SKCPQPCRNGGKICGSKCKCSKGYQGD LCSKFPVCEPGCGAGHTCHEPNKQCQEG WHGRHCNKRYEASLIHALRPAGAQLRQH TPSLKKAERDRPPESNYIW
13876	27777	A	14046	18	274	YSQEVLCENRSGVVSNTIKRGWAWWOLT TTIPALWEAEVGGLEPRSLRLASPQPP QHEDYSMSYCAQPRFSLCIRGFIFYSLW F
13877	27778	A	14047	177	441	GGSHYAWPNITFIFTKLIQFFCFFEMQ SCSVARLECRGAISAHCNLHLPSSNSP VMAQILKNQRKSNFDEDTLLGLSYTLL GEI
13878	27779	A	14048	136	319	DVFLLLPHSNYFLFFETGSHSVSQAGVK WCDLSSLQPPPLGSSDPPTSASRVPALE FFLEF
13879	27780	A	14049	388	128	ELKLEPSYKGQSPQLSLRRYFADLIAIVS NRFTLCPSARHLAVYLLDLFMDRYDISI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QQLHLVALSCLLLASKYESDLHDWKFLMFI
13880	27781	A	14050	262	3	VIVNYISVRPPFNHYHTFYTLSEFLYLS THHTHTHTHTHTQRETGHVCVCIYTYM YMCNYAKWWYKFTFLISGKARIHTHLHP CI
13881	27782	A	14051	149	423	YPHLC AFLLLPSISSFRAGVFFFSYLSL TAYPLTWKPEPPATPQPTPNPPPGHPA TRGPKSALLDHSYACASAPPLGTEGTAP SPSFALI
13882	27783	A	14052	2	1440	FVAVTAMAAFCLLRQGRAGALKTMLQEA QVFRGLASTVLSAESGKSEKQGPQNSK KQSPKKNVVEPKERGLLATQTAAELSK NLSSPSSYPFAVNKGRKVASPSPSGSVL FTDEGVPKFLSRKTLVEFPQKVLSPFRK QGSDEARQVGRKVTSPSSSSSSSSSDS ESDDEADVSEVTPRVVS KGRGGLRKPEA SHSFENRAFRVTVSAKEKTLQKPHVDI TDPEKPHQPKKKGSPAKPSEGRENARPK TTMPRSQVDEEFLKQSLKEKQLQKTFRL NEIDKESQKPFVKGPLPVHTKSGLSAP PKGSPAPAVLAEEARAEGQLQASPPGAA EGHLEKPVPEPQRKAAPLPRKETSGTQ GIEGHLKGGQAIIVEDQIPPSNLETVPVE NNHGFHEKTAALKLEAEGEAMEDAAAPG NDRGGTQEPAPVPAEPFDNTTYKNLQHH DYSTYTFDLNLELSKFRMPQPSGRES PRH
13883	27784	A	14053	177	1253	EKKRTLPRSVTGELOGKSLSDLAAGTM DSEKKRFTTEATKYFRERVSPVHLQILL TNNEAWKRFVTAELPRDEADALYEALK KLRTYAAIEDBYVQKDEQFREWFLKEF PQVKRKIQESIEKLRLANGIEEVHRC TISNVVSSSTGAASGIMSLAGLVLPFT AGTSLALTAAGVGLGAASAVTGITTSIV EHSYTSSAEAEASRLTATSIDRLKVFE VMRDI TPNNLSLLNNYIEATQTIGSEIR AIRQARARALPVTWRISAGSGGQAER TIAGTTRAVSRGARILSATTSGIFLALD VVNLVYESKHLHEGAKSASAEELRRQAQ ELEENLMELTQIYQRLNPCHTH
13884	27785	A	14054	1585	2099	ICVKTFFPLALQVRMAAEHHSSGLPY WPLYLTAETLKNRMGHQPPPTQOHSITD NSLSLKTSPSERLLYPLPPSAPPSADDNL KTPPECLLTPLPPSALPSADDNLKTPAE CLLYPLPPSADDNLKTPPECLFTPLPPS APPSVDDNLKTPPECVCSLFFHPQRMII SRN
13885	27786	A	14055	2	2865	ALPDGGASVASDRAEGRPAKPSKTAARE KTEGAVAAVGGGPSSFRCCYGCCEARL GRTS LPRGVIML TEASLSIWGWGSLGIV LFLITFGPFVIFYLTFYILCFVGGGLVV TLLEFGKTNSEKYLEQCEHSFLPPTSPGV PKCLEBMKREARTIKIDRRLTGANIIDE PLQQVIQFSLRDYVQYWYTTLSDDDESFL LEIROTLQNALIQFATRSKEIDWQPYFT TRIVDDFGTHLRVFRKAQQKITEKDDQV KGTAE DLVDTFFFEVEMEKEVCRDLVC

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						TSPKDEEGFLRDLCEVLLYLLPPGDFQ NKIMRYFVREILARGILLPLINQLSDPD YINQYVIWMIRDSNCNYEAFMNI IKLSD NIGELEAVRDKAABELQYLRSLDTAGDD INTIKNQINSLLFVKKVCDSRIQRLQSG KEINTVKLAANFGKLCCTVPLDSILVDNV ALQFFMDYMQQTGGQAHLFWMFVGEYR VTAQQQLEVLRSRQDQKHQTNQTKGLL RAAAVGIYEQYLSEKASPRVTVDYLVA KLADTLNHEDPTPEIFDDIQRKVYELML RDERFYPSFRQNALYVRMLAELDMKDP SFRGSDDGDESFNCSPTGSINLSDDL SNVSSDDSVQLHAYISDTYADYDPYAV AGVCNDHGKTYALYAITVHRRNLNSEEM WKTYRRYSDFHDFHMRITEQFESLSSIL KLPEKKTFFNNMDRDFLEKRRKDLNAYLQ LLLAPEMMKASPALAHYVYDFLENKAYS KGKGFARMDTFVNPLRNSMRNVNAV KSLPDSLAEGMTKMSDNMGKMSERLQGD IKQSFFKVPPLIPKTDSDPEHRRVSAQL DDNVDDNIPLRVMLLLMDEVFDLKERNQ WLRNLIKNLQQLIRATYGDTINKRIVD HVDWMTSPEQVADSVKFRDAFWPENGIL AEAVPCRDKSIRMTRVAGTKLLAIMP GE
13886	27787	A	14057	311	150	FLCFKYRRGFATLHSGCLKLGSSDPSS TSQIPGITGTSKCVQPTHFLFLALS
13887	27788	A	14058	53	211	RQHITCLDIFFIHMNYKVKYINILYSIY LSIYLSIYLIYLSISHSSYITERA
13888	27789	A	14059	1	1642	RDGRKMATATIALQVNGQQGGSEPA AAVVAAGDKWKPQQTDSIKMENQGSTA AKLGLPPLTPQEALQKAKYAMEQSI KSVLVKQTIHQQQQLTNLQMAAQRQRA LAIMCRVYVGSIIYELGEDTIRQAFAPF GPIKSIDMSWDSVTMKHKGFAFVEYEV EAAQLALEQMNVSMLGGRNIKVGRESNI GQAQPIIDQLAEEARAFNRIVVASVHQD LSDDDIKSVFEAFGKIKSCTLRDPTTG KHKGYGFIYEKAQSSQDAVSSMNLFDL GGQYLRVGKAVTPPMPLLPATPGGLPP AAVAAAAATAKITAEAVAGAAVLGTL GTPGLVSPALTLAQPLGTLPAVMAAQA PGVITGVTPARPPIPVTIPSVGVVNPIL ASPPTLGLLEPKKEKEEEELFPESERPE MLSEQEHMSISGSSARHVMQKLLRKQE STVMVLRNMVDPKIDDDLEGEVTEECG KFGAVNRVIYQEKQGEEDAEIVKIF VEFSIASETHKAIQALNGRWFAGRKVVA EVDQERFDNSDLA
13889	27790	A	14060	1238	1474	VLAQEGRPWRREPASIDACRLNFORLR RGKFSNVLPFGLAQEALYSGGYHLKFAD ELMGNLKKSTADASGSRGHQL
13890	27791	A	14061	266	400	GQWARPVIPALWEAKAGGSLEPSMLRPA GQHIKTPSVLITSKKT
13891	27792	A	14062	2178	1881	VLQAPSILLDAPRTDGGDMGRAMVARLG LWLLLLALLLPTQIYSSETTGTSSNS QSTSTGLAPNPTNATTKAAGGALQSTA SLFVVSLSLLHLYS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13892	27793	A	14063	261	1	NSVLTALALFSLHVLPPPPSGVTDTAG ALSTGGPPSPSTSVTGRGPAHSHASQLPP APGFBAPLNESECRGWAGBAFLERFPDAW VDP
13893	27794	A	14064	2384	1115	QHFSRRGLCVVEQRSSVTSWTSWGAWS PCPPSNASCNTLHTRDWASPDGGQGS GESPGPAPPGQLHTLDTDLHSLAQIGK SPVAGVGNNGSLWPRESPTANGHSP TPPGPGPPGPCPTKRRLPAGEAPDVSS EEEGPAPRRRRGSLGHPTAANSSDAKAT PFWSHLLPGPKSPVLDPTDCGPMGRRLK GARRLKLSPLRSRLKGPGLSPPRASPV PTPAVSRTLLGNFEESLLRGRFAPSGHI EGFTAEIGASGSYCPQHVTLPVTVTFD VSEQNAPAPFLGIVDLNPLGRKGYSVPK VGTVQVTLFNPNTQTVVMFLVTFDFSDM PAAHMTFLRHRLFLVPVGEGBNANP LLCYLLHLRFRSSRSRSLHGDRL SRRSLELDTGLPYELQAVTEAPHNPRYS PLP
13894	27795	A	14065	232	416	GWAVQLGIGTEGKEGTSSSERQREG GNRKTGRRREGRRSTKTDPSPYPAHRP RSKLI
13895	27796	A	14067	238	45	IQTCGSHSFCIPSIWEAKAGGLEPRSL SPACPTQKDPISHLGSELQSFRLILRL VPLPLSAC
13896	27797	A	14068	3	1705	SCESKATPWRAVSASQELQHPQGGQ LPGDLTPARPNPAYPLTVEQCRSCSRV PAPLEPHTHPGSSCFYSSFSFITKATA PGAQRRAVTQAEGRMGFLGTGTWILVL VLPQAPFPKPGSQDKSLHNRELSAERP LNEQIAEAEEDKIKKTYPPENKPGQSNY SFVDNLNLLKAITKEKIKERQSISS PLDNKLNVEDVDSTKNRKLIDDYDSTKS GLDHKFDQDDPGLHOLDGTPLTAEIVH KIAARIYEENDRAVFDKIVSKILNLGLI TESQANTLEDEVAEVLQKLISKEANNYE EDPNKPTSWTENQAGKIPKVTFMAAIQ DGLAKGENDETVSNTLTTLNGLERRTKT YSEDNFEELQYFPNPFYALLKSIDSEKEA KEKETLITIMKTLIDFVMMVKYGTISP EEGVSYLENLDEMIALQTKNLEKNATD NISKLFPAPSEKSHEETDSTKEEAAKME KEYGSLKDDSTKDDNSNPGGKTDEPKGT EAYLEAIRKNIEWLKKHDKGKNKEDYDL SKMRDFINKQADAYVEKGILDKEEAEAI KRIYSSL
13897	27798	A	14069	1	140	NTSVAIQTIEYSAFKRKETLTHVPLWM NLKDTMLREISQSQKDTV
13898	27799	A	14071	212	104	HTNHQCQTVLPAGQALATPQGLAPSPV PQSCLRMV
13899	27800	A	14072	358	112	FPLTVMLNVFLWQNLKHFCWFIOEQLM FFFFFLRTGSHYVQAGLELLGSTNLP ASVSRVAGTTGIHNCTQFNPLHTLHL
13900	27801	A	14073	3	151	YMGFHHVGYAGLELLTSSDLPWPWPKCW DYRHEPSCLAMFFYFALIAPE
13901	27802	A	14074	8	1493	VTIHHLFVQAVRADTLKKKSPSCLLCI VFIPVPRIDLNTIDQVAVIFKHFPVGR

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						GDAVLKTWAPAQCLCSRMGPAWLWLLGT GILASVHCQPLLAHGDKSLQGPQPPRHQ LSEPAPAYHRITPTITNFALRLYKELAA DAPGNIFFSPVSIISTTLALLSLGAQANT SALILEGLGFNLTTETPEADIHQGFRLSLL HTLALPSPKLELKVGNLSFLDKRLKPRQ HYLDSIKELYGAFAPFSANFTDSVTGRQ INDYLRRQTYGQVVDCLPEFSQDTFMVL ANYIFFKAKWKHPFSRYQTQKQESFFVD ERTSLQVPMMHQKEMHRFLYDQDLACTV LQIEYRGNALALLVLPDPGKMKQVEAAL QPQTLRKWGQLLLPDLLDLHLPRFSISG TYNLEDILPQIGLTNINLEADFGVGTG QLNKTISKVSHKAMVDMSEKGTAGAAS GLLSQPPSLNTMSDPHAHFNRPFLLLLW EVTTQSLFLGKVVNPVAG

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-13901, a mature protein coding portion of SEQ ID NO: 1-13901, an active domain of SEQ ID NO: 1-13901, and complementary sequences thereof.
- 5 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 10 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 15 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
- 20 7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively
25 associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - 30 (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NOS: 1-13901.
11. A composition comprising the polypeptide of claim 10 and a carrier.
- 35 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

5 b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

10 a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

15 c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

20 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

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17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

30 b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-13901, a mature protein coding portion of SEQ ID NO: 1-13901, an active domain of SEQ ID NO: 1-13901, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-13901, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 13902-27802, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NOS: 1-13901.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.
- 5 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 10 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.